



STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 126550

TO: Phuong Bui
Location: REM-2A15/2C18
Art Unit: 1638
Monday, July 12, 2004

Case Serial Number: 09/857522

From: Toby Port
Location: Biotech-Chem Library
Remsen 1A59
Phone: 571-272-2523

toby.port@uspto.gov

Search Notes

Dear Examiner Bui,

Here are the results of your search.
Please feel free to contact me if you have any questions.

Toby Port

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: July 9, 2004, 08:38:29 ; Search time 7664 Seconds

(without alignments)
11016.731 Million cell updates/sec

Title: US-09-857-522B-3

Perfect score: 1948
Sequence: 1 gtgcaccacacgcgcgcgcgcac.....taaaaaaaaaaaaaaaaaa 1948

Scoring table: IDENTITY NUC
Gap 10.0 , Gapext 1.0

Searched: 3470272 seqs, 2167151695 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: gb_ba:*
2: gb_htg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1195.8	61.4	1838	8	D82035
2	1195.8	61.4	2213	8	AK100591
3	1195.8	61.4	2245	8	AK072723
4	1195.6	61.4	1899	8	BT009004
5	1186.8	60.9	1872	8	D82038
6	1186.8	60.9	2161	8	D82036
7	1164	59.8	1770	8	OSU55768
8	1159.6	59.5	2927	8	AK065206
9	1037.8	53.3	1542	8	HVU7990
10	1026.2	52.7	1539	8	HVBKIN12M
11	988.2	50.7	1809	8	RYERKIN1
12	817.4	42.0	2073	8	AK067158
13	815.8	41.9	2209	8	D82039
14	795	40.8	1453	8	HVBKIN2
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16	784.2	40.3	2100	8	AF062479
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18	780.2	40.1	1539	8	AK505467
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ALIGNMENTS

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LOCUS D82035 1838 bp mRNA linear PLN 06-FEB-1999
DEFINITION Oryza sativa mRNA for OSK4, complete cds.
ACCESSION D82035
VERSION D82035.1 GI:4107000
KEYWORDS OSK4.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE
AUTHORS Takano,M., Kajiyama,Kanegae,H., Funatsuki,H. and Kikuchi,S.
TITLE Rice has two distinct classes of protein kinase genes related to

Pred. No. is the number of results predicted by chance to have a

SNP1 of Saccharomyces cerevisiae, which are differently regulated in early seed development
Mol. Gen. Genet. 260 (4), 388-394 (1998)
JOURNAL
MEDLINE
PUBMED
99086251
2 (bases 1 to 1838)
Takano, M.
REFERENCE
AUTHORS
TITLE
JOURNAL
Direct Submission
Submitted (15-DEC-1995) Makoto Takano, National Institute of Agrobiological Resources, Department of Molecular Genetics, 2-1-2 Kannondai, Tsukuba, Ibaraki 305-8602, Japan
(E-mail:mtakano@abr.affrc.go.jp, Tel:81-298-38-7446, Fax:81-298-38-7408)

FEATURES
source

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polya_site

1838
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ORIGIN

Query Match 61.4%; Score 1195.8; DB 8; Length 1838;
Best Local Similarity 85.9%; Pred. No. 3.9e-309;
Matches 1326; Conservative 0; Mismatches 217; Indels 0; Gaps 0;

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DB 140 TACAATCTAGGAACATTTAGTATGTGTTCATTTGGAAGAAAGTGAAGATTGCAGACAT 199
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DB 200 AAGCTTACAGGGCACAAGTGTCTATAAGATCCTGAACCGTCGCCAAATGAGAAATATG 259
QY 341 GAATGGAAGGAAGGAAGAGAAATGCAAGATTAATGAAGTTGCATTCACCCCAT 400
DB 260 GAATGGAAGGAAGGAAGGAAGAAATCAAGATTAATGAAGTTGCATTCACCCCAT 319
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DB 320 ATCATTCGGCTTTATGAGGTATATACCTCTACAGATATATATGTTGATGAGATAT 379
QY 461 TGTAAATGAGCGAGATTATTTGATTACATTTGTGAGAAAGGACAGATTACAGAAATGAA 520
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QY 521 GCTGTGTGAATCTTCAGCAGATCATATCTGCGTCAATATCTCCATAGAAATATGTT 580
DB 440 GCTGTGTGAATCTTCAGCAGATCATATCTGCGGTCAATATCTCCATAGAAATATGTT 499

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DB 620 AGTCCGAATCTGCTGTCCAGAGGTATCTGTTAAATTAATGCTGGACCCGAGGTT 619
QY 761 GATGATGAGAGTTGGGGTGAATCTTATGCTCTTCTTGTGGAACCTTCCATTTGAT 820
DB 680 GATGATGAGAGCTGTGGAGTATCTTATGCTCTTCTTGTGATCTTCCATTTGAT 729
QY 821 GATGAGATTTTCCCAATCTGTTCAAAAAAATTAAGGAGGTATCTACACTTCCAACT 880
DB 740 GACGAGAAATCTCCCAACTATTCAAAAAGATTAAGGAGGTATTAATATCTTCCAACT 799
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DB 800 CATTTATCTGCTCTGGCAGAGATTGATCCCAAGATGCTTGTGATCCCAATGAAG 859
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QY 1421 AGATGGAAGGAATGGGCACTCAAGTGAATGCAAGATGAGTGTGCCAGGTTTCTGAA 1480
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Db 756 AGTCCGAATATGCTGCTCCAGAGAGTATCTGTGTAATATATATGTGACCCGAGT 815
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RESULT 3
AK072723 2245 bp mRNA linear PLN 24-JUL-2003
LOCUS AK072723
DEFINITION Oryza sativa (japonica cultivar-group) cDNA clone:J023135H07, full insert sequence.

ACCESSION VERSION KEYWORDS SOURCE ORGANISM REFERENCE AUTHORS

AK072723
AK072723.1 GI:32982746
FLI CDNA: CAP trapper.
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.

TITLE JOURNAL MEDLINE PUBMED REFERENCE AUTHORS

The Rice Full-length CDNA Consortium, National Institute of
Agrobiological Sciences Rice Full-length CDNA Project Team;
Kikuchi, S., Satoh, K., Nagata, T., Kawagashira, N., Doi, K.,
Kishimoto, N., Yazaki, J., Ishikawa, M., Yamada, H., Ooka, H., Hotta, I.,
Kojima, K., Namiki, T., Ohneda, E., Yahagi, W., Suzuki, K., Li, C.,
Ohtsuki, K., Shishiki, T., Foundation of Advancement of International
Science Genome Sequencing & Analysis Group; Ohtsuki, K.,
Iida, Y., Sugano, S., Fujimura, T., Suzuki, Y., Tsunoda, Y.,
Kurosaki, T., Kodama, T., Masuda, H., Kobayashi, M., Xie, Q., Lu, M.,
Narikawa, R., Sugiyama, A., Mizuno, K., Yokomizo, S., Nishikura, J.,
Ikeda, R., Ishibiki, J., Kawamata, M., Yoshimura, A., Miura, J.,
Kusumegi, T., Oka, M., Ryu, R., Ueda, M., Matsubara, K., RIKEN;
Kawai, J., Carninci, P., Adachi, J., Aizawa, K., Arakawa, T., Fukuda, S.,
Hara, A., Hashidume, W., Hayatsu, N., Imotani, K., Ishi, Y., Itoh, M.,
Kagawa, I., Kondo, S., Konno, H., Miyazaki, A., Otsu, N., Ota, Y.,
Saito, R., Sasaki, D., Sato, K., Shibata, K., Shinagawa, A., Shiraki, T.,
Yoshino, M., and Hayashizaki, Y.
Collection, mapping, and annotation of over 28,000 cDNA clones from
japonica rice
Science 301 (5631), 376-379 (2003)
22752273
12869764

TITLE JOURNAL COMMENT

Submitted (05-DEC-2001) Shoshi Kikuchi, National Institute of
Agrobiological Sciences, Department of Molecular Genetics, Head of
Laboratory of Gene Expression; 2-1-2 Kamondai, Tsukuba, Ibaraki
305-8602, Japan (E-mail: skikuchi@nias.affrc.go.jp,
Tel:81-29-838-7007, Fax:81-29-838-7007)
This clone is one of the 28k full-length cDNA clones from japonica
rice.
URL: <http://cdna01.dna.affrc.go.jp/cdna/>
NIAS Rice Full-length CDNA Project Team: Kikuchi, S., Satoh, K.,
Nagata, T., Kawagashira, N., Doi, K., Kishimoto, N., Yazaki, J.,
Ishikawa, M., Yamada, H., Ooka, H., Hotta, I., Kojima, K., Namiki, T.,
Ohneda, E., Yahagi, W., Suzuki, K., Li, C., Ohtsuki, K., Shishiki, T., and
Yamamoto, M.
FAIS Genome Sequencing & Analysis Group: Ohtsuki, Y., Iida, Y.,
Fujimura, T., Ikeda, R., Ishibiki, J., Kawamata, M., Kobayashi, M.,
Kodama, T., Kurosaki, T., Kusumegi, T., Lu, M., Masuda, H., Miura, J.,
Mizuno, K., Narikawa, R., Nishikura, J., Oka, M., Ryu, R., Sugano, S.,
Sugiyama, A., Suzuki, Y., Tsunoda, Y., Ueda, M., Xie, Q., Yokomizo, S.,
Yoshimura, A., Matsubara, K., and Murakami, K.

Genome Exploration Research Group in Riken Genomic Sciences Center
and Genome Science Laboratory in Riken: Adachi, J., Aizawa, K.,
Akimura, T., Arikawa, T., Carninci, P., Fukuda, S., Hanagaki, T.,
Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K.,
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Sogabe, Y., Tagami, M., Tagami-Takeda, Y., Tagawa, A., Takehashi, F.,
Takaku-Akahira, S., Tanaka, T., Tomaru, A., Toyota, T., Waki, K.,
Tsunishi, A., and Hayashizaki, Y.

FEATURES

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ORIGIN

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Matches 1326;	Conservative 0;	Mismatches 217;	Indels 0;	Gaps 0;

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Qy	521	GCTGCTCGAATCTTCCAGAGATCATATCTGCGCGTCAATCTCCATAGAAACATGCTT	580
Db	572	GCTGCGGGAATCTTCCAGAGATCATATCTGCGGTTGAATCTCCACAGAAACATGCTT	631
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Db	692	GCTGACTTTGTGTGATGATGTCATGCATGATGCGCAATTTTAAAGACAAGCTGCGGG	751
Qy	701	AGTCGGAACATATGCTGCTCAGAGGTAATTCGTGTAACTATATATGCTGGAACCTGAGCTC	760
Db	752	AGTCGGAATTAATGCTGCTCAGAGGTAATTCGTGTAAATTAATATATGCTGGAACCTGAGCTC	811
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Db	812	GATGATGGAAGCTGTGGAAGTATCCTTTATATGCTCTCTTGTGGAATCCTTCCATTTGAT	871
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[illegible]

LOCUS DB2036 2161 bp mRNA linear PLN 06-FEB-1999
DEFINITION Oryza sativa mRNA for OSKs, complete cds.
ACCESSION DB2036
VERSION DB2036.1 GI:4107002
KEYWORDS OSKs.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Erihartoideae; Oryzaceae; Oryza.
REFERENCE
AUTHORS Takano, M., Kajiya-Kanegae, H., Funateuki, H. and Kikuchi, S.
TITLE Rice has two distinct classes of protein kinase genes related to
SNP1 of Saccharomyces cerevisiae, which are differentially regulated
in early seed development
Mol. Gen. Genet. 260 (4), 388-394 (1998)
JOURNAL 99086251
MEDLINE 9807074
PUBMED 9870704
2 (bases 1 to 2161)
AUTHORS Takano, M.
TITLE Direct Submission
JOURNAL Submitted (15-DEC-1995) Makoto Takano, National Institute of
Agricultural Resources, Department of Molecular Genetics; 2-1-2
Kamondai, Tsukuba, Ibaraki 305-8602, Japan
(E-mail:mtakano@abr.affrc.go.jp, Tel:81-298-38-7446,
Fax:81-298-38-7408)
FEATURES
source Location/Qualifiers
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DEFINITION	Oryza sativa SNF1-related protein kinase (RSK1) mRNA, complete cds.		
ACCESSION	U55768		
VERSION	U55768.1	GI:1477683	
KEYWORDS			
SOURCE	Oryza sativa		
ORGANISM	Oryza sativa		
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzae; Oryza.		
AUTHORS	1 (bases 1 to 1770)		
TITLE	Snf1, T.-H. and Le, H.-T.		
JOURNAL	SNF1-related protein kinase of rice		
REFERENCE	2 (bases 1 to 1770)		
AUTHORS	Tsai, T.-H.		
TITLE	Direct Submission		
JOURNAL	Submitted (19-Apr-1996) Teh-Huei Tsai, Life Science, National Tsing-Hua University, Hsinchu 30043, Republic of China		
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Query Match	59.8%;	Score 1164;	DB 8; Length 1770;
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RESULT 8
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ACCESSION AK069206
 VERSION AK069206.1 GI:32979230
 KEYWORDS FLI CDNA; CAP trapper.
 SOURCE Oryza sativa (japonica cultivar-group)
 ORGANISM Oryza sativa (japonica cultivar-group)
 BUKARYOTA: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophytes; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Euphorbiaceae; Oryzaceae; Oryza.

REFERENCE
 AUTHORS 1
 The Rice Full-length cDNA Consortium, National Institute of

Agrobiological Sciences Rice Full-length cDNA Project Team,
 Kikuchi, S., Satoh, K., Nagata, T., Kawagashira, N., Doi, K.,
 Kishimoto, N., Yazaki, J., Ishikawa, M., Yamada, H., Ooka, H., Hotta, I.,
 Kojima, K., Namiki, T., Ohneda, E., Yahagi, W., Suzuki, K., Li, C.,
 Ohtsuka, K., Shishiki, T., Foundation of Advancement of International
 Science Genome Sequencing & Analysis Group, Ootomo, Y., Murakami, K.,
 Iida, T., Sugano, S., Fujimura, T., Suzuki, Y., Tsunoda, Y.,
 Kurosaki, T., Kodama, T., Masuda, H., Kobayashi, M., Xie, Q., Lu, M.,
 Narikawa, R., Sugiyama, A., Mizuno, K., Yokomizo, S., Mikiura, J.,
 Ikeda, R., Ishibiki, J., Kawamata, M., Yoshimura, A., Miura, J.,
 Kusumegi, T., Oka, M., Ryu, R., Ueda, M., Matsubara, K., RIKEN:
 Kawai, J., Carninci, P., Adachi, J., Aizawa, K., Arakawa, T., Fukuda, S.,
 Hara, A., Hashidume, W., Hayatsu, N., Imotani, K., Ishii, Y., Itoh, M.,
 Kagawa, I., Kondo, S., Komano, H., Miyazaki, A., Oato, N., Ota, Y.,
 Saito, R., Sasaki, D., Sato, K., Shibata, K., Shinagawa, A., Shiraki, T.,
 Yoshino, M., and Hayashizaki, Y.
 Collection, mapping, and annotation of over 28,000 cDNA clones from

JAPONICA RICE
 Science 301 (5631), 376-379 (2003)

JOURNAL MEDLINE
 PUBMED 12869764
 REFERENCE 2 (bases 1 to 2927)
 AUTHORS Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Carninci, P., Doi, K.,
 Fujimura, T., Fukuda, S., Hanagaki, T., Hara, A., Hashidume, W.,
 Hayashida, K., Hayashizaki, Y., Hayatsu, N., Hiramoto, K., Hirooka, T.,
 Hori, F., Hotta, I., Iida, J., Iida, Y., Ikeda, R., Imamura, K.,
 Imotani, K., Ishibiki, J., Ishii, Y., Ishikawa, M., Itoh, M., Kagawa, I.,

TITLE

Kanagawa, S., Katoh, H., Kawagashira, N., Kawai, J., Kawamata, M.,
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 Yamada, H., Yamamoto, M., Yasunishi, A., Yazaki, J., Yokomizo, S., and
 Yoshimura, A.

COMMENT

Submitted (05-DEC-2001) Shoshi Kikuchi, National Institute of
 Agrobiological Sciences, Department of Molecular Genetics, Head of
 Laboratory of Gene Expression; 2-1-2 Kannondai, Tsukuba, Ibaraki
 305-8602, Japan (E-mail: skikuchi@nias.affrc.go.jp,
 Tel:81-29-838-7007, Fax:81-29-838-7007)
 This clone is one of the 28k full-length cDNA clones from japonica
 rice.

URL: <http://cdna01.dna.affrc.go.jp/cDNA/>
 NIAS Rice Full-length cDNA Project Team: Kikuchi, S., Satoh, K.,
 Nagata, T., Kawagashira, N., Doi, K., Kishimoto, N., Yazaki, J.,
 Ishikawa, M., Yamada, H., Ooka, H., Hotta, I., Kojima, K., Namiki, T.,
 Ohneda, E., Yahagi, W., Suzuki, K., Li, C., Ohtsuka, K., Shishiki, T., and
 Yamamoto, M.

FAIS Genome Sequencing & Analysis Group: Ootomo, Y., Iida, Y.,
 Fujimura, T., Ikeda, R., Ishibiki, J., Kawamata, M., Kobayashi, M.,
 Kodama, T., Kurosaki, T., Kusumegi, T., Lu, M., Masuda, H., Miura, J.,
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 Sugiyama, A., Suzuki, Y., Tsunoda, Y., Ueda, M., Xie, Q., Yokomizo, S.,
 Yoshimura, A., Matsubara, K., and Murakami, K.
 Genome Exploration Research Group in Riken Genomic Sciences Center
 and Genome Science Laboratory in Riken: Adachi, J., Aizawa, K.,
 Akimura, T., Arakawa, T., Carninci, P., Fukuda, S., Hanagaki, T.,
 Hara, A., Hashidume, W., Hayashida, K., Hayatsu, N., Hiramoto, K.,
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FEATURES

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 Qy 575 ATGGTTGTCACACCTGACCTTAAGCCGGAACCTTGTTACTGATTCGAAAGTATATGTA 634
 Db 1594 ATGGTTGTCACACCTGACCTTAAGCCGGAACCTTGTTACTGATTCGAAAGTATATGTA 1653
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 Db 1654 AATCTTGCGATTTTGGTCTGAGCAATGTCATGCAATGAGCCATTTTCTGAAGACTAGC 1713
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 Db 1714 TTGTTGAGTCCGAACTATGCTGCTCCAGAGTATATCTGTTAACTATATGCTGAGACT 1773
 Qy 755 GAGTTCAGATGATGAGTTGTTGAGGATGATTTTATGCTCTCTTGTGAACTCTTCCA 814
 Db 1774 GAGTTCAGATGATGAGTTGTTGAGGATGATTTTATGCTCTCTTGTGAACTCTTCCA 1833
 Qy 815 TTGATGATGAGAAATTTCCCAATCTGTTCAAAAATTAAGAGGATATCTACACTT 874
 Db 1834 TTGATGATGAGAAATTTCCCAATCTGTTCAAAAATTAAGAGGATATATATCTCTC 1893
 Qy 875 CCAAGTATTTGTTGCTTTGGCCAGAGATTTGATCCCAAGAACTGTTGTTGAGCCT 934
 Db 1894 CCAAGTATTTGTTGCTTTGGCCAGAGATTTGATCCCAAGAACTGTTGTTGAGCCT 1953
 Qy 935 ATGAGAGAAATCACAATTTAGGGAATTCGGAGCATCAATGTTCCAGATTCGCTTCCA 994
 Db 1954 ATGAGAGAAATCACAATTTAGGGAATTCGGAGCATCAATGTTCCAGATTCGCTTCCA 2013
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 Qy 1115 AGCAGACTTCAAAATGAGGCAACTGTTGATATTTACTATTTGAGCAATCGGTTTGA 1174
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RESULT 9
 HVU7990
 LOCUS
 DEFINITION
 ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM

HVU7990 1542 bp mRNA linear PLN 22-JUL-1998
 Hordeum vulgare mRNA for SnRK1-type protein kinase, partial.
 A2007990
 A2007990.1 GI:3341451
 kn12a gene; Snrk1-type protein kinase.
 Hordeum vulgare subsp. vulgare
 Hordeum vulgare subsp. vulgare
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Poideae; Triticeae; Hordeum.

1
 Slocumbe,S.P., Bertini,L., Beaudoin,F., Dickinson,J.R. and
 Halford,N.G.
 Molecular cloning of Bsnr1, a novel putative SNF4-related protein
 identified in a two-hybrid screen with barley seed Snrk1 protein
 kinase
 Unpublished
 2 (bases 1 to 1542)
 Slocumbe,S.P.
 Direct Submission
 Submitted (21-JUL-1998) Slocumbe S.P., Salami Department, Max
 Planck Institut fuer Zuechtungsforchung, Carl-von-Linne Weg 10,
 D-50829 Koeln, GERMANY

FEATURES
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NRLV"

ORIGIN

Query Match 52.7%; Score 1026.2; DB 8; Length 1539;
Best Local Similarity 80.2%; Pred. No. 1.2e-263;
Matches 1234; Conservative 0; Mismatches 293; Indels 12; Gaps 2;

QY 173 ATGATGGAAGTAAAGGAGTGGGATTCGAGCATTAAGAACTACACCTGGGA 232
DB 1 ATGATGGAACAACAGAGGAGTGGACATTCGAGCATTAAGAACTACACCTAGGC 60
QY 233 AGACCTTAGGTATCGGTATCTTGAAGAAAGTGAAGATGAGACATTAAGCTTACTGGA 292
DB 61 AAAACATTAAGGTATGAGAACATTTGAGATGTGAAGTTGCAAGCTTAACGGA 120
QY 293 CATAGGTTGCTATTAAGATCATCACTCCGCCAAATGAGAAATATGAAATGAAAG 352
DB 121 CAGAGAGTGTATTAAGATCTGAACCGTGTAAATGAGAACTATGAAATGAAAG 180
QY 353 AAAGCAAGAGAAATTCAGATATTGAATG-----TTCACTTACCCCATATC 403
DB 181 AAAGCAATAGAGAAATTCAGATATTGAATGTTTCATTTGATTCATTCATTCATTCATTC 240
QY 404 ATTCGGCTTATGAGTATATACACCTACAGATATATATGTTGATGGAATATTGT 463
DB 241 ATCCGGGTTATGAGTATATGAGACACCTAAGATATATTCGTTGATGGAATATTGC 300
QY 464 AAGTATGCGAGTATATTGATTCATTTGAGAAAGCAGATTTACAGAGATGAAGCT 523
DB 301 AATAATGCGAGTATATTGATTCATTTGAGAAATGCGGTTACAGAGATGAAGCT 360
QY 524 CGTGAATCTTCAGAGATCATATCTGGCGTGAATATCTGCCATGAAACATGTTGTC 583
DB 361 CGTGAATCTTCAGAGATTTTATGCTGTGTGAATATCTGCCATGAAATATGTTGTC 420
QY 584 CACCGTACCTTAAGCCGGAACCTGTTACTTGAATCAAGTATTAATGTAACCTTGGC 643
DB 421 CATGTATCTTAAGCCAGAAACCTGTACTTGAATCAAGTATTAATGTAACCTTGGC 480
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QY 704 CCGAATATGCTGCTCCAGAGTATATCTGTGAACCTATATGCTGAGCTGAGTGCAT 763
DB 541 CTAAATATGCTGCTCCAGAGATATCTCAAGTAAATATATGCTGAGCTGAGTGCAT 600
QY 764 GTATGAGTTGTGGGAGATCTTATGCTCTTCTTGTGGAACCTTCACTTGAATGAT 823
DB 601 GTTTGAGCTGTGGGAGTATCTTATGCTCTTCTTGTGCTCTGTTCACTTGAATGAT 660
QY 824 GAGATATTCCTCATCTTCAAAAATTAAGGAGATCTTACACACTTCCAAATCAT 883

DB 661 GACATATTCCTAGCCTGTTCAGAAAGATTAAGGAGTACTTATATCTTCCAGCTAT 720
QY 884 TTGCTGCTTTGGCCAGGATTTGATCCCGAATGCTGTGTGAGCTTATGAGAGA 943
DB 721 TTATCTATTTCTGCGAGGATTTGATCCAAATTTGTTAATATGATTCAAATGAGAG 780
QY 944 ATCAATTAAGGAAATTCGAGGATCAATGATTCAGATTCGCTTCCAGCTTACTTG 1003
DB 781 ATCAATTTATGAAATTCAGATTCAGATTCAGATTCAGATTCAGATTCAGATTCAG 840
QY 1004 GCGATGCTCCACAGATACGACCAACCAACCAAAATGATGATGAGATACCTTGA 1063
DB 841 GCAATGCTCCACAGATACGACCAACCAACCAAAATGATGATGAGATACCTTGA 900
QY 1064 GATCTGTTATATGGAATTTAACAACAAGTGTGTGTAATGCTGTGTAATGAGCTG 1123
DB 901 GAGGTGTCAACCTGAGATATGATTAAGATATGATGATGATGATGATGATGATGAT 960
QY 1124 CAATATGAGCAACTGTTGATATTTATTTATTTATTTATTTATTTATTTATTTATTT 1183
DB 961 CAATATGAGCAACTGTTGATATTTATTTATTTATTTATTTATTTATTTATTTATTT 1020
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QY 1304 AGTGTGTTGGGCGCATTTATTTCTGTTGAAGAAATGAGGCGCTGATTCAGTCTCG 1363
DB 1141 GGTGCTTACGCGCATATTTACCCGTTACAAAGAAATGAGGCTATGAGGTTGCACTCG 1200
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QY 1424 TGAAGAAGAAATGAGGCTCAACAGTAAATGAGATGATGATGATGATGATGATGATGAT 1483
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DB 1321 AGCGATATGTTGTTAATGATGATGATGATGATGATGATGATGATGATGATGAT 1380
QY 1541 GATGATCTAATGAGGAGCTACTTGTGATCAAGTTGAATTCAGCTTTACAGAGC 1600
DB 1381 GCGAATGCTGATGAGGAGCTACTTGTGATCAAGTTGAATTCAGCTTTACAGAGC 1440
QY 1601 AAGGAGCAAGTACCTTTAATGATGATGATGATGATGATGATGATGATGATGATGAT 1660
DB 1441 AAGGATTAACAAGTACCTGATGATGATGATGATGATGATGATGATGATGATGAT 1500
QY 1661 GACTTGTGCGGCTTCTTACCAAGCTTAAGGTTCTA 1699
DB 1501 GAATTTGTGGGCTTCTTACCAAGCTTAAGGTTCTA 1539

RESULT 11
RYERKINI
LOCUS 1809 bp mRNA linear PLN 27-Apr-1993
DEFINITION Secale cereale RKINI mRNA, complete CDS.
ACCESSION M74113
VERSION M74113.1 GI:169835
KEYWORDS protein serine/threonine kinase.
SOURCE Secale cereale (rye)
ORGANISM Secale cereale
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Poideae; Triticeae; Secale.
1 (bases 1 to 1809)
REFERENCE
Alderson,A., Sabelli,P.A., Dickinson,J.R., Cole,D., Richardson,M.,

Kreis, M., Shewry, P. R. and Halford, N. G.
Complementation of snfi, a mutation affecting global regulation of
carbon metabolism in yeast, by a plant protein kinase cDNA
Proc. Natl. Acad. Sci. U.S.A. 88 (19), 8602-8605 (1991)

JOURNAL
MEDLINE
PUBMED
92020901
1924320

COMMENT
Original source text: Secale cereale (cultivar Gazelle) seed
endosperm cDNA to mRNA.

FEATURES
source
location/Qualifiers

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gene

CDS

ORIGIN

Query Match 50.7%; Score 988.2; DB 8; Length 1809;
Best Local Similarity 80.7%; Pred. No. 1.8e-253;
Matches 1235; Conservative 0; Mismatches 248; Indels 48; Gaps 5;

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358 CATGTGACACCGAAGATATTTTGTGTTGATGAAATATTCGCAAAATGGTGCATATT 417
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418 GGCATTAACATTTGAGAAAGGCGGTTACAGAAAGGAGGCTGTGAACCTTCAGCA 477
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601 GGAAGAACTTGTACTTGAATCAAGTATATATGTAAGAACTTGCAGATTGCTGAGCAA 660
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Db 658 AGAGTCAATCTGAGTAATATGATAGCTGAGCTGAGATTGATGATTGAGGCTGAGGCT 717
Qy 781 GATCTTATATGCTCTCTTTGTAAGCTCTGATTTGATGATGATGATGATGATGATGAT 840
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Qy 901 GATTTGATCCAGATGCTGTTGTTGAGCTTATGAGAGATCAATTAAGGAAAT 960
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Qy 961 TGGAGAGCATCAATGTTCCAGATTGCGCTTCCAGCTTACTTGGCAGTCTCCACCA 1020
Db 898 TCGAAAAACTCATGTTTCAAGATGCGCTTCTCGCTACTGCGAGTCTCCACCA 957
Qy 1021 TAGACACAAACAGCCAAAATGATGATGAGATGATGATGATGATGATGATGATGAT 1080
Db 958 TAGATGACAGCAAGCCAAAATGATGATGAGATGATGATGATGATGATGATGATGAT 1017
Qy 1081 ATTTAACAAGAACCATGTTGTTGATGATGATGATGATGATGATGATGATGATGATGAT 1140
Db 1018 ATATGATTAAGATCAATGTTGTTGATGATGATGATGATGATGATGATGATGATGATGAT 1077
Qy 1141 TGATATTTATTTATCTATGAGCAATGCTTTTGAAGCACTGATGCTATCTTGGGCA 1200
Db 1078 TGATATTTATTTATCTATGAGCAATGCTTTGAGGCTTATTTGAGGCTCTCA 1137
Qy 1201 TTATCAAGATCAATGAGACAGAAATTAATCAAGCTGGGCTATCTGAATCATCTAGTT 1260
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Db 1228 TTACCGGCTTGAAGAAATGAGGCTGTTGAGGCTTCCAGAGCTCTCCCTGCTGC 1287
Qy 1378 AATATGTTGAGGCTTAAAGCACTCAAGAAATTAACGATGAGTGAAGAGAAATG 1437
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Qy 1438 GCA---CTACACGTAAGATGAGATGAGTCCAGAGGTTTCTGAAGTTAATGACA---C 1491
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Db 1468 TAGTATGATGAGGCTGATGATCAAGTTTGAATTCAGCTTAAACAGAGAGAGCA 1527
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Db 1588 GGCCTTCTTACCAAGCTTGGGTTCTATAG 1618

RESULT 12
AK067158 2073 bp mRNA linear PLN 24-JUL-2003
LOCUS AK067158

DEFINITION	<i>Oryza sativa</i> (japonica cultivar-group) cDNA clone:J013094M16, full insert sequence.
ACCESSION	AK067158
VERSION	AK067158.1 GI:32977176
KEYWORDS	Full cDNA; CAP trapper.
SOURCE	<i>Oryza sativa</i> (japonica cultivar-group)
ORGANISM	<i>Oryza sativa</i> (japonica cultivar-group)
REFERENCE	1. Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; <i>Oryza</i> .
REFERENCE	2. The Rice Full-Length cDNA Consortium, National Institute of Agricultural Sciences Rice Full-Length cDNA Project Team; Kikuchi, S., Satoh, K., Nagata, T., Kawagashira, N., Doi, K., Kishimoto, N., Yazaki, J., Ishikawa, M., Yamada, H., Ooka, H., Hotta, I., Kojima, K., Namiki, T., Ohneda, B., Yahagi, W., Suzuki, K., Li, C., Ohtsuki, K., Shishiki, T., Foundation of Advancement of International Science Genome Sequencing & Analysis Group; Ootomo, Y., Murakami, K., Iida, Y., Sugano, S., Fujimura, T., Suzuki, Y., Tsunoda, Y., Kurosaki, T., Kodama, T., Masuda, H., Kobayashi, M., Xie, Q., Lu, M., Marikawa, R., Sugiyama, A., Mizuno, K., Yokomizo, S., Nikura, D., Ikeda, R., Ishibiki, J., Kawamata, M., Yoshimura, A., Miura, J., Kusumegi, T., Oka, M., Ryu, R., Ueda, M., Matsubara, K., RIKEN; Kawai, J., Carninci, P., Adachi, J., Aizawa, K., Arakawa, T., Fukuda, S., Hara, A., Hashidume, W., Hayatsu, N., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kondo, S., Kono, H., Miyazaki, A., Ootomo, N., Ota, Y., Saito, R., Sasaki, D., Sato, K., Shibata, K., Shinagawa, A., Shiraki, T., Yoshino, M., and Hayashizaki, Y.
TITLE	Collection, mapping, and annotation of over 28,000 cDNA clones from japonica rice
JOURNAL	Science 301 (5611), 376-379 (2003)
MEDLINE	22752273
PubMed	12869764
REFERENCE	2 (bases 1 to 2073)
AUTHORS	Aizawa, K., Aizawa, K., Akimura, T., Arakawa, T., Carninci, P., Doi, K., Fujimura, T., Fukuda, S., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayashizaki, Y., Hayatsu, N., Hiramoto, K., Hirooka, T., Horii, P., Hotta, I., Iida, J., Iida, Y., Ikeda, R., Imamura, K., Imotani, K., Ishibiki, J., Ishii, Y., Ishikawa, M., Itoh, M., Kagawa, I., Kanagawa, S., Katoh, H., Kawagashira, N., Kawai, J., Kawamata, M., Kikuchi, S., Kishikawa-Hirozane, T., Kishimoto, N., Kobayashi, M., Kodama, T., Kojima, K., Kojima, Y., Kondo, S., Kono, H., Kouda, M., Koya, S., Kurihara, C., Kurosaki, T., Kusumegi, T., Li, C., Lu, M., Masuda, H., Matsubara, K., Matsuyama, T., Miura, J., Miyazaki, A., Mizuno, K., Murakami, K., Murata, M., Nagata, T., Nakamura, M., Namiki, T., Narikawa, R., Numata, E., Ohno, M., Ohtsuki, K., Oka, M., Ooka, H., Ootomo, N., Ota, Y., Ootomo, Y., Ryu, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Sato, K., Satoh, K., Satoh, K., Shiraki, T., Shishiki, T., Sogabe, Y., Sugano, S., Sugiyama, A., Suzuki, K., Suzuki, Y., Tagami, M., Tagami, T., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Tanaka, T., Tomaru, A., Toya, T., Tsunoda, Y., Ueda, M., Waki, K., Xie, Q., Yahagi, W., Yamada, H., Yamamoto, M., Yasunishi, A., Yazaki, J., Yokomizo, S., and Yoshimura, A.
TITLE	Direct Submission
JOURNAL	Submitted (05-DEC-2001) Shoshi Kikuchi, National Institute of Agricultural Sciences, Department of Molecular Genetics, Head of Laboratory of Gene Expression; 2-1-2 Kannondai, Tsukuba, Ibaraki 305-8602, Japan (E-mail:skikuchi@nias.affrc.go.jp, Tel:81-29-838-7007, Fax:81-29-838-7007)
COMMENT	This clone is one of the 28k full-length cDNA clones from japonica rice. URL: http://cdna01.dna.affrc.go.jp/cdna/NIAS_Rice_Full-Length_cDNA_Project_Team_Kikuchi_S_Satoh_K_Nagata_T_Kawagashira_N_Doi_K_Kishimoto_N_Yazaki_J_Ishikawa_M_Yamada_H_Ooka_H_Hotta_I_Kojima_K_Namiki_T_Ihikawa_M_Yamada_H_Ooka_H_Hotta_I_Kojima_K_Namiki_T_Yamamoto_M_Yahagi_W_Suzuki_K_Li_C_Ohtsuki_K_Shishiki_T_and_Yamamoto_M_FAIRS_Genome_Sequencing_and_Analysis_Group_Ootomo_Y_Iida_Y_Fujimura_T_Ikeda_R_Ishibiki_J_Kawamata_M_Kobayashi_M_Kodama_T_Kurosaki_T_Kusumegi_T_Lu_M_Masuda_H_Miura_J_Mizuno_K_Narikawa_R_Nikura_J_Oka_M_Ryu_R_Sugano_S_

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Best Local Similarity	72.4%; Pred. No. 1.e-207;
Matches 1074; Conservative	0; Mismatches 406; Indels 3; Gaps 1;
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 ACCESSION DB2039.1 GI:4107008
 VERSION
 KEYWORDS OSK1.
 SOURCE Oryza sativa
 ORGANISM Oryza sativa
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Ehrhartoideae; Oryzaceae; Oryza.
 REFERENCE 1 (sites)
 AUTHORS Takano,M., Kajiya-Kanegae,H., Funatsuki,H. and Kikuchi,S.
 TITLE Rice has two distinct classes of protein kinase genes related to
 SNF1 of Saccharomyces cerevisiae, which are differently regulated

JOURNAL in early seed development
 MEDLINE Mol. Genet. 260 (4), 388-394 (1998)
 PUBMED 99086251
 9870704
 REFERENCE 2 (bases 1 to 2209)
 AUTHORS Takano,M.
 TITLE Direct Submission
 JOURNAL Submitted (15-DEC-1995) Makoto Takano, National Institute of
 Agrobiological Resources, Department of Molecular Genetics, 2-1-2
 Kamondai, Tsukuba, Ibaraki 305-8602, Japan
 (E-mail:mtakano@abr.affrc.go.jp, Tel:81-298-38-7446,
 Fax:81-298-38-7408)

FEATURES

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ORIGIN

Query Match 41.9%; Score 815.8; DB 8; Length 2209;
 Best Local Similarity 72.4%; Pred. No. 3.1e-207;
 Matches 1073; Conservative 0; Mismatches 407; Indels 3; Gaps 1;

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Dp	763	GATGTGTGGAAGTTGTGGTTATTTCTTATATGCTCTTCTTGTGGAACCTTCCATTGAT	822
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Qy	881	CATTGTCTGCTTGTGGCCAGGATTTGATCCACGAATGCTGTTGTGAGCTTATGAAG	940
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Qy	1181	AGTGGCTATCTTTGGGGCAGATTTATACAAGATCAATGACAGGAATTTAAATCAGCTGGG	1240
Dp	1183	AGTGGCTATCTTTGGGGCAGATTTATACAAGATCAATGATTAATGGAATCTTCTCGCTCAAGTAACT	1242
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Qy	1361	CGGGGCCACCTCGTGAATAATATGTTGAGCTTTAAAAAGCACTTCAGAAATTAACGTC	1420
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Qy	1421	AGATGGAAGAAATGGGCACCTACCAAGCTGAATCAGATGGTGGCCAGGGTTCCTGAA	1480
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Qy	1541	GATGATGTTAATGGGAGGCTACTTATCTGATCAAGTTTGAATTCAGCTTATCAAGAGC	1600
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Dp	1600	AGGAGTAAAAATATACCTTCTTGACCTTGAAGGGGTCAGTGGACCAACAGCTTCTCTTCTG	1658
Qy	1661	GACTTCTGTGGGGCTTCTTACCAAGCTTATAGGCTTATATGAT	1703
Dp	1660	GACCTGTGCTGTGCTTCTTAACTCAGCTGAGAGCTCTTTTAT	1702

RESULT 14			
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LOCUS	1453 bp	mRNA	linear
DEFINITION	H.vulgaris mRNA for SNF1-related protein kinase.		
			PLN 18-SEP-1995

ACCESSION VERSION KEYWORDS SOURCE ORGANISM	REFERENCE AUTHORS TITLE	JOURN. MEDLINE PUBMED REFERENCE AUTHORS TITLE JOURNAL
X62548 X62548.1 GI:575291 BKIN2 gene; SNF1 protein kinase. Hordeum vulgare subsp. vulgare Hordeum vulgare subsp. vulgare Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta, Liliopsida; Poales; Poaceae; Poideae; Triticeae; Hordeum.	1 Hannappel,U., Vicente-Carbalosa,J., Barker,J.H., Shewry,P.R. and Halford,N.G. Differential expression of two barley SNF1-related protein kinase genes	JOURN. MEDLINE PUBMED REFERENCE AUTHORS TITLE JOURNAL
	Plant Mol. Biol. 27 (6), 1235-1240 (1995)	95284374
	7766906	
	2 (bases 1 to 1453)	
	Halford,N.G. Direct Submission Submitted (07-NOV-1994) N.G. Halford, Institute of Arable Crops Research, Long Ashton Research Station, University of Bristol, Bristol BS18 9AF, UK	

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ORIGIN

Query Match	40.8%;	Score 795;	DB 8;	Length 1453;
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Matches 1071; Conservative	0;	Mismatches 380;	Indels 18;	Gaps 3;

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QY	290	GGCATATGAGTTCTCTATAAGATCATCATCACTGCCCGCCAATGAGAAATATGAAATGAA	349
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QY	410	CTTTATGAGGTCTATATACACCTCAAGATATATATGTTGTATGGAATTTGTAAGTAT	469
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QY	470	GGCGAGTTATTGTTGATTCAATTGTTGAGAAAGGCAGATTACAGAAAGATGAAGCTGCTGCA	523
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Dd	1424 TCTGCTTTCTAACCCACGCTGAGAGTCT	1452

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DEFINITION	Lycopersicon esculentum SNF1 (SNF1) mRNA, complete cds.				
ACCESSION	AF143743				
VERSION	AF143743.1	GI:7672781			
KEYWORDS					
SOURCE	Lycopersicon esculentum (tomato)				
ORGANISM	Lycopersicon esculentum				

REFERENCE
AUTHORS
1 (bases 1 to 1948)
Bradford, K.J., Downte, A.B., Gee, O.H., Alvarado, V., Yang, H. and

TITLE
Abstract Acid and Gibberellin Differentially Regulate Expression of
Genes of the SNF1-Related Kinase Complex in Tomato Seeds
JOURNAL
Plant Physiol. 132 (3), 1560-1576 (2003)
MEDLINE
22742410

REFERENCE
AUTHORS
TITLE
JOURNAL

2 (bases 1 to 1948)
Bradford, K.J., Dahal, P., Downie, B., Nonogaki, H. and Alvarado, V.
Yeast SNF1 kinase homolog from tomato
Unpublished

BRIDFORD, K. J., DAHAL, P., DOWNIE, B., NOMOGAKI, H. and ALVARADO, V.
 Direct Submission
 Submitted (15-APR-1999) Vegetable Crops, University of California,
 Davis, One Shields Ave, Davis, CA 95616, USA

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1. 1948
/organism="Lycopersicon esculentum"
/mol_type="mRNA"
/db_xref="taxon:4081"

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gene
gibberellin (4+7) for 24 hours"
1. .1948
/note="gibberellin deficient mutant of Money-maker
cultivar; isolated from seeds imbibed in 100-µM
gibberellin (4+7) for 24 hours"

```
CDS      33..1577
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         /note="similar to yeast SNF1 kinase"
         /codon_start=1
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/feature_id="AAFC6639.1"
/db_xref="GI:7672782"
/translation="MDGAAVOGSSVDFLRNYVLTGLIGISFGKVIAEHTLTGK
VAVILNRKRIKMDMEKKVREIKIIRLPMPHPIIALYEIETPSPIIYVMEYVSG

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DENT.PNL.FKKIKGCIYTLPHLSAGARDL.PRM.I.VDPMKMT.PETRLHPYFPAHL.P
RYLA.VPDPDTTQAKKIDELIJOBVSGMGDRNNLTESLNRONCTEVAHYLLDLNR
HRVSTGYLGA.FOESMEYGNRINSNSTALS.PVCGORF.PGMTDY.OOAGAROP.PLERKKA

ORIGIN
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AQLRVL"

Query Match	40.6%;	Score 791.2;	DB 8;	Length 1948;
Best Local Similarity	71.5%;	Pred. No. 1.2e-200;		

Matches 1074; Conservative 0; Mismatches 413; Indels 15; Gaps 2;

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Oy 212 TTAGGAACCTCAACCTGGGAGAACTTTAGTATCGGTACATTGGGAAAGTAAAGTT 271
Db 78 TTACGAACCTCAACCTGGGAGAACTTTAGTATCGGTACATTGGGAAAGTAAAGTT 137
Oy 272 GCAGAGCATTAAGCTTACTGACATAGGTTGCTTAAGATCATCACTGGCCAAATG 331
Db 138 GCTGAACATTAAGCTTACTGACATAGGTTGCTTAAGATCATCACTGGCCAAATG 197
Oy 332 AGAATATGGAATGGAAGAGAAAGCAAGAGATTCAGATTTGAAGTTGTTCACTT 391
Db 198 AGAATATGGAATGGAAGAGAAAGCTCGTAGAGAAATCAAAATATGAGTTGTTCACT 257
Oy 392 CACCCCATATCATTCGGCTTATGAGGTCATATACACCTCAAGATATATATGTTG 451
Db 258 CATCTCATATTAATGAGCTTATGAGGTCATAGAGACACATGATATATATGTTG 317
Oy 452 ATGGAATATTTGAATAGGAGGAGTTATTTGATTAATCATTTGTAAGAAAGGAGATTACAG 511
Db 318 ATGAGATATGGAATATCTGGGAGTTATTTGATTAATCATTTGTAAGAGGAGATTGAG 377
Oy 512 GAATGAAGCTCGTCGATCTTCCAGCAATCATATCGCGCTGGAATCTGCCATGA 571
Db 378 GAGATGAAGCTCGTAACTTTTTCAGCAGATTAATTTCTGGTGTGAGTACTGCCATGA 437
Oy 572 AACATGTTGTCACCGTCACTTAAGCCGGAATCTTTACTTTGATTCAAAGTATAT 631
Db 438 AACATGTTGTTCAATAGAGCTTAAAGCTTAAACCTCTTCTGAGCTCCAAATGAT 497
Oy 632 GTAAAACTTGGGATTTTGTCTGAGCAATGTCATGATGCGCATTTTCTGAAGACT 691
Db 498 GTGAAGATCGAGATTTTGTGTTGAGCAATCATGCGCATTTTCTGAAGACA 557
Oy 692 AGCTGGGAGCTCCGAATATGCTGCTCCAGAGGTAAATATGTTAACTATATGCTGA 751
Db 558 AGTTGCCGAAGCCCAACTATATGCTGCCCAAGAGTTATATCAGTTAATGTATGCTG 617
Oy 752 CCTGAGGTCGATGATGAGGTTGAGGCTGATCTTTATAGCTCTTCTTGGAACCTT 811
Db 618 CTTGAGGTCGATGATGAGGTTGAGGCTGATCTTTATAGCTCTTCTTGGAACCTT 677
Oy 812 CCATTGATGATGAAATATCCCAATCTGTTCAAAAAAATTAAAGGAGTATCAACA 871
Db 678 CCGTTGACGATGAAACATACCAATCTTTTAAAGAAATTAAGGAGTATATATCT 737
Oy 872 CTTCAAGTCACTTTGCTGCTTGGCCAGAGATTTGATCCACGAATGCTTTGTTGAG 931
Db 738 CTGCCAGCCATTTATCAGCTGTGCGAGGATTTGATCCGAGATGCTTATAGTGCAC 797
Oy 932 CCTATGAAGAAATCAACATTAAGGAAATTTGGAGCATCAATGTTCCAGATTCGCTT 991
Db 798 CCAATGAAGCGAAATGACTATCTGAGATTTGCTGCAACCTTGTGTTCAAGCTCATTTG 857
Oy 992 CCAAGTTACTTGGAGTGCCTCCACAGATGACACACAACCAAGCCAAATGATTGATGA 1051
Db 858 CCAAGCTATTTGGCGCTGCTCCACAGATCAACCAACCAAGCAAGAAAGATGATGA 917
Oy 1052 GATACACTTGCAGATGTTGTTAATATGGAATTTAAACAAGAACATGTGTGAATCACTG 1111
Db 918 GAGATTTCTCAAGAGTGTTAATAGTGGATTTGACAGGAACAACCTTACTGAGTCTT 977
Oy 1112 TGCAGCAGACTTCAAAATGAGGCACTGTGCAATATTTAATTTGACATCGGTTT 1171
Db 978 CGCAATAGAGTTCAAAATGAGGCACTGTGCAATATTTAATTTGACATCGGCAAT 1037
Oy 1172 AGAGCACTAGTGCCTATCTTGGGAGATTTATCAAGATCAATGACAGGAATTTAAAT 1231
Db 1038 CGTGTTCACACTGCTATCTTTGAGCTGAATTTCAAGAGTCCATGAAATATGTTACAC 1097
Oy 1232 CAGCTGCGTCATCTGAATCATCTAGTTCTGGTACGAGAAATTAATGTTCCAGAAAGCA 1291
Db 1098 CGGATCAATTTCAATGAACCGCTGCTCCCTGTGTGTCAAAGTTCCAGAAATATG 1157
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Oy 1292 GATCCATAGCAGTGTGTTGCGGCCATATATCTGTGAAAAGAAATGAGCGCTTGA 1351
Db 1158 GATTATACGAAGCTGTGTGCAAG--ACAGTTCCCATTAAGAAATATGAGCTTTGGC 1214
Oy 1352 CTTCACTCTGCGGCCCACTCGTGAATATATGTTGAGGTCTTTAAAGCACTTCAAGAA 1411
Db 1215 CTCAGTCTGAGGCGCATCCACCGTGAATATATGCTGAAGTTTGAAGGCTTCCAGAA 1274
Oy 1412 TTAAAGTCAGATGGAAGAAAGATGAGCACTACAGCTGAATATGCAATGTGTGCCAGG 1471
Db 1275 CTGAATATATGTTGAAAAGATTTGTCAGATTAACATGAATGTGATGAGTTCTAGC 1334
Oy 1472 TTCTCAAGTTAATGACAGTTAGATGCA-----GCAACAGCTTCTTGTG 1519
Db 1335 TTACTGTGATCATGGAAGCATGGTGTATATTCATGCAATGGAATCAAGTTTGA 1394
Oy 1520 GACTCTACATCATGATTAATGATGATCTTAATGGAAGGCTACTGATGATCAAGTTT 1579
Db 1395 GATGATTCATGCATCATTTGAAGATGATGAGGCGCAAAAGTTAACAAATGTGTCAAGTTT 1454
Oy 1580 GAATTCAGCTTTTCAAGAGAGAGACGACAGTACTTTAGATATGCAAGAGTTACT 1639
Db 1455 GAATTCAGCTTTTCAAAACCAAGAGAGAGATCTTGTGACCTTCAAGAGCTTCAAG 1514
Oy 1640 GGAACCTGAGCTGCTCTTCTTGACTTCTGTCGCGGCTTCTTCAAGCTTAAAGGCTTCA 1699
Db 1515 GGTCACAATTCCTTCTTCTGAGTCTGTGCTGCTTCTTCTGCTCAAGTCTTCAAGTCTT 1574
Oy 1700 TA 1701
Db 1575 TA 1576
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Search completed: July 9, 2004, 13:46:10
Job time : 7672 secs

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CC Arabidopsis thaliana, Cucumis sativus, Glycine max and Oryza sativa. The
 CC protein is involved in carbon catabolite repression, and so the gene and
 CC protein can be used in plants to control the nitrogen and carbon
 CC partitioning pathways during plant growth and development. They can also
 CC be used to alter the accumulation of carbohydrates, lipids and proteins
 CC during plant growth

XX Sequence 1948 BP; 572 A; 380 C; 461 G; 535 T; 0 U; 0 other;

Query Match 100.0%; Score 1948; DB 3; Length 1948;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1948; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 GTGACCCACGCGCCGACCAAGCGGCGATACGCCCCCAAGTCCAAAAGCCCTCTCC 60
 1 GTGACCCACGCGCCGACCAAGCGGCGATACGCCCCCAAGTCCAAAAGCCCTCTCC 60
 61 GCGCCGCTCTCCACCTGAGTGTCTCCCGCTCTCCCGCGCATCTGCTCGCGCG 120
 61 GCGCCGCTCTCCACCTGAGTGTCTCCCGCTCTCCCGCGCATCTGCTCGCGCG 120
 121 GCAGAAAGTTGACCTGCGAGGCGCGCGCAACCCGCTAGTGAAGTGAATGATGG 180
 121 GCAGAAAGTTGACCTGCGAGGCGCGCGCAACCCGCTAGTGAAGTGAATGATGG 180
 181 AAGTATGAAGGAGTGGGCACTTCTGAAGCATTAAGAACTACAACTGGGGAAGACTTT 240
 181 AAGTATGAAGGAGTGGGCACTTCTGAAGCATTAAGAACTACAACTGGGGAAGACTTT 240
 241 AGGTATCGGTACATTTGGAAAAGTGAAGATTGACAGCATTAAGCTTCTGACATAGGCT 300
 241 AGGTATCGGTACATTTGGAAAAGTGAAGATTGACAGCATTAAGCTTCTGACATAGGCT 300
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 301 TGCATTAAGATCATCACTGCGCCCAATGAGAAATATGAAATGGAAGAAAGCAA 360
 361 GAGAGATTCAGATTTGAAAGTTGTCATTCACCCCATTCATTCGAGCTTTATGAGT 420
 361 GAGAGATTCAGATTTGAAAGTTGTCATTCACCCCATTCATTCGAGCTTTATGAGT 420
 421 CATATACACACCTACAGATATATATGTTGATGAAATATTTGAAATGATGCGAGTATT 480
 421 CATATACACACCTACAGATATATATGTTGATGAAATATTTGAAATGATGCGAGTATT 480
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 481 TGATTAATCTGTGAGAAAGGCAATTAACAGAAAGATGAAGCTGTGAATCTTCCAGCA 540
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 601 GAAAACTTGTACTTGAATCAAGATATATGTAATAAATCTGGGATTTTGTCTGAGCAA 660
 601 GAAAACTTGTACTTGAATCAAGATATATGTAATAAATCTGGGATTTTGTCTGAGCAA 660
 661 TGTATGCAATGAGCCATTTTCTGAAAGACTAGCTGTGGAGTCCGAACATATGCTGCTCC 720
 661 TGTATGCAATGAGCCATTTTCTGAAAGACTAGCTGTGGAGTCCGAACATATGCTGCTCC 720
 721 AGAGGTATATCTGTGTAATCTATATGCTGACCTGAGGTGATATAGAGTTGTGGGGT 780
 721 AGAGGTATATCTGTGTAATCTATATGCTGACCTGAGGTGATATAGAGTTGTGGGGT 780
 781 GATTCCTTATGCTCTTCTTGTGAACTCTTCAATTTGATGATGAAGAATATTCACATCT 840
 781 GATTCCTTATGCTCTTCTTGTGAACTCTTCAATTTGATGATGAAGAATATTCACATCT 840
 841 GTTCAAAAAAATTAAGGAGATATCTACACTTCCAAAGTCAATTTGTCTGTGGCCAG 900
 841 GTTCAAAAAAATTAAGGAGATATCTACACTTCCAAAGTCAATTTGTCTGTGGCCAG 900

901 GGATTTGATCCACGATGCTGTTGTTGAGCCTATGAAAGATCAATTAAGGAAAT 960
 901 GGATTTGATCCACGATGCTGTTGTTGAGCCTATGAAAGATCAATTAAGGAAAT 960
 961 TCGGAGCATCAATGTTTCCAGATTTGCGCTTCCAGCTTACTTGGCAGTGTCTCACCA 1020
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 1021 TACGACCAACAAGCCAAATGATGTAAGTACCTCGATGTTGTTAATATGGG 1080
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 1081 ATTTAACAAGAACCATGTGTGTGAATCACTGTGACAGCACTTCAAAATGAGGCACTGT 1140
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 1141 TGCATATTTATCTATTTGACAACTGGTTTAAAGCACTAGTGGCTATCTTGGGCA 1200
 1201 TTAATCAAGATCAATGAGACAGAAATTTAAATCAGTGGCGCTCATCTGAATCATCTAGTT 1260
 1201 TTAATCAAGATCAATGAGACAGAAATTTAAATCAGTGGCGCTCATCTGAATCATCTAGTT 1260
 1261 TGGTACGAGAAATTAATGTTCCAGAAAGCAAGTATCTCATAGCAGTGTGGGCA 1320
 1261 TGGTACGAGAAATTAATGTTCCAGAAAGCAAGTATCTCATAGCAGTGTGGGCA 1320
 1321 TTAATCTGTTGAAAGAAATGGCGCTTGAATCTTCACTGCGGCGCCACCTGTGTAAT 1380
 1321 TTAATCTGTTGAAAGAAATGGCGCTTGAATCTTCACTGCGGCGCCACCTGTGTAAT 1380
 1381 AATGTTGAGCTCTTAAAGCACTTCAAGAAATTAACGTGATGGAAGAAATGGGCA 1440
 1381 AATGTTGAGCTCTTAAAGCACTTCAAGAAATTAACGTGATGGAAGAAATGGGCA 1440
 1441 CTAACAAGTGAATGAGATGAGTGGCCAGGCTTCTGAAGTTAATGACAGTTAATGC 1500
 1441 CTAACAAGTGAATGAGATGAGTGGCCAGGCTTCTGAAGTTAATGACAGTTAATGC 1500
 1501 CAGCAACAGCTTCTTGTGATCTTACATCATATGATGATGATGATGATGATGATGATG 1560
 1501 CAGCAACAGCTTCTTGTGATCTTACATCATATGATGATGATGATGATGATGATGATG 1560
 1561 ACCTACGTGATCAAGTTGAAATTCAGCTTCAAGACGAAGACGACAGTACCTTT 1620
 1561 ACCTACGTGATCAAGTTGAAATTCAGCTTCAAGACGAAGACGACAGTACCTTT 1620
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 1621 AGATATGACAGAGTTAATCTGACCTGAGCTGCTCTTGAATCTTGTGCGGCTTCTCT 1680
 1681 TACCAAGCTTAAAGGCTTCTATATGCTGTCATCATATGTCGAAATTTTCACTGTGGAAT 1740
 1681 TACCAAGCTTAAAGGCTTCTATATGCTGTCATCATATGTCGAAATTTTCACTGTGGAAT 1740
 1741 AACGGAAGCATGTAATATAGAACTTGTCTGCTCTTGTGACAAAGCAATGTTGAG 1800
 1741 AACGGAAGCATGTAATATAGAACTTGTCTGCTCTTGTGACAAAGCAATGTTGAG 1800
 1801 TGAATGCTTGTGTTGAGGCGCTTAAAGGTCATGTAATCTTAGTTAGTATTTTCTGT 1860
 1801 TGAATGCTTGTGTTGAGGCGCTTAAAGGTCATGTAATCTTAGTTAGTATTTTCTGT 1860
 1861 TCTTAAATATTTTGTGCTGCTGCTAGTATGTTCAATTTTGAACATAAAGCTTGAATA 1920
 1861 TCTTAAATATTTTGTGCTGCTGCTAGTATGTTCAATTTTGAACATAAAGCTTGAATA 1920
 1921 AAAAAAGTAAAAAATTAAGGAGATATCTACACTTCCAAAGTCAATTTGTCTGTGGCCAG 1948
 1921 AAAAAAGTAAAAAATTAAGGAGATATCTACACTTCCAAAGTCAATTTGTCTGTGGCCAG 1948

RESULT 2
ID ACC00743
ACC00743 standard; cDNA; 1948 BP.
XX
AC ACC00743;
XX
16-MAY-2003 (first entry)
XX
Zea mays oil trait related cDNA sequence SEQ ID NO:235.
DE
XX
XX plant; oil trait; oil phenotype; altered lipid profile; MAP kinase;
XX receptor-like protein kinase; mitogen activated protein kinase; oil;
XX LIPID-1-like transcription factor caleosin; ATP citrate lyase; SNF1;
XX CAC-like transcription factor; antisense inhibition; co-suppression;
XX transgenic plant; gene; ss.
OS
XX Zea mays.
XX MO2003002751-A2.
XX
XX 09-JAN-2003.
XX
XX 27-JUN-2002; 2002MO-US020152.
XX
XX 29-JUN-2001; 2001US-0301913P.
XX
XX (DUPO) DU PONT DE NEMOURS & CO E I.
XX (PION-) PIONEER HI-BRED INT INC.
XX
XX Allen SM, Allen WB, Cahoon RE, Epelbaum S, Famodu OO, Harvell LT,
XX Jones TJ, Kinney AJ, Klein TM, Li C, Oliveira IC, Sakai H, Shen B,
XX Terczynski MC;
XX
XX MPI; 2003-201509/19.
XX P-PSDB; ABR40708.
XX
XX Novel nucleotide fragment encoding polypeptides having receptor-like
XX protein kinase activity, caleosin-like activity, useful for altering oil
XX phenotypes in plants such as sunflower, coconut, soybean, wheat and rice.
XX
XX Claim 18; Page 272-273; 542pp; English.
XX
XX The present invention describes an isolated nucleotide fragment (I)
XX comprising a nucleic acid sequence (NS) chosen from a NS encoding a
XX polypeptide (PP) having receptor-like protein kinase activity, mitogen
XX activated protein kinase (MAP)-kinase activity, lipid-like transcription factor
XX activity, caleosin-like activity, ATP citrate lyase activity, SNF1-like
XX activity and CAC-like transcription factor activity. Also described: (1)
XX complement (II) of (I); (2) a chimeric construct (III) comprising (I) or
XX (II), operably linked to a regulatory sequence; (3) a plant (IV)
XX comprising (III) in its genome; (4) seeds (V) obtained from (IV); and (5)
XX oil obtained from (V). (I) or its part can be used in antisense
XX inhibition or co-suppression in a transformed plant. (III) is useful for
XX altering the oil phenotype in a plant such as corn, soybean, wheat, rice,
XX canola, Brassica, sorghum, sunflower or coconut. (III) is also useful for
XX creating transgenic plants having altered lipid profiles. (I) can also be
XX used as a hybridisation probe. ACC00626 to ACC00868 and ABR40581 to
XX ABR40879 represent sequences used in the exemplification of the present
XX invention
XX
XX Sequence 1948 BP; 572 A; 380 C; 461 G; 535 T; 0 U; 0 Other;
Query Match 100.0%; Score 1948; DB 7; Length 1948;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1948; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GTGACCCAGCGCGCGGACCAAGCGGGGATACGCGCCCAAGTCCAAAGCCCTTCC 60
DB 1 GTGACCCAGCGCGCGGACCAAGCGGGGATACGCGCCCAAGTCCAAAGCCCTTCC 60
QY 61 GCCCGGCTCTCCACTGTAGTGTCTCCCGCTCTCCGCGCGCACTCGCTCGCGCG 120
DB 61 GCCCGGCTCTCCACTGTAGTGTCTCCCGCTCTCCGCGCGCACTCGCTCGCGCG 120

QY 121 GCAGGAAGTTGACTGTGAGGGGCGGCGAACCCGGTAAGTAAGTGAAGTGG 180
DB 121 GCAGGAAGTTGACTGTGAGGGGCGGCGAACCCGGTAAGTAAGTGAAGTGG 180
QY 181 AAGTAGTAAGGAGAGTGGGCAATTCAGACATTAAAGCACTACACCTGGAGAACTTT 240
DB 181 AAGTAGTAAGGAGAGTGGGCAATTCAGACATTAAAGCACTACACCTGGAGAACTTT 240
QY 241 AAGTAGTGGTACATTTGGAAAAAGTGAAGATTGACAGACATTAAGCTTAAGAGT 300
DB 241 AAGTAGTGGTACATTTGGAAAAAGTGAAGATTGACAGACATTAAGCTTAAGAGT 300
QY 301 TGCTATTAAGATCATCACTGCGCCCAAAATGAAGAAATATGAAGTAAGAGAAAGCAA 360
DB 301 TGCTATTAAGATCATCACTGCGCCCAAAATGAAGAAATATGAAGTAAGAGAAAGCAA 360
QY 361 GAGAGAAATTCAGAAATATGAAGTGTTCATTCACCCCATATCATTCGCTTTATAGGT 420
DB 361 GAGAGAAATTCAGAAATATGAAGTGTTCATTCACCCCATATCATTCGCTTTATAGGT 420
QY 421 CATATACACCTTACAGATATATATGTTGATGAAATTTGTAATGGCAATTAT 480
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QY 481 TGATTAATGTTGAGAAAGGAGATTAACAGAAATGAAGTCTGTCGATCTTCCAGCA 540
DB 481 TGATTAATGTTGAGAAAGGAGATTAACAGAAATGAAGTCTGTCGATCTTCCAGCA 540
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DB 541 GATCATATCTGGGCGTGAATATGCGCATAGAAACATGTTGTCACCGTACCTAAAGCC 600
QY 601 GGAAGAACTTGTATCTTGATTCAGAAATATATGTAATGTAATCTTGGGATTTGCTGAGCAA 660
DB 601 GGAAGAACTTGTATCTTGATTCAGAAATATATGTAATGTAATCTTGGGATTTGCTGAGCAA 660
QY 661 TGTCATGCAATGAGGAGGCAATTTCTGAAAGTCTGAGGAGTCCGAACTATCTGCTCC 720
DB 661 TGTCATGCAATGAGGAGGCAATTTCTGAAAGTCTGAGGAGTCCGAACTATCTGCTCC 720
QY 721 AGAGGTAAATATCTGTAATATATATATGCTGAGCTGAGTGTAGTGTGGGCT 780
DB 721 AGAGGTAAATATCTGTAATATATATATGCTGAGCTGAGTGTAGTGTGGGCT 780
QY 781 GATTTCTTATGCTCTTCTTTTGGAACCTTCCATTTGATGATGAGAAATTTCCAACT 840
DB 781 GATTTCTTATGCTCTTCTTTTGGAACCTTCCATTTGATGATGAGAAATTTCCAACT 840
QY 841 GTTCAAAAAAATTAAGGAGGATCTTCAACACTTCAAGTCAATTTGCTGCTTGGCCAG 900
DB 841 GTTCAAAAAAATTAAGGAGGATCTTCAACACTTCAAGTCAATTTGCTGCTTGGCCAG 900
QY 901 GATTTGATCCAGATGCTTGTGTTGAGCTTATGAAGAGATCAATTAAGGAAAT 960
DB 901 GATTTGATCCAGATGCTTGTGTTGAGCTTATGAAGAGATCAATTAAGGAAAT 960
QY 961 TCGGAGAGCATCAATGCTTCCAGATGCTTCCAGCTTACTTGGCAGTGTCCACAGCA 1020
DB 961 TCGGAGAGCATCAATGCTTCCAGATGCTTCCAGCTTACTTGGCAGTGTCCACAGCA 1020
QY 1021 TACGACACCAAGCCCAAAATGATGATGAAGTACATTCGAGATGTTTAAATATGGG 1080
DB 1021 TACGACACCAAGCCCAAAATGATGATGAAGTACATTCGAGATGTTTAAATATGGG 1080
QY 1081 ATTTAACAAGAACCATGTGTGTAATCACTGTGACAGACATCTTAATTAAGGCACTGT 1140
DB 1081 ATTTAACAAGAACCATGTGTGTAATCACTGTGACAGACATCTTAATTAAGGCACTGT 1140
QY 1141 TGCATATTAATTAATTAATGAGCAATGCTTTAGAGCACTAGTGTGCTATCTTGGGCAAG 1200
DB 1141 TGCATATTAATTAATTAATGAGCAATGCTTTAGAGCACTAGTGTGCTATCTTGGGCAAG 1200

QY 1201 TTATCAAGAAATCAATGAGACAGAAATTTAAATCAGCTGGCGCATCTGAATCATCTAGTTC 1260
 DB 1201 TTATCAAGAAATCAATGAGACAGAAATTTAAATCAGCTGGCGCATCTGAATCATCTAGTTC 1260
 QY 1261 TGGTACAGGAAATTAATGTTCCAGAGACAGATGCTCATAGAGTGGTTGGCGGCATA 1320
 DB 1261 TGGTACAGGAAATTAATGTTCCAGAGACAGATGCTCATAGAGTGGTTGGCGGCATA 1320
 QY 1321 TTATCTGTTGAAGAAATGGGGCGCTTGACCTTCACTTCGGGCCCAACCTCGTGAAT 1380
 DB 1321 TTATCTGTTGAAGAAATGGGGCGCTTGACCTTCACTTCGGGCCCAACCTCGTGAAT 1380
 QY 1381 AATGTTGAGGCTTTAAAGACCTTCAAGAAATTAAGTCAGATGAGAAGAAATGGGCA 1440
 DB 1381 AATGTTGAGGCTTTAAAGACCTTCAAGAAATTAAGTCAGATGAGAAGAAATGGGCA 1440
 QY 1441 CTACACAGTGAATGACAGATGTCGCCAGGGTTTCTGAAGTTATGACACGTTAGATGC 1500
 DB 1441 CTACACAGTGAATGACAGATGTCGCCAGGGTTTCTGAAGTTATGACACGTTAGATGC 1500
 QY 1501 CAGCAAGAGCTTTTGTGTGCTTACATCATGAGTAAGTATGCTATATGGAGGCT 1560
 DB 1501 CAGCAAGAGCTTTTGTGTGCTTACATCATGAGTAAGTATGCTATATGGAGGCT 1560
 QY 1561 ACTACTGTGATCAAGTTTGAATTCAGCTTTACAGACGAGACGACAAATGACTCTT 1620
 DB 1561 ACTACTGTGATCAAGTTTGAATTCAGCTTTACAGACGAGACGACAAATGACTCTT 1620
 QY 1621 AGATATGACAGAGTACTGAGACCTGACCTGCTTCTTCTGACTTCTGTGGCGCTTCT 1680
 DB 1621 AGATATGACAGAGTACTGAGACCTGACCTGCTTCTTCTGACTTCTGTGTGGCGCTTCT 1680
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 DB 1681 TACCAAGCTTAAGGTTCTATATGTGTGCTCATCATGAGTAAGTATGCTATATGGAGT 1740
 QY 1741 AACCGAAGCATGTAATATAGGAACCTTGTCTGCTTTTGGACAAGCAATGTTGAG 1800
 DB 1741 AACCGAAGCATGTAATATAGGAACCTTGTCTGCTTTTGGACAAGCAATGTTGAG 1800
 QY 1801 TGACTGCTTGTGTGAGCGCGTAAGGTCATGATATCTTAGGTAAGTATTTTCT 1860
 DB 1801 TGACTGCTTGTGTGAGCGCGTAAGGTCATGATATCTTAGGTAAGTATTTTCT 1860
 QY 1861 TCTTAATATTTGTGCTGCTAGTATGATCTTTTGAACCTTAAGCTTACGAATTA 1920
 DB 1861 TCTTAATATTTGTGCTGCTAGTATGATCTTTTGAACCTTAAGCTTACGAATTA 1920
 QY 1921 AAAAAAGATAAAAA 1948
 DB 1921 AAAAAAGATAAAAA 1948

RESULT 3
 ACC00753
 ID ACC00753 standard; cDNA; 1899 BP.
 XX
 AC ACC00753;
 XX
 XX 16-MAY-2003 (first entry)
 XX
 DE Triticum aestivum oil trait related cDNA sequence SEQ ID NO:255.
 XX
 KW plant; oil trait; oil phenotype; altered lipid profile; MAP kinase;
 KW receptor-like protein kinase; mitogen activated protein kinase; oil;
 KW Lipid-like transcription factor caleosin; ATP citrate lyase; SNF1;
 KW CKC-like transcription factor; antisense inhibition; co-suppression;
 KW transgenic plant; gene; ss.
 XX
 XX Triticum aestivum.
 XX
 PN MO2003002751-A2.
 XX

PD 09-JAN-2003.
 XX
 PF 27-JUN-2002; 2002MO-US020152.
 XX
 XX 29-JUN-2001; 2001US-0301913P.
 PR
 PA (DUPO) DU PONT DE NEMOURS & CO E. I.
 PA (PION-) PIONEER HI-BRED INT INC.
 PI Allen SM, Allen WB, Caloon RE, Epelbaum S, Farnold OO, Harvell LT;
 PI Jones TJ, Kinney AJ, Klein TM, Li C, Oliveira IC, Sakai H, Shen B;
 PI Tarczy-Hornoch MC;
 PI
 DR WPI; 2003-201509/19.
 DR P-PSDB; ABR40718.
 XX
 XX Novel nucleotide fragment encoding polypeptides having receptor-like
 PT protein kinase activity, caleosin-like activity, useful for altering oil
 PT phenotypes in plants such as sunflower, coconut, soybean, wheat and rice.
 XX
 PS Claim 18; Page 296; 542pp; English.
 CC
 CC The present invention describes an isolated nucleotide fragment (I)
 CC comprising a nucleic acid sequence (NS) chosen from a NS encoding a
 CC polypeptide (PP) having receptor-like protein kinase activity, mitogen
 CC activated protein (MAP)-kinase activity, Lipid-like transcription factor
 CC activity, caleosin-like activity, ATP citrate lyase activity, SNF1-like
 CC activity and CKC-like transcription factor activity. Also described: (1)
 CC complement (II) of (I); (2) a chimeric construct (III) comprising (I) or
 CC (II), operably linked to a regulatory sequence; (3) a plant (IV)
 CC comprising (III) in its genome; (4) seeds (V) obtained from (IV); and (5)
 CC oil obtained from (V). (I) or its part can be used in antisense
 CC inhibition or co-suppression in a transformed plant. (III) is useful for
 CC altering the oil phenotype in a plant such as corn, soybean, wheat, rice,
 CC canola, brassica, sorghum, sunflower or coconut. (III) is also useful for
 CC creating transgenic plants having altered lipid profiles. (I) can also be
 CC used as a hybridisation probe. ACC00626 to ACC00868 and ABR40591 to
 CC ABR40879 represent sequences used in the exemplification of the present
 CC invention
 XX
 SQ Sequence 1899 BP; 572 A; 364 C; 462 G; 501 T; 0 U; 0 Other;
 Query Match 61.4%; Score 1195.6; DB 7; Length 1899;
 Best Local Similarity 85.8%; Pred. No. 4.1e-308;
 Matches 1327; Conservative 0; Mismatches 219; Indels 0; Gaps 0;
 QY 166 AGTGAATATGAGAGAGTGTAAAGGAGTGGGCTTCTGAAGCATTAAGAACTACAA 225
 DB 60 AGTGAATATGAGAGAGTGTAAAGGAGTGGGCTTCTGAAGCATTAAGAACTACAA 119
 QY 226 CTGGGAAGAACTTTAGGTATCGGTACATTTGGAAAAGTGAATGACAGAGCATTAAGCT 285
 DB 120 TGTGGGAGAACTTAGTATAGGACATTTGAAAAGTGAATGACAGAGCATTAAGCT 179
 QY 286 TACTGACATAGAGGTTGCTATTAAGATCATCACTGCCGCAATGAGAAATATGAAAT 345
 DB 180 TACAGGGCATTAAGTGTCTATTAAGATTCGAACCGTCGCAATGAGAACTATGAAAT 239
 QY 346 GAAAGAAAGCAAAAGAGAAATTCAGAGATTTGAAGTGTTCATTCACCCCATATCAT 405
 DB 240 GAGAGAAAGCAAAAGAGAGATCAAGATTTGAAGTGTTCATTCACCCCATATCAT 289
 QY 406 TCGGCTTATGAGGTCATATACACACTACAGATATATATGTTGTGATGGAATATGTA 465
 DB 300 CCGGCTTATGAGGTCATATACACACTACAGATATATATGTTGTGATGGAATATGTA 359
 QY 466 GTATGGAGATTTATGATTAATCATTTGTGAAAAGGAGATTAACAGAGATGAAGCTCG 525
 DB 360 GTATGGAGATTTATGATTAATCATTTGTGAAAAGGAGGCTTACAGAGATGAAGCTCG 419
 QY 526 TCGAATTTCCAGACATATATCTGGCGTCAATATCTGCAATGAAGAACTGTTGTCCA 565
 DB 420 TCGAATTTCCAGACATATATCTGGTGTGAATCTGCAAGAAACTGTTGTCTCA 479

QY	586	TCGTACCTTAAGCCGGAACCTTGTACTGTGATTCGAAGTAATGTATGTAAACTTCGGCA	645
Db	480	TCGTGATCTTAAGCCAGAACCTGTACTGTATTCGAATACATGTGAAACTTCGCCGA	539
QY	646	TTTTGTCTGAGCAATGTCATGCAATGATGCGCATTTTCTGAAGACTGACGTGGAGTCC	705
Db	540	CTTTGGGTTAAGTAAATGTCAATGCAATGACATGTCATTTCTGAAGACTGACGTGGAGTCC	599
QY	706	GACATATCTGCTCCAGAGGTAAATATCTGTGTAATCTATATGCTGGAACCTGAGGCTGAGT	765
Db	600	AAACTATCTGCAACAGAGGTATCTCAGATAAATTAATACGTGGACCTGAGGTGAAGT	659
QY	766	ATGAGATGTGGGGTGAATTTCTTTATGCTCTTCTTTGTGGAACTCTTCCATTTGATGATGA	825
Db	660	TTGGAGCTGCGGGGTGATACCTTTATGCTCTTCTTTGTGGACCTTCCATTTGATGATGA	719
QY	826	GAAATATTTCCCAATCTGTTCAAAAATAATTAAGGAGGTATCTACACACTTCCAGTCAATTT	885
Db	720	CAATATTTCCCAACGTGTTCAAAATAATTAAGGAGGCATCTATATCTTCCAAAGTCAATTT	779
QY	886	GTCGTCCTTTGGCAGAGGATTTGATCCCAAGATGCTGTGTGTGTGGCCCTAATGAAGAAAT	945
Db	780	ATCTGCTCTTGCAAGGAAATTTGATCCCAAGAAATGCTGTGTGTGATCTTAATGAAGAAAT	839
QY	946	CACAAATTAAGGAAATTCGGAGCATCAATGTTTCCAAATTCGCTTCACGTTAATTGCTGGC	1009
Db	840	CACAAATTCGTGAATTTCCAGAAACACCAATGGTTTCAAGATGCTTCCTTCGCTGACTGGC	899
QY	1006	AGTGCCTCCACAGATATGACACACACAGCCAAATATGATATGAAGATACACTTCAGAA	1066
Db	900	AGTGCCTCCACAGACAGCGCGCAGCAAGCCAAATATGATATGAAGATACACTTTAAAGA	959
QY	1066	TGTTGTTATATATGAGGATTTTAAACAAGACCATGTGTGATATCACTGTGCAGACACTTCA	1125
Db	960	GATTTGTCACCTGGGATATGATTAAGACACATGTGTGTGATATCATTTGTGTGCATATAGGCTCA	1019
QY	1126	AAATGAGCAACTGTTGCAATTAATTTATCTATTTGGACAAATGCGTTTAAGCAACTGATGG	1185
Db	1020	AAATGAGCAACTGTTGCAATTAATTTATCTTGGACAAATGCGTTCGCGGACACTGATGG	1079
QY	1186	CTATCTTGGGGCAGATTTATCAAGAAATCAATGGAACAGAAATTTAAATACAGCTGGCGTATC	1245
Db	1080	CTATTTGGGGGCTGACTATCTACATCAATGAGGTATGAGATTTAATCAAGTTTACTTCAATT	1139
QY	1246	TGAATCATCTAGTTCTGTGTGAGAGGAATTAATGTTCCAGAGAACATGATCTCATTAAGCAG	1305
Db	1140	GGAATCAGCAAGCCCAAGTACAGGCAATCTTCCAGACAGCAATGATTTCTCAAGCAG	1199
QY	1306	TGCTTTGGGCGCATTTATCTCTGTGAAAGAAATGCGCGCTTGGACCTTCACTGCTCGGCG	1365
Db	1200	TGGCTTGGGCGCATTTATCCCCGTGAAAGAAATGGGCTCTTGGGCTCCAGTCTCGAGC	1259
QY	1366	CCACCTCGTGAATAATGTTGAGAGTCTTTAAAGCACTTCAAGAAATTAACGTCAGATG	1425
Db	1260	TCAACTCTGTAGAAATATGATCGAGGCTCTTAAGGCACTTCAAGAAATTAATGTCTGCTG	1319
QY	1426	GAAAGAAATGCGCACATCAACATGTAATGCAATGATGTGCCAGGGCTTCTGTAAGTTAA	1485
Db	1320	GAAAGAAATGCGACACTCAACATGTAATGCAAGGTGTGCCCTCGGGTTCCTCAGGTAG	1379
QY	1486	TGACACGTTAATGCGCAGCAAGCTTCTTGTGTGACTCTACATCAATGAAATTAACGCGCA	1545
Db	1380	TGAATATGTTAATGCGCACACAGCTTGTGTGTGATGACTCTACATCAATGAAATTAACGCGCA	1439
QY	1546	TGCTAATGGAGGCTACCTACTGTGATCAAGTTTGAATTCAGCTTTAACAAGACGAAGGA	1605
Db	1440	TGCTAATGGAGGCTACCTGCGGTGATCAAGTTTGAATTCAGGCTTTAACAAGACGAAGGA	1499
QY	1606	CGAACAAGTACTTTAAGTATGACAGAGGTTAATCTGAGACCTCAGCTGCTCTTCTTGACTT	1665
Db	1500	TGACAAGTACTGCTAAGTATGACAGAGGTTAATCTGAGACCTCAGCTCTCTTCTTGAAGTTT	1559

Oy		1666 CTGCGCCGCCCTTCTTAACGAAGTTAGGGTTCATTATGGGTCAACC	1711
Db		1560 TTGGCGGCCTTCTTAACAACCTTAGGTTCTATAATGATGCTCC	1605
<hr/>			
RESULT 4			
ID	AAA52769	standard; cDNA; 2107 BP.	
XX	AAA52769;		
AC	03-JAN-2001	(first entry)	
XX			
DE	Corn putative catabolite repression protein SNF1 coding sequence #3.		
XX			
KW	Corn; carbon catabolite repression; sucrose non-fermenting protein 1;		
XX	SNF1; plant growth; ss.		
OS	Zea mays.		
XX			
FT	Key	Location/Qualifiers	
FT	CDS	2..1739	
FT		/tag= a	
FT		/product= "SNF1"	
FT		/partial	
XX			
PN	WO200036115-A2.		
PD	22-JUN-2000.		
XX			
PF	15-DEC-1999;	99WO-US029824.	
XX			
PR	16-DEC-1998;	98US-O112563P.	
XX			
PA	(DUPO) DU PONT DE NEMOURS & CO E I.		
Allien SM,	Hephard EP, Sakai H, Weng Z, Helentjaris TG, Macool DJ;		
Miso G;			
DR	WPI; 2000-431593/37.		
P-PSDB;	AAB03417.		
XX			
XX	New nucleic acids encoding sucrose non-fermenting 1 (SNF1) proteins		
PT	involved in carbon catabolite repression in plants and seeds, useful for		
PT	controlling carbon and nitrogen partitioning pathways during plant growth		
PT	and development.		
XX			
PS	Claim 2; Page 37; 59pp; English.		
XX			
XX	The present sequence is a putative sucrose non-fermenting protein SNF1		
CC	coding sequence from corn. The sequence was isolated by searching a corn		
CC	stem cDNA library for sequences similar to those encoding SNF1 in		
CC	Arabidopsis thaliana, Cucumis sativus, Glycine max and Oryza sativa. The		
CC	protein is involved in carbon catabolite repression, and so the gene and		
CC	protein can be used in plants to control the nitrogen and carbon		
CC	partitioning pathways during plant growth and development. They can also		
CC	be used to alter the accumulation of carbohydrates, lipids and proteins		
CC	during plant growth		
SQ	Sequence 2107 BP; 578 A; 454 C; 484 G; 591 T; 0 U; 0 Other;		
Query Match	41.3%; Score 804.2; DB 3; Length 2107;		
Best Local Similarity	71.7%; Pred No. 1.1e-203;		
Matches 1084;	Conservative 0; Mismatches 418; Indels 9; Gaps 2;		
Oy	190 AGGAGTGCGCATTTCTAGACATTAAAGAACTAACACCTGGAGAAGAACTTTAGGTATCGG	249	
Db	238 AGCGGAAAGAGATGCCAACCCTTTGACGCGTTACAGAAATGGCAAACCTCGGGAATTGG	297	
Oy	250 TAACATTGGAAGAAAGTGAAGATTGACAGCAGCTAAAGCTTACTGAGACATAGGCTGTCTAAAA	309	
Db	298 GTGCTTGGTAAAGTGAAGATCGCGGAACATTATATTACATGCTATTAAGGTGGGATCAAA	357	

CC (II), operably linked to a regulatory sequence; (3) a plant (IV)
 CC comprising (III) in its genome; (4) seeds (V) obtained from (IV); and (5)
 CC oil obtained from (V). (I) or its part can be used in antisense
 CC inhibition or co-suppression in a transformed plant. (III) is useful for
 CC altering the oil phenotype in a plant such as corn, soybean, wheat, rice,
 CC canola, Brassica, sorghum, sunflower or coconut. (III) is also useful for
 CC creating transgenic plants having altered lipid profiles. (I) can also be
 CC used as a hybridisation probe. ACC00626 to ACC00868 and ABR40591 to
 CC ABR40879 represent sequences used in the exemplification of the present
 CC invention

XX Sequence 2107 BP; 578 A; 454 C; 484 G; 591 T; 0 U; 0 Other;

Query Match 41.3%; Score 804.2; DB 7; Length 2107;

Best Local Similarity 71.7%; Pred. No. 1.1e-203; Mismatches 418; Indels 9; Gaps 2;

Matches 1084; Conservative 0; Mismatches 418; Indels 9; Gaps 2;

QY 190 AGGAGTGGGCACTTCTGAGCATTAAAGAACTACAACTGGGAAAGAACTTATGCTATCG 249
 DB 238 AGGGGAAAGATGCCAACCTTTGAGGGTTACAGATTGGCAAAACCTGGGAATTGG 297
 QY 250 TACATTTGAAAAGTGAAGATGCAAGCATTAAGCTTAAGCAATAGGGTGTCTATAA 309
 DB 298 GTCTTGGTAAAGTGAAGATGCGGAAATATATGCTGCTATAGGTCGATCAA 357
 QY 310 GATCATCACTGCGCCAAATGAAATATGAAATGAAAGAAAGAAAGAAAGAAAT 369
 DB 358 GATTCTCAATCGCAAGAAAGATCAAGAGATGATATGAGAAAGAAAGTAAAGAAAT 417
 QY 370 CAAGATTTGAAGTGTTCATTCACCCCATATCATTCGGCTTATGAGTCATATAC 429
 DB 418 CAAGATCTGAGATTATTTATGATCCATCATACCGCTTATAGGATAGATAC 477
 QY 430 ACCATCAATATATATGTTGATGAAATTTGAATATGCGAATTTATTTATCAT 489
 DB 478 ACCGCTGAATATGTTGTTGATGAGATGATTAATCTGGAAGTGTGTTGATTCAT 537
 QY 490 TGTGAAAGAGGAGATTAACGAAAGTGAAGTCTGCGAATCTTCCAGAGATCATATC 549
 DB 538 CATTGAAGAGAGAGGCTTACGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGATC 597
 QY 550 TGGCGTGAATATCTGCAATAGAAACATGTTGTCACCGTGAAGCTTAAAGCGAAATCT 609
 DB 598 TGGTGTGAATATGCAATAGAAACATGTTGTCACCGTGAATTTAAAGCGAAGATCT 657
 QY 610 GTTACTTGAATCAAGATTAATGTAATCTTGGGATTTGCTGAGCAATGTCATGCA 669
 DB 658 TCTTTGATTCAAATGCAATGTTAAGATTGCGGATTTGGCTTAAGTATATATGCG 717
 QY 670 TGAATGGCATTTCTGAAAGCTAGCTGCGGAGTCCGAATCTATGCTCCAGAGATAT 729
 DB 718 TGAATGGCATTTCTTAAAGAGAGTGTGAGCCCAATTTATGACACACCTGAGTCAT 777
 QY 730 ATCTGTAATCTATATGCTGAGCTGAGTGAATGATGAGTGTGGGATTTCTTAA 789
 DB 778 ATCTGTAATCTATATGCTGAGCTGAGTGAATGATGAGTGTGGGATTTCTTAA 837
 QY 790 TGGCTTTCTTTGGAATCTTTCATTTGATGATGAGATATTCATCTGTTCAAAA 849
 DB 838 TGGCTTTCTTTGGAATCTTTCATTTGATGATGAGATATTCATCTGTTCAAAA 897
 QY 850 AATTAAGGAGATATCTACACATCTTCAAGCTTTGCTGCTTTGGCGGAGATTTGAT 909
 DB 898 AATTAAGGAGATATATACCTTCTAGCATTTGTCACCTTCACGAGGAGCTTGAT 957
 QY 910 CCCAGCAATCTTGTGTTGAGCTATGAGAGATCAATTAAGGAAATTCGGAGCA 969
 DB 958 TCCAGAAATCTGTTGTTGATCAATGAAGATTAAGATTAAGTAAATCTGTGAACA 1017
 QY 970 TCAATGTTCAAGATTTGCTTCAAGTATCTTGGAGTGTCTCACAGATACAGACA 1029
 DB 1018 TGTGTGTTCAAGATTCGACTCGCGCTATTTGGCTGTGCGGCTCTCAGACACTGCTCA 1077

QY 1030 ACAAGCCAAATGATGATGAGATACACTTCGAGATGTTGTTATATGAGATTAACAA 1089
 DB 1078 ACAAGTTAAAGATGCAAGAGAACTTTATGATGTTATTAAGATGGTTTGACAA 1137
 QY 1090 GAACCATGTGTGTAATCACTGTGACAGACATTCAAATGAGCACTGTGATTTA 1149
 DB 1138 GAATCAGCTAATGAATCTGTGAAAACAGATTCAGAAATGAGCAACAGTGTCTATTA 1197
 QY 1150 TTTACTATTTGACATATGTTTATGAGCACTAGTGTCTATCTTGGGCAATTAACA 1209
 DB 1198 TTTACTCTTGACATATGAGCTGTGACACAGTGTATCTGATCTGATTTCAAGA 1257
 QY 1210 ATCAATGACAGAAATTAATATCAAGCTGGGTCATCTGATATCTTATGTTCTGTAGAG 1269
 DB 1258 ATCTATGATCATCTTTGTTCTA--AGTAATGCTGAAACACCACTTCAGCACTGA 1314
 QY 1270 GAATTAATGTTCCAGAAAGATGATCTCTATGAGAGTGTGCGGCAATTAATCTGT 1329
 DB 1315 ACTTCGACAGATGGGTTTCAAGATCTCAAGTGTGCTGAGGAGCATTTTGACAGC 1374
 QY 1330 TGAAGAAATGAGGCGCTTGACCTTCAGTCTCGGCGCCACCTCTGTAATTAATGTTGA 1389
 DB 1375 TGAAGAAATGAGGCGCTTGACCTTCAGTCTCGGCGCCACCTCTGTAATTAATGTTGA 1434
 QY 1390 GGTCTTAAAGCACTTCAAGATTAATCAAGTCAAGTGAAGAAAGATGGGCACTACAGCT 1449
 DB 1435 AGTCTTAAAGCTCTGCAAGATCTGAATGTTTACTGAAAGAAATGGAACATACAT 1494
 QY 1450 GAAATGCAATGTTGCGCCAGGCTTCTGAAGTTAATGACACGTTAGTCCAGCAAG 1509
 DB 1495 GAAATGCAATGTTGCGCCAGGCTTCTGAAGTTAATGACACGTTAGTCCAGCAAG 1548
 QY 1510 CTTTCTGTGATCTTCAATCAATGATATGATGATGATGATGATGATGATGATGATGAT 1569
 DB 1549 CTTTCTGTGATCTTCAATCAATGATATGATGATGATGATGATGATGATGATGATGAT 1608
 QY 1570 GATCAATGTTGAATTCAGCTTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGATGCA 1629
 DB 1609 AGTGAATGTTGAATTCAGCTTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGATGCA 1668
 QY 1630 GAGAGTACTGACCTTCAAGCTTCTTCTTGAATCTTCTGCGGCTTCTTCAAGCT 1689
 DB 1669 AAGGTCAGAGATCAATCTTCTTCTTGAATCTTCTGCGGCTTCTTCAAGCT 1728
 QY 1690 TAGGTTCTAT 1700
 DB 1729 GAGAGTTCTTT 1739

RESULT 6
 ACC00745
 ID ACC00745 standard; cDNA; 2052 BP.
 XX ACC00745;
 AC
 XX
 DT 16-MAY-2003 (first entry)
 XX
 DE Zea mays oil trait related cDNA sequence SEQ ID NO:239.
 XX
 XX Plant; oil trait; oil phenotype; altered lipid profile; MAP kinase;
 KM receptor-like protein kinase; mitogen activated protein kinase; oil;
 KM LIP5-like transcription factor caleosin; ATP citrate lyase; SNF1;
 KM CMC-like transcription factor; antisense inhibition; co-suppression;
 KM transgenic plant; gene; ss.
 XX
 XX Zea mays.
 OS
 PN MO2003002751-A2.
 XX
 XX 09-JAN-2003.
 PD
 XX
 PF 27-JUN-2002; 2002MO-US020152.
 XX

PR 29-JUN-2001; 2001US-0301913P.
 XX (DUPO) DU PONT DE NEMOURS & CO B I.
 PA (PION-) PIONEER HI-BRED INT INC.
 XX Allen SM, Allen WB, Cahoon RE, Ebelbaum S, Famodu OO, Harvell LT,
 PI Jones TJ, Kinney AJ, Klein TM, Li C, Oliveira IC, Sakai H, Shen B,
 XX Tarczynski MC;
 XX WPI; 2003-201509/19.
 DR P-PSDB; ABR40710.
 XX Novel nucleotide fragment encoding polypeptides having receptor-like
 PT protein kinase activity, caleosin-like activity, useful for altering oil
 PT phenotypes in plants such as sunflower, coconut, soybean, wheat and rice.
 XX Claim 18; Page 277-278; 542pp; English.
 PS
 XX The present invention describes an isolated nucleotide fragment (I)
 CC comprising a nucleic acid sequence (NS) chosen from a NS encoding a
 CC polypeptide (PP) having receptor-like protein kinase activity, mitogen
 CC activated protein (MAP)-kinase activity, lipid-like transcription factor
 CC activity, caleosin-like activity, ATP citrate lyase activity, SNF1-like
 CC activity and CLK-like transcription factor activity. Also described: (I)
 CC complement (II) of (I); (2) a chimeric construct (III) comprising (I) or
 CC (II), operably linked to a regulatory sequence; (3) a plant (IV)
 CC comprising (III) in its genome; (4) seeds (V) obtained from (IV); and (5)
 CC oil obtained from (V). (I) or its part can be used in antisense
 CC inhibition or co-suppression in a transformed plant. (III) is useful for
 CC altering the oil phenotype in a plant such as corn, soybean, wheat, rice,
 CC canola, Brassica, sorghum, sunflower or coconut. (III) is also useful for
 CC creating transgenic plants having altered lipid profiles. (I) can also be
 CC used as a hybridisation probe. ACC00626 to ACC00868 and ABR40591 to
 CC ABR40879 represent sequences used in the exemplification of the present
 CC invention
 CC
 XX Sequence 2052 BP; 563 A; 445 C; 481 G; 563 T; 0 U; 0 Other;
 SQ
 Query Match 40.7%; Score 793.4; DB 7; Length 2052;
 Best Local Similarity 72.4%; Pred. No. 7.9e-201;
 Matches 1079; Conservative 0; Mismatches 391; Indels 21; Gaps 3;
 QY 210 CATTAGAACTACACCTGGAGAACTTTAGGTATCGTATCTTGGAAAGTGAAGA 269
 Db 244 CGTTAGGAATTTATCGATTGGCAAGACTCTCGAATTTGGCTCATTCGGGAAGTGAAGA 303
 QY 270 TTGAGAGCATACCTTACTGAGCATAGGCTTCTATTAAGATCATCACTGCCGCAAA 329
 Db 304 TTGGGAGCATATGAGCATGAGCAAGGTGGCAATCAAGATTTCTAACCGCGTAAAA 363
 QY 330 TGAGAAATATGAGAAATGAGAGAAAGCAAGAGATTCAGATTTTGAAGTTGTCA 389
 Db 364 TCAAGGCGATGAGATGAGAGAAAGTTAAAGAGATTTAGATTTAGGTTATTTA 423
 QY 390 TTCAACCCCATATCATTTGGCTTTATGAGGTATATACACCTTACAGATATATATGTTG 449
 Db 424 TGCATTCACATATATTCGCTCTATGAGGTTATAGACACCGGCTGATATTTATGTTG 483
 QY 450 TGATGGAATATTTAGATGATGAGCGAGTTATTTATATCATTTGTGAGAAAGCGATTA 509
 Db 484 TTATGAGATATGTTAAGTGTGGGAAATTTATTTGATTCATTTGTGAAGAAAGTGGCTG 543
 QY 510 AGGAAGATGAAAGCTCGTGAATCTTCCAGAGATCATATCTGGCGTGAATATCTGCATA 569
 Db 544 AAGGAAGAAAGCTCGCGCTTTCTTCCAGATTAATATCGGCTTGAATATTTGCCATA 603
 QY 570 GAAACATGTTGTCACCGTACCTAAAGCGGAAAACTTGTATCTTGATTTCAAGATATA 629
 Db 604 GAAACATGTTGTCACCGTACCTAAAGCGGAAAACTTGTATGATTTCAAGATATA 663
 QY 630 ATGTAATACTTGGCGATTTTGTCTGAGCAATGTCATGATGAGCCATTTTCTGAAGA 689
 Db 664 ATGTAAGATTTGCGATTTTGTGCTTAAGTATGTTATGCGGAGATGTCATTTTCTGAAGA 723

QY 690 CTAGCTGGAGAGTCCGAACTATGCTGCTCCAGAGGTAATATCTGTTAACTATATGCTG 749
 Db 724 CAGTGTGTGTACCCAAATTTATGCTGCTCCAGAGGTAATATCTGTTAACTATATGCTG 783
 QY 750 GACCTGAGTGTGATGATGAGAGTGTGGGGTATCTTTATGCTCTTCTTTGTGAATC 809
 Db 784 GACCTGAGTGTGATGATGAGAGTGTGGGGTATCTTTATGCTCTTCTTTATGCTGCTC 843
 QY 810 TTCCATTTGATGATGAGAGTGTGGGGTATCTTTATGCTCTTCTTTATGCTGCTC 869
 Db 844 TGCATTTGATGATGAGAGTGTGGGGTATCTTTATGCTCTTCTTTATGCTGCTC 903
 QY 870 CACTTCCAGATCATTTGTCTGCTTTGCGCAGAGATTTGATCCACAGATGCTTTGTTG 929
 Db 904 CCGTCCAGCATTTTGTCTGCTTTGCGCAGAGATTTGATCCACAGATGCTTTGTTG 963
 QY 930 AGCTTATGAAAGAGATTCATATTAAGGAAATTTGGAGCATCAATGCTTCAGATTCGCC 989
 Db 964 ATCTTATGAAAGCGATTCATATTAAGGAAATTTGGAGCATCAATGCTTCAGATTCGCC 1023
 QY 990 TTCCAGTATCTTGGAGTGTGCTTCCAGATTCAGACAAAGCAAGCAAGTATGATG 1049
 Db 1024 TCCCGGCTATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1083
 QY 1050 AAGATCACTTCCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1109
 Db 1084 AAGAACTCTCCGTAAGTGTGATGATGATGATGATGATGATGATGATGATGATGATG 1143
 QY 1110 TGTGACAGACATTTCAAAATGAGGCACTGTCATATTTATTTATTTGATGATGATG 1169
 Db 1144 TCCAAAAAAGGCTGCAAAATGAGGCACTGTCATATTTATTTATTTGATGATGATG 1203
 QY 1170 TTAGAGCACTAGTGTGATCTTGGGCGAGATTAATCAAGATCAATGAGACAGAAATTTA 1229
 Db 1204 TCCGTAAACAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1263
 QY 1230 ATCAGCTGGCGTATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1289
 Db 1264 CAACATGCGATCATATGAAAGCAAAAGTTGACAGAGTGGGATGACAGCAATATTTA 1323
 QY 1290 GTGATCTCTATGACAGATGATGATGATGATGATGATGATGATGATGATGATGATG 1349
 Db 1324 TGGAGTCTC---CAGTGGCTTGAAGACCATCTTCCAGCTGAGAGAAATGGGCTCTTG 1380
 QY 1350 GACTCAGTCTGGGCGCAACCTCGTGAATAATGTTGAGTCTTAAAGCACTTCAAG 1409
 Db 1381 GTCTTCACTTCAAGACATTCGAAAGAAATATGTTGAGTCTTAAAGCACTTCAAG 1440
 QY 1410 AATTAAACGTCAAGTGAAGAAAGATGAGCACTTCAAGCGTAAATGAGATGATGATG 1469
 Db 1441 AATTAAATGTTTATGAGAAAGATGAGTCACTATTAATGAGATGAGATGATGATG 1500
 QY 1470 GGTTCCTGAAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1529
 Db 1501 GCTTCTCTGCTCAAAATTCATTAACATATTAATCTCA-----GTGAGGGT 1545
 QY 1530 TCAATGATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1589
 Db 1546 CAAATGAACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1602
 QY 1590 TTTACAAAGCAAGAGCAAGCAAGTACTCTTATGATATGAGAGATTAATGAGCTTCAAG 1649
 Db 1603 TGTACAAAACAAAGAGCAAGAAATTAATCTTCAATTTGCAAGAGTCAAGGAGCCACAG 1662
 QY 1650 TGCCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1700
 Db 1663 TCCCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1713

RESULT 7
 AAAS2772
 ID AAAS2772 standard; cDNA; 2123 BP.

XX AAA52772;
 AC 03-JAN-2001 (first entry)
 XX
 DE Soybean putative catabolite repression protein SNF1 coding sequence #2.
 XX
 KM Soybean; carbon catabolite repression; sucrose non-fermenting protein 1;
 KM SNF1; plant growth; ss.
 XX
 OS Glycine max.
 XX
 FH Key Location/Qualifiers
 FT CDS 123..1667
 FT /*tag= a
 FT /product= "SNF1"
 FT
 PN WO200036115-A2.
 XX
 PD 22-JUN-2000.
 XX
 PF 15-DEC-1999; 99WO-US029824.
 XX
 PR 16-DEC-1998; 98US-0112563P.
 XX
 PA (DUPO) DU PONT DE NEMOURS & CO E I.
 XX
 PI Allen SM, Heppard EP, Sakai H, Weng Z, Helentjaris TG, Macool DJ,
 PI Miao G;
 XX
 DR WPI: 2000-431593/37.
 DR P-PSDB: AAB03420.
 XX
 PT New nucleic acids encoding sucrose non-fermenting 1 (SNF1) proteins
 PT involved in carbon catabolite repression in plants and seeds, useful for
 PT controlling carbon and nitrogen partitioning pathways during plant growth
 PT and development.
 XX
 PS Claim 2; Page 42-43; 59pp; English.
 CC The present sequence is a putative sucrose non-fermenting protein SNF1
 CC coding sequence from the soybean. The sequence was isolated by searching
 CC a pod cDNA library for sequences similar to those known to encode SNF1 in
 CC Arabidopsis thaliana, Cucumis sativus, Glycine max and Oryza sativa. The
 CC protein is involved in carbon catabolite repression, and so the gene and
 CC protein can be used in plants to control the nitrogen and carbon
 CC partitioning pathways during plant growth and development. They can also
 CC be used to alter the accumulation of carbohydrates, lipids and proteins
 CC during plant growth
 CC
 SQ Sequence 2123 BP; 593 A; 395 C; 477 G; 658 T; 0 U; 0 Other;
 Query Match 40.2%; Score 782.6; DB 3; Length 2123;
 Best Local Similarity 71.1%; Pred.No. 6.1e-198;
 Matches 1072; Conservative 0; Mismatches 414; Indels 21; Gaps 2;

Db 409 TGAAGTATGTAAGTCTGAGAGCTTTTCATTAATAGTAAGTAAGTAAGTTCAGG 468
 Qy 513 AAGATGAAGCTCGTCAATCTTCCAGACATCATATTCGCGTCGATATCTGCATGAA 572
 Db 469 AAGATGAAGCTCGTCAATCTTCCAGACATCATATTCGCGTCGATATCTGCATGAA 528
 Qy 573 ACATGATGTCACCGTACCTAAAGCCGGAACCTTACTGATGTCGAATATATG 632
 Db 529 ATATGATGTCATAGAGATTTTGAAGCTGAGATTTACTTTGAGCTCCAAATGTATG 588
 Qy 633 TAAATCTGCGATTTTGTCTGAGCAATGTCATGATGTCATTTCTGAAGACTA 692
 Db 589 TCAAGATTTGCGATTTTGGCTGAGCAATCATAGCTGATGTCATTTCTTAAGAA 648
 Qy 693 GCTGTGGAAGTCGCAATATGCTGCTCAAGATATATCTGTAACTATGCTGAC 752
 Db 649 GTTGTGAAGCCCTTAATGATGAGCTCTGAGGTATCTCTGGGAAATGTATGCTGAC 708
 Qy 753 CTGAGTCGATGATGAGATTTGAGGCTGATTTCTTATGCTCTTGTGGAACCTTC 812
 Db 709 CTGAAGTGAAGTCTGAGCTGTGTGTAATTTATATGCTCTTGTGGAACCTTC 768
 Qy 813 CATTTGATGATGAGATATTTCCCAATCTGTTCAAAAAATTAAGGAGATATCAAC 872
 Db 769 CTTTGTATGATGAAATATTTCCAAATCTCTCAAGAAATTAAGGATTTACATC 828
 Qy 873 TTCAGATCAATTTGCTGCTTTGGCCAGGATTTGATCCACGATCTTGTGTGAGC 932
 Db 829 TTCCAGATCAATTTGCTGCTTTGGCCAGGATTTGATCCACGATCTTGTGTGAGC 888
 Qy 933 CTATGAAGAAATCAATATAGGAAATTTGGAGATCAATGTTCCAAATTCGCTTC 992
 Db 889 CTATGAAGAAATCAATATAGGAAATTTGGAGATCAATGTTCCAAATTCGCTTC 948
 Qy 993 CAGTTACTTGGAGTCTCCACAGATATGACACAAACAAGCCAAATGATGATGAAG 1052
 Db 949 CAGTTACTTGGAGTCTCCACAGATATGACACAAACAAGCCAAATGATGATGAAG 1008
 Qy 1053 ATACACTTCAGATGTTGTTAATATGAGATTTAAACAAGCAATGTGTGATCACTGT 1112
 Db 1009 AGATCTCTCAGAAAGTGTGAAATAGGATTTACAGGAATCAATGTGTGAAATCTTGT 1068
 Qy 1113 GCAAGACATTTCAAAATGAGCAACGTGTCATATTTATTAATGATGAAATGCGTTA 1172
 Db 1069 GGAACAGAAATCAAAATGAGCAACGTGTCATATTTATTAATGATGAAATGCGTTA 1128
 Qy 1173 GAGCACTAGTGTATCTTTGGGAGATTTATCAAGATCAATGACAGAAATTTAAT 1232
 Db 1129 GTGTTCCAGTGTATCTTTGGGAGATTTATCAAGATCAATGACAGAAATTTAAT 1188
 Qy 1233 AGCTGGCGTATCTGAATCATCTAATCTGTTGTCGAGAAATTAATGTCAGAAACATG 1292
 Db 1189 AATATGATCTCAAGTAACTGTTCTCAATGTTGGAACCGCTTCCAGCTCAATG 1248
 Qy 1293 ATCTCATACAGTGTGTCGCGCATATATCTCTGTGAAGAAATGCGCTTGGAC 1352
 Db 1249 AATATCAAGAGTATGATATGAGCAACAGTCTCTGTGAAGAAATGCGCTTGGAC 1308
 Qy 1353 TTCAAGTCTGGGCGCCACCTCGTGAATTAATGTTGAGCTTAAAGCACTCAAGAT 1412
 Db 1309 TTCAAGTCTGGGCGCCACCTCGTGAATTAATGAGTGTCTTAAAGCTTTTGAAGAT 1368
 Qy 1413 TAAACGTCAATGAGAAAGATGGGCACTAACAAGTGAATGCAATGTCAGAGGT 1472
 Db 1369 TAAATGTTTGTGAAGAAATGTCATCAACAAGTGAATGTCAGAGGTGTCAGAG 1428
 Qy 1473 TTCTCTG-----AAGTTATGACAGTTAATGTCAGAGCAACGCTTCTTG 1517
 Db 1429 TTCTCTGTCACCAAGAAAGATGTTAACAATATGTCAGATTAATCAATTAATCTTGGAG 1488
 Qy 1518 GTGACTTACCATCATGATTAATGATGATGCTAATGAGGAGCTACCTACTGTATCAAGT 1577

Db	1489	ATGATTCACACTATTATGAAATGATGCTGTTTCT------ACTTCAAAATGTGGTCAAGT	15412
Oy	1578	TTGAATTCACAGCTTTTACAAGACGAACGACACAGTACTCTTGATATGACGAGAGTTA	1637
Db	1543	TTGAAGTCCAGCTTTTACAAAACCCCGGGAAGAAAGTATCTCGATCTTTCAAAAGGGGTGC	1602
Oy	1638	CTGAGCCCTCAGCTGCTCTTCCTGACCTCTGAGGGGCGCTTCCTTACCAAGCTTAGGGGTTG	1697
Db	1603	AGGGTCCACAGCTTTCTTTTCTTGATCTATGTGCTGCTTTCTTGACACAGCTTGCTGTC	1662
Oy	1698	TATAGTGTG	1704
Db	1663	TCTAGAG	1669
RESULT 8			
ACC00749			
ID	ACC00749	standard; cDNA; 2123 BP.	
XX	AC	ACC00749;	
XX	AC	16-MAY-2003 (first entry)	
DT	XX		
XX	XX	Glycine max oil trait related cDNA sequence SEQ ID NO:247.	
DE	XX		
XX	XX	Plant; oil trait; oil phenotype; altered lipid profile; MAP kinase;	
KM	XX	receptor-like protein kinase; mitogen activated protein kinase; oil;	
KM	XX	lipid-5-like transcription factor caleosin; ATP citrate lyase; SNPL;	
KM	XX	CRC-like transcription factor; antisense inhibition; co-suppression;	
KM	XX	transgenic plant; gene; ss.	
OS	XX		
XX	XX	Glycine max.	
XX	XX		
XX	XX	WO2003002751-A2.	
PD	XX		
XX	XX	09-JAN-2003.	
PF	XX	27-JUN-2002; 2002WO-US020152.	
XX	XX		
PR	XX	29-JUN-2001; 2001US-0301913P.	
XX	XX		
PA	XX	(DUBO) DU PONT DE MEMOURS & CO E I.	
PA	XX	(PION-) PIONEER HI-BRED INT INC.	
PI	XX	Allen SM, Allen WB, Cahoon RE, Epelbaum S, Famodu OO, Harvey IJ;	
PI	XX	Jones TJ, Kinney AJ, Klein TW, Li C, Oliveira IC, Sakai H, Shen B;	
PI	XX	Tarczynski MC;	
DR	XX	WPI; 2003-201509/19.	
DR	XX	P-PSDB; ABR40714.	
PT	XX		
PT	XX	Novel nucleotide fragment encoding polypeptides having receptor-like	
PT	XX	protein kinase activity, caleosin-like activity, useful for altering oil	
PT	XX	phenotypes in plants such as sunflower, coconut, soybean, wheat and rice.	
XX	XX	Claim 18; Page 286-287; 542pp; English.	
PS	XX		
XX	XX	The present invention describes an isolated nucleotide fragment (I)	
CC	XX	comprising a nucleic acid sequence (NS) chosen from a NS encoding a	
CC	XX	polypeptide (PP) having receptor-like protein kinase activity, mitogen	
CC	XX	activated protein (MAP)-kinase activity, lipid-5-like transcription factor	
CC	XX	activity, caleosin-like activity, ATP citrate lyase activity, SNPL-like	
CC	XX	activity and CRC-like transcription factor activity. Also described: (1)	
CC	XX	complement (II) of (1); (2) a chimeric construct (III) comprising (I) or	
CC	XX	(II), operably linked to a regulatory sequence; (3) a plant (IV)	
CC	XX	comprising (III) in its genome; (4) seeds (V) obtained from (IV); and (5)	
CC	XX	oil obtained from (V). (I) or its part can be used in antisense	
CC	XX	inhibition or co-suppression in a transformed plant. (III) is useful for	
CC	XX	altering the oil phenotype in a plant such as corn, soybean, wheat, rice,	
CC	XX	canola, Brassica, sorghum, sunflower or coconut. (III) is also useful for	
CC	XX	creating transgenic plants having altered lipid profiles. (I) can also be	
CC	XX	used as a hybridisation probe. ACC00626 to ACC00868 and ABR40591 to	
CC	XX	ABR40879 represent sequences used in the exemplification of the present	

CC	invention
xx	Sequence 2123 BP; 593 A; 395 C; 477 G; 658 T; 0 U; 0 Other;
50	Query Match 40.2%; Score 782.6; DB 7; Length 2123; Best Local Similarity 71.1%; Pred. No. 6.1e-198; Matches 1072; Conservative 0; Mismatches 414; Indels 21; Gaps 2;
QY	213 TAAGAACTACACCTGGGAAAGACCTTAGTACCGGTACATTGGAAAAGTGAAGTTG 272
DB	169 TACCAATTTAATAATTTGGAAAAACCTCGGATTTGATCTTTTGGCAAGTGAATTTG 228
QY	273 CAGAGCATTAAGCTTACTGACATATGGGTGTGTATAAGATCATCACTGCCGCAATGA 332
DB	229 CAGAACATGTGTACTGTGGCCATTAAGTTGGATCAAGATCTCTTAACGAGCAAGATTA 288
QY	333 GAAATATGGAATGGAAGAGAAACCAAGAGACATTCMAAGATTTGAAGTTGCTTC 392
DB	289 AGAACATGGAATGGAAGAAAGAAAGTGAAGAGAAATCAAAATTTAAGATTGCTCATGC 348
QY	393 ACCCCATATCATTTCCGCTTTATATAGGTCATATCACACCTACAGATATATATGTTGA 452
DB	349 ATCTCATATTATTCGACTTTTATTAAGTCATAGAACTCCAACTGACATATATGTGCA 408
QY	453 TGAATATTTAGTATGCGCAGATTATTTGAATTCATTTGTGAGAAAGCAGATTACAG 512
DB	409 TGGAGTATGTAAGTCTGAGAGAGCTTTTCATTCATAGTAGAAGAGGTAGGTTGCAGG 468
QY	513 AAGATGAAGCTGCGTCGAACTCTTCAGAGAGATCATATCTGCGTCGATTCGCCATGAA 572
DB	469 AAGATGAAGCTGCGTAATTTTGTGAGCAGATACTCTGGGTTGAGTACTGTCAACGSA 528
QY	573 ACATGTTGTCACCGCTGACCTTAAGCCGGAACCTTGTAATTACTGATTCAAAGTATATG 632
DB	529 ATATGTTGTTTCAATAGAGATTGGAAGCTGGAATTTACTTTTGGACTCCAAATGTAATG 588
QY	633 TAAAACCTTGGCGATTTTGGTCTGAGCAATGTCATGATGGCATTTTCTGAAGCTA 692
DB	589 TCAAGATTGCTGATTTTGGCTTGAGCAACATCAAGCGTATGTCACCTTTCTTAAAACAA 648
QY	693 GCTGGGAGTCCGAACTATGCTGCTCCAGAGGTAAATCTGTAATCTATATCTGGAG 752
DB	649 GTTGTGAGAGCCCTAACATATGACACTCTGAGGTTATCTCTGGAAATTTGATGCTGAC 708
QY	753 CTGAGCTGATGTATGAGATGTTGGGGGTGATCTTTATGCTCTTTTGTGAACTCTTC 812
DB	709 CTGAAGTGTGATGTCTGGAGCTGTGTGTAAATTTATATATGCTCTTTTGTGGCACCTTC 768
QY	813 CATTTGATGAGAAATATATCCCAATCTGTTCAAAAAATTAAGGGAGGTATCTACACAC 872
DB	769 CTTTGTGATGAGAAATATATTCCAATCTCTTCAGAAATTAAGGGAGGTATTTACACTC 828
QY	873 TTCCAAATGATTTGCTTGTGGCCAGAGATTTGATCCACAGATCTTTGTTGTGAGC 932
DB	829 TTCCCAATGATCTATACACCGGTCCTGAGATTTGATATCCAGGGATGCTTGTGGTTGACC 888
QY	933 CTATGAAGAGATCACAATTAAGGAAATTTGGAGCATCAATGTTCTCAATTTGCTTC 992
DB	889 CTATGAGAGATACACATATCTTAGATTCGCTCAACCAATGTTCTCAAGCTCGACTTC 948
QY	993 CACGTTACTTGGCAGTGCCTCACACAGATACGACACAAGCCAAATATATTGATGAAG 1052
DB	949 CACGTTATTTAGCTGTGCCACACCAATATACATGCAACAGGCCAAAATGATGATGAG 1008
QY	1053 ATPACATTCGAGATGTTGTATATATGGAATTTAACAGAACCAATGTGTGATCACTGT 1112
DB	1009 AGATCTCTCAGGAAGTGTGAAATTTGGATTTTGACAGAAATCAATTTGTGAATCTCTTG 1068
QY	1113 GCACGAGCTTCAAAATGAGGCACTGTGTGATATTTTACTATTTGGAACAATGGGTTTA 1172
DB	1069 GGAACAGAGATACAAAATGAGGGTACTGTGGGATATCTATTTGTTATTTGACACCAATTC 1128
QY	1173 GAGCAACTAGTGGCTATCTTGGGGCAGATTTATCAAGATCAATGACAGAAATTTAATC 1232

Db 1129 GTGTTTCCAGTGGCTATCTTGAGCTGATGTTCAAGAGACATGATTCGGGTTTATATC 1188
Qy 1233 AGCTGGGCTATCTGATCATCTAGTTCTGGTAGAGAAATTATGTTCCAGAAAGCATG 1292
Db 1189 AATATGCAATTCAGAGAACTTCTCTTCAAGTTGTTGAAACCGGTTCCAGCTACATAGG 1248
Qy 1293 ATCTCATAGAGAGTGTGTGGCCATATATCTCTGTTGAAAGAAATGGCGGCTGGAC 1352
Db 1249 AATATTCAGAGTAGATGAGGCAAGTCCCTGTTGAAAGAAATGGCGGCTGGAC 1308
Qy 1353 TTCACTCGGGCCACCCCTGTAATAATGTTGAGTCTTAAAGCACTTCAAGAT 1412
Db 1309 TTCACTCGGGCCACCCCTGTAATAATGTTGAGTCTTAAAGCTTTCAGAGAT 1368
Qy 1413 TAAACGTACATGAGAGAGAAATGGGCACTTCAAGTGAATGATGATGCCAGGCT 1472
Db 1369 TAAATGTTTGTGAGAGAAATGGTCTCACTCAACATGATGATGATGATGCCAGGCA 1428
Qy 1473 TTCTCTG-----AAGTTATGACAGTTAGATGACAGCAACAGCTTCTTG 1517
Db 1429 TTCTCTGTCACCAAGAGAAATGTTAACTAATGTCATATGATCATTACTTTGAG 1488
Qy 1518 GTGACTTACCATGATGATATGATGATGATGATGATGATGATGATGATGATGATGAT 1577
Db 1489 ATGATTCACATATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1542
Qy 1578 TTGAATTCAGCTTTTACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGT 1637
Db 1543 TTGAAGTACAGCTTTTACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGT 1602
Qy 1638 CTGACCTCAGCT 1697
Db 1603 AGGATTCAGAGCTTTCT 1662
Qy 1698 TATAGT 1704
Db 1663 TCTAGAG 1669

RESULT 9
AAAF62011
ID AAF62011 standard; DNA; 1929 BP.
XX
AC AAF62011;
XX
DT 02-MAY-2001 (first entry)
XX
DE Tomato LesNFI (sucrose nonfermenting yeast homologue) gene.
XX
KW Sucrose non-fermenting; SNF-4; SNF-1; tomato; sugar metabolism; seed;
KW source-sink; fruit; enhanced quality; sugar accumulation; LesNFI;
KW stress resistance; transgenic plant; germination stimulation; ds.
XX
OS Lycopersicon esculentum.
XX
PN W0200107570-A1.
XX
PD 01-FEB-2001.
XX
PF 21-JUL-2000; 2000WO-US019981.
XX
PR 21-JUL-1999; 99US-00359161.
XX
PA (REGC) UNIV CALIFORNIA.
XX
PI Bradford KJ, Peetambar D, Yang H, Cooley M, Downie B, Gee OH;
XX
DR WPI; 2001-168545/17.
XX
PT New sucrose non-fermenting (SNF1) and SNF4 polynucleotides and expression
PT cassettes containing the polynucleotides for modulating source-sink
PT relationships in plants and enhancing yield or quality of harvested plant

PT products.
XX
PS Claim 19; Page 39; 43pp; English.
XX
CC This invention relates to polynucleotide sequences encoding plant sucrose
CC non-fermenting SNF-4 or SNF-1 polypeptides. Specifically included in the
CC invention are tomato LesNFI-4 and LesNFI-1 polynucleotide sequences. A
CC recombinant expression vector comprising SNF-4 or SNF-1 polynucleotide
CC sequences is useful for modulating sugar metabolism in a plant. The
CC recombinant expression cassette comprising the DNA sequence is useful for
CC modulating source-sink relationships in plants and therefore enhances
CC yield or quality of harvested plant products, such as fruit. SNF-4 and
CC SNF-1 DNA can be used to enhance sink activity or starch or lipid
CC accumulation in seeds. Also they can be used to enhance sugar
CC accumulation in fruits. The expression cassettes can also be used to
CC enhance responsiveness to stress conditions in plants. Enhanced
CC expression of SNF1 and SNF4 polynucleotides or polypeptides is used to
CC alter expression of sugar related genes or to enhance resistance to
CC stress. Inhibition of endogenous SNF1 or SNF4 genes modulates the
CC activity of enzymes associated with sugar metabolism. In seeds,
CC inhibition of SNF4 expression can be used to break dormancy and stimulate
CC germination. The present sequence represents the tomato LesNFI-1 gene
XX
SQ Sequence 1929 BP; 546 A; 384 C; 442 G; 557 T; 0 U; 0 Other;
Query Match 40.1%; Score 780.8; DB 4; Length 1929;
Best Local Similarity 71.5%; Pred. No. 1.ee-197;
Matches 1074; Conservative 0; Mismatches 412; Indels 16; Gaps 3;
Qy 212 TTAAGAACTACAACTGGAGAGAACTTATGATCGTACATTTGGAGAAAGTGAAGATT 271
Db 78 TTACGAACTATTAACCTCGGAGAAACCTTGATGATGATGATGATGATGATGATGATGAT 137
Qy 272 GCAAGCATAGCTTACTGACATAGGTTGCTTAAAGATCATCACTGCCGCAATG 331
Db 138 GCTGAACATAGCTTAAACAGGCGCAAAAGTGTCTCAAGATCTTAACTCTCAAAATC 197
Qy 332 AGAAATATGAAATGAG 391
Db 198 AGAAATATGAG 257
Qy 392 CACCCCATATCATTCGGCTTTATGAGAGATATACACACTACAGATATATATGTTG 451
Db 258 CATTCATATTTATACGGCTTTATGAGAGATATAGAGACATCATATATATGTTG 317
Qy 452 ATGAAATATTTATGATGAGAGATATTTGATTAATGTTGAGAGAGAGAGAGAGAGAG 511
Db 318 ATGAGATATGAAATCTGCGAGATTAATTTGATTAATGTTGAGAGAGAGAGAGAGAG 377
Qy 512 GAAGATGAACCTGCTGGAATCTTCCAGAGATCATATGTCGCTCCAAATCTGCCATAGA 571
Db 378 GAGATGAACCTGCTGGAATCTTCCAGAGATCATATGTCGCTCCAAATCTGCCATAGA 437
Qy 572 AACATGTTTCCACCGTGAACCTTAAAGCCGAGAACTTGTACTGTTCAAGATTAAT 631
Db 438 AACATGTTTCCACCGTGAACCTTAAAGCCGAGAACTTGTACTGTTCAAGATTAAT 497
Qy 632 GTAACCTTGGAGATTTGCTGAGCAATGTCATGATGATGATGATGATGATGATGATGAT 691
Db 498 GTAACCTTGGAGATTTGCTGAGCAATGTCATGATGATGATGATGATGATGATGATGAT 557
Qy 692 AGCTGAG 751
Db 558 AGCTGAG 617
Qy 752 CTTGAGTGTATGAG 811
Db 618 CTTGAGTGTATGAG 677
Qy 812 CCAATTGATGAG 871
Db 678 CCGTTGAG 737

QY 872 CTTCCAGTATTTGCTGCTTTGGCCAGGATTTGATCCGCAATGCTGTGTGAG 931
 DB 738 CTGGCCAGCATTTATCAGTCGTGGAGGATTTGATTCGAGGATTTATAGTGAC 797
 QY 932 CTTATGAGAGATCACAATTAGGAAATTCGGAGCATCAATGTTCCAGATTCGCTT 991
 DB 798 CCAATGAGGAAATGACTATTCGAGATTCGCTGCACTTGTGTCAGACCATTTG 857
 QY 992 CCACTTACTTTGGAGTCCCTCCACAGATPACACACAAAGCCAAATGATGATGAA 1051
 DB 858 CCAAGCTATTTGGCTGCTCCACAGATPACACCAAGCAAGAAAGATGATGAA 917
 QY 1052 GATACCTTGAGATGTTGTTAATATGAGATTTAAACAAGACATGTGTGATCACTG 1111
 DB 918 GAGATTTTCAAGAGGTGTTAATGATGGATTTACAGAAACATTTAGATCTTCTT 977
 QY 1112 TGACGACAGCTTCAAAATGAGGCACTGTGCAATTTATTTACTTATGACATCGGTT 1171
 DB 978 CGCAATGAGTTCAAAATGAGGCACTGTGCAATTTATCTGCTCCGACATCGCAT 1037
 QY 1172 AGACCACTGTGCTATCTTTGGGGAGATTTACAGATCAATGACAGGAATTTAAAT 1231
 DB 1038 CGTGTTCACCTGCTATCTTTGAGCTGATTTACAGAGTCCATGAAATGTTACAC 1097
 QY 1232 CAGCTGCGTCATCTGATCATCTAGTTCTGTGACAGGATTTATGTTCCAGAAAGCAT 1291
 DB 1098 CGGATCAATTTATGAAACCGCTGCTTCCCTGTGTGCAAGCTTTCCAGGAATATG 1157
 QY 1292 GATCTCATAGCACTGTGTGCGGCCCATTTATCTGTGAAAGAAATGGGCGCTTGA 1351
 DB 1158 GATATATGACAAAGCTGTGCAAG--ACAGTCCCATTTGAAAGAAATGGGCTCTTGGC 1214
 QY 1352 CTTAGCTGTGGGGCCACCTCGGAAATATGTTGAGGCTTAAAGCACTTCAAGAA 1411
 DB 1215 CTCAGTCTGAGGCACTCCAGTAATATGCTGAAGTTTGAAGCTCTTCAAGAA 1274
 QY 1412 TTAAACGTCAAGTGAAGAAATGGGCACTACACGTGAATGAGATGTGCGCAGG 1471
 DB 1275 CTGAATGATGTGGA--AGATTTGTCAGTATTAACATGAAATGTCATGGCTCTAGC 1333
 QY 1472 TTTCTGAAATTATGACACCTTGATGCCA-----GCAACAGCTTTCTTGT 1519
 DB 1334 TTACCTGTATCATGAGGATGGGTATTAATTCATGATGAGAAATCACTTCTTGA 1393
 QY 1520 GACTCTACATCATGATATGATGATGCTAATGGAGGCTTACCTAGTATCAAGTT 1579
 DB 1394 GATGATTCATCATGATGATGATGAGGCGCCAAAGTTAACAATGTGTCAAGTT 1453
 QY 1580 GAATTCAGCTTTAACAAGCAGAGCAGCAAGTACCTTTAGATATGACAGAGTTACT 1639
 DB 1454 GAATTCAGCTTTAACAAGCAGAGGAGAAAGTACTTGAAGCTTCAAGAGCTTCAAG 1513
 QY 1640 GGACCTCAGCTGCTTCTTGAATCTGTGCGGCTTCTTACCAAGCTTAGGTTCTA 1699
 DB 1514 GGTCCACAAATCTCTTCTGTGATCTGTGCTGCTTCTTGTCTCAGCTTCAAGTACTT 1573
 QY 1700 TA 1701
 DB 1574 TA 1575

RESULT 10

AB212357 standard; DNA; 1539 BP.

AB212357;

21-JAN-2003 (first entry)

Arabidopsis thaliana stress regulated gene SEQ ID NO 162.

Arabidopsis thaliana; plant; gene; stress; transgenic; ds.

XX

OS Arabidopsis thaliana.

PN W0200216655-A2.

XX 28-FEB-2002.

PF 24-AUG-2001; 2001WO-US026685.

XX 24-AUG-2000; 2000US-0227666P.

PR 26-JAN-2001; 2001US-0264647P.

PR 22-JUN-2001; 2001US-0300111P.

XX (SCRI) SCRIPPS RES INST.

PA (SYGN) SYNGENTA PARTICIPATIONS AG.

PI Harper JF, Kreps J, Wang X, Zhu T;

PT WPI; 2002-304127/34.

PS Identifying a stress condition to which a plant cell has been exposed and producing plants with increased tolerance to these abiotic stresses.

XX Claim 144; SEQ ID NO 162; 577bp + Sequence Listing; English.

CC The invention relates to identifying a stress condition to which a plant cell has been exposed, comprising: (a) contacting nucleic acid

CC representative of expressed polynucleotides in the plant cell with an array or probes representative of the plant cell genome; and (b)

CC detecting a profile of expressed polynucleotides in the plant cell

CC characteristic of a stress response. The method is useful in the production of transgenic plants, cells and seeds and in producing plants

CC with increased tolerance to abiotic stress. The present sequence is that of an Arabidopsis thaliana stress regulated gene (AB212196-AB217574) used

CC in methods of the invention. Note: The sequence data for this patent is not represented in the printed specification but is based on sequence

CC information supplied to Derwent by the European Patent Office

XX SQ Sequence 1539 BP; 439 A; 291 C; 369 G; 440 T; 0 U; 0 Other;

QY Query Match 40.1%; Score 780.2; DB 6; Length 1539;

DB Best Local Similarity 70.2%; Pred. No. 2.3e-197; Matches 1046; Conservative 0; Mismatches 443; Indels 0; Gaps 0;

QY 212 TTAAAGAACTACCACTGGGAGAACTTTAGTATCGTACATTTGGAAAGTGAAGATT 271

DB 49 TTACGATTTACAAAGCTTGTATAAAGCTTGAATGGGCTTTGGAGAGTGAATA 108

QY 272 GCAGAGCATTAAGCTTACTGACATAGGGTGTATTAAGTATCAATGCGCCCAATG 331

DB 109 GCAGAGCATTTGTCAAGGCGCATTAAGTTGCTATCAAAATCCTTAATCGTGAAGATC 168

QY 332 AGAAATATGGAATGGAAGAAAGCAAGAAATTCAGATATGAAAGTTGATTCAT 391

DB 169 AAGAACATGGAATGGAAGAAAGTGAAGAGGAGCAATTAAGTTCTACGCTGTTATG 228

QY 392 CACCCCATATCATTCGGCTTTATGAGTCAATPACACACTACAGATATATATGTTG 451

DB 229 CATCTCATATTTATGGCGATATGAGGTATGAGACCAAGTACATTTATGTTG 288

QY 452 ATGGAATATGTAAGTATGCGGAGTATTTGATTAATTTTGAAGAAAGCAATTAAC 511

DB 289 ATGAGATATGCAAGTCTGAGAGAGCTTTGATTAATTTGTAAGAAAGCAATTAACA 348

QY 512 GAAGATGAAGCTGTGGAATCTTCCAGACATCATATCTGGCGTCAATTCGCCATAGA 571

DB 349 GAAGATGAGCTGTGAATCTTTTCCAGATATATATCTGTATGATCTGCCATCT 408

QY 572 AACATGTTGCCACCGTGAAGTAAAGCCGGAATCTTTACTTGAATTAAGTATAT 631

DB 409 AATATGTTTCCATATGAGACCTGAAGCTTGAATTTACTATTTGATGAGGTATAT 468

QY 632 GTAAACTGCGAATTTTGTGTGAGCAATGTCATGATATGAGCCATTTTGAAGACT 691

469 ATTAAGATGCGAGCTTTGGGTTGAGTAATGTATGCGGATGGCTATTTCTAAAGACG 528
QY
692 AGCTGTGGGAGTCCGAATCTATGCTGTCAGAGGTAATATGTGTAACATATATGCTGGA 751
DB
529 AGTTGTGAAGCCCCCACTACGCTGCCGAGGTATATCAAGTAATATATATGCTGGA 588
QY
752 CCTGAGGTCGATGATGAGTGTGGGGTGAATCTTTATGCTCTCTTTGGGAACCTT 811
DB
589 CTTGAAGTAGATGATGAGTGTGGAGTTATATGACCTATATATGCGTACTCTT 648
QY
812 CCATTTGATGATGAGAAATATCCCAATCTGTTCAAAAAAATTAAGGAGGATCTACACA 871
DB
649 CCTTTGATGATGAGAAACATTCACACCTTTTCAAGAAATTAAGGGATTTACACT 708
QY
872 CTTTCAAGTCAATTTGTCTGCTTTGGCCAGGATTTGATCCACGAATGCTTTGTTGAG 931
DB
709 CTTTCAAGTCAATTTATATCATGAGCTAGAGACCTGATCCCAAGATGCTTTATGTTGAC 768
QY
932 CCTATGAGAGAAATCACAAATTAAGGAAATTCGGGAGCTCAATGTTCCAGATTCGCTT 991
DB
769 CCGGTGAAGAGAAATCACCAATTCCTGAGATCCGTCAACCGTTGGTTCCAGACTCATCTC 828
QY
992 CCAGTTACTTGGAGTGCCTCCACAGATTCAGACACAAAGCCAAATGATGATGAA 1051
DB
829 CCTGTTATCTTGTCTGCTCCACCGGATACAGTAGAGCAGGCTAAAAAGATCAATGAG 888
QY
1052 GATACACTTGCAGATGTTGTTAATATGAGATTTAAACAAGAACCTGTGTGATCACTG 1111
DB
889 GAGATAGTTCAAGAAAGTGTATACATGAGATTTATAGAAACAGGTTTGAATCTCTA 948
QY
1112 TGCAGAGACTTCAAAATGAGGCAACTGTTGATATTTACTATTGAGCAATCGGTTT 1171
DB
949 CGCAACGAGAACAAACAGATGCTACTGTTACATCTACTGTTATGAGTAACCGGTTT 1008
QY
1172 AGAGCAACTAGTGTCTATCTTGGGCAAGATTAATCAGAAATCAATGACAGGAATTTAAT 1231
DB
1009 CGTGTTCAGAGTGTCTATCTAGAAATCGAGTTTACGAGGACAAACAGACAGTTCAT 1068
QY
1232 CAGTGGCGTATCTGAATCATCTAGTCTGTGACAGAAATTAATGTTCCAGAGCACT 1291
DB
1069 CCAATGGGCACACCTGAAAGCGGCGCTCACCTGAGCCCTGATTCCTGCAATGTG 1128
QY
1292 GATCCTCATAGCACTGGTTTGGGCAATATTAATCTGTGTAAGAAATGGGCGCTTGA 1351
DB
1129 GATCCTACAGGTTGGGAGCAAGATCACTAGTCCCTGTGTGCAAAATGGGCTTTGGA 1188
QY
1352 CTTGAGTCTCGGGCCCACTCTGTGAATAATGTTGAGTCTTTAAAGCACTTCAAGAA 1411
DB
1189 CTTGAGTCTCATGGGCATCTCTGTGAATCATGATGAGTTTGAAGCTCTTCAAGAA 1248
QY
1412 TTAAAGCTCAGATGAGAGAGAAATGGGCACTACAACTGAATCAGATGGTCCCAAGG 1471
DB
1249 CTCATGTGTGTGAAAGAAATGTGTCATACAACTGAATGTCAATGGGTCTCTGGT 1308
QY
1472 TTTCTGAAGTTATGACAGTTAGATCCAGCAACGCTTCTTGGGACTTACCATC 1531
DB
1309 TTACCTGATGTGCAATATCTATGTCAACATACGCTGCACCTTCAAGATGAATCCAGC 1368
QY
1532 ATGATATGATGATGCTATATGAGAGGCTACTACTGTGATCAAGTTGATTCAGCTT 1591
DB
1369 ATCATTTGAGATGACTGTGCATATCTTCACTGCTGTCAATCAAAATTTGAATTCAGCTA 1428
QY
1592 TACAAGACGAAAGACGACAGTACCTCTTAGATATGACAGAGTTACTGACCTCAGCTG 1651
DB
1429 TACAAGACCCCGGAAAGAAATACTTGTGATATACAGAGTTAAACGGTCCCAAGTTT 1488
QY
1652 CTCTTCCTGACTCTGTGAGGCGCTTCTTACCAAGCTTAGGTTCTAT 1700
DB
1489 CTCTTCTTGATCTATAGCGCGCTTCTTACAGAGCTTCTGTGATCT 1537

ID AAC44825 standard; DNA; 1792 BP.
XX
AC AAC44825;
AC
DT 18-OCT-2000 (first entry)
XX
DE Arabidopsis thaliana DNA fragment SEQ ID NO: 44271.
XX
KM Hybridisation assay; genetic mapping; gene expression control;
KM protein identification; signal transduction pathway; metabolic pathway;
KM promoter; termination sequence; ss.
XX
OS Arabidopsis thaliana.
XX
EN EP1033405-A2.
XX
PD 06-SEP-2000.
XX
PF 25-FEB-2000; 2000BP-00301439.
XX
PR 25-FEB-1999; 99US-0121825P.
PR 05-MAR-1999; 99US-0123180P.
PR 09-MAR-1999; 99US-0123548P.
PR 23-MAR-1999; 99US-0125788P.
PR 25-MAR-1999; 99US-0126264P.
PR 29-MAR-1999; 99US-0126785P.
PR 01-APR-1999; 99US-0127462P.
PR 06-APR-1999; 99US-0128234P.
PR 08-APR-1999; 99US-0128714P.
PR 16-APR-1999; 99US-0129845P.
PR 19-APR-1999; 99US-0130077P.
PR 21-APR-1999; 99US-01300449P.
PR 23-APR-1999; 99US-0130510P.
PR 23-APR-1999; 99US-0130891P.
PR 28-APR-1999; 99US-0131449P.
PR 30-APR-1999; 99US-0132048P.
PR 30-APR-1999; 99US-0132407P.
PR 04-MAY-1999; 99US-0132484P.
PR 05-MAY-1999; 99US-0132485P.
PR 06-MAY-1999; 99US-0132486P.
PR 07-MAY-1999; 99US-0132487P.
PR 07-MAY-1999; 99US-0132863P.
PR 11-MAY-1999; 99US-0134256P.
PR 14-MAY-1999; 99US-0134218P.
PR 14-MAY-1999; 99US-0134219P.
PR 14-MAY-1999; 99US-0134221P.
PR 14-MAY-1999; 99US-0134370P.
PR 18-MAY-1999; 99US-0134768P.
PR 19-MAY-1999; 99US-0134941P.
PR 20-MAY-1999; 99US-0135124P.
PR 21-MAY-1999; 99US-0135353P.
PR 24-MAY-1999; 99US-0135629P.
PR 25-MAY-1999; 99US-0136021P.
PR 27-MAY-1999; 99US-0136392P.
PR 28-MAY-1999; 99US-0136782P.
PR 01-JUN-1999; 99US-0137222P.
PR 03-JUN-1999; 99US-0137528P.
PR 04-JUN-1999; 99US-0137502P.
PR 07-JUN-1999; 99US-0137724P.
PR 08-JUN-1999; 99US-0138094P.
PR 10-JUN-1999; 99US-0138540P.
PR 10-JUN-1999; 99US-0138647P.
PR 14-JUN-1999; 99US-0139119P.
PR 16-JUN-1999; 99US-0139452P.
PR 17-JUN-1999; 99US-0139453P.
PR 18-JUN-1999; 99US-0139454P.
PR 18-JUN-1999; 99US-0139455P.
PR 18-JUN-1999; 99US-0139456P.
PR 18-JUN-1999; 99US-0139457P.
PR 18-JUN-1999; 99US-0139458P.
PR 18-JUN-1999; 99US-0139459P.
PR 18-JUN-1999; 99US-0139460P.


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D 482 CATCCATATATTTCCGAGATATAGGTAATAGACCAAGATGACATTTATGTGTG 541
Q 452 ATGAATATATGTAATGAGAGATTAATTTGATTAATGTTGGAAGAGATTAAG 511
D 542 ATGAGATATGCAAGTCTGGAGAGCTTTGATTAATTTGTTGGAAGAGATTAACA 601
Q 512 GAAGATAGAGCTGCTCAATCTTCAGAGATCATATCTGGCCGCAATATCTGCATAGA 571
D 602 GAAGATAGAGCTGCTCAATCTTTCCAGCAGATTAATCTGTGTAGAGTACTGCATCCT 661
Q 572 AACATGTTGTCAACCGTGAACCTTAAGCCGGAAAACTTTGTTACTGATTCAAAGTATAT 631
D 662 AATATGTTGTCAATAGAGACCTGAAGCTGAATTAATTAATTAATGATTCAGAGTAAAT 721
Q 632 GTAAACTTGGGAGTTTGTGTCTAGAGATCATATGATATGAGCATTTTCTGAAGACT 691
D 722 AATTAAGATGCAAGCTTTGGGTTAGTAATTTATGAGGGAGTGTCAATTTTCAAAACG 781
Q 692 AGCTGGGAGTCCGAGCTATGCTCTCCAGAGGTAATATCTGGTAAACTATATGCTGA 751
D 782 AGTTGTGAAGCCCAACTAGCTGCTCCGAGGTTATATCAGGTAATTAATATGCTGGA 841
Q 752 CTTGAGTCAATATATGAGAGTTGTGGGAGTAATCTTTATGCTCTTGTGTGAACCTTT 811
D 842 CTTGAAGTATGATGATGAGTTGCGGAGTTATATTAATGATGCTATATGCGGTAATCTT 901
Q 812 CCATTTGATGATGAGTAATTTCCCAATCTGTTCAAAAAATTAAGGAGTATCTACCA 871
D 902 CTTTGTATGATGATGAAAAATTTCCCACTTTTCAAGAAAAATTAAGGAGTATTAACCT 961
Q 872 CTTTCAAGTCAATTTGCTGCTTTGCGAGGAGTTTGAATCCCAAGATGCTTGTGTGAG 931
D 962 CTTTCAAGTCAATTTATATCTGAGGCTTAGAGACTGATCCAGAGATGCTTATATGTTGAC 1021
Q 932 CCTATGAAGAGATCAACATTTAGGAAAAATTCGGAGATCAATGTTCCAGATTCGCTT 991
D 1022 CCGGTGAAGAGAAATCAACATTTCCGAGATTCGTCACACCGTTGTTCCAGATCTCATCTC 1081
Q 992 CCACGTTAATTTGGAGAGTCTCCACAGATTCGACACCAACGCAAAATGATGATGA 1051
D 1082 CTTGCTATCTTGTCTCTCTCCACCGGATACAGTATGAGCGCTTAAAGATCAATGAG 1141
Q 1052 GATACACTGAGATGTTGTTAATATGAGATTAACAAGAACATGATGATCACTG 1111
D 1142 GAGATAGTTCAAGAGATGTTTAACAATGAGATTTAATGAACCAAGTTTGGATCTCTA 1201
Q 1112 TGACAGAGATTTCAAAAATGAGGCAACTGTTGATATTAATTAATTAATGAGATG 1171
D 1202 CGCAACAGAAACAAAAAGATGCTACTGTTAATCAATCACTGTTATGATTAACGGTTC 1261
Q 1172 AGAGCAACTGATGCTATCTTTGGGCGAGATTAACAAGATCAATGACAGAAATTTAAT 1231
D 1262 CGTGTTCAGAGTGGCTATCTTGAATCCGAGTTTCAAGAGACAGAGTGTTCACAT 1321
Q 1232 CAGTGGGCTCATGATATCAATCTAGTCTGTACAGGAATTAATGTTCCAGAGAGAGT 1291
D 1322 CTTATGCGCACCTGAGCGGGGCTTACCTTATAGGCCCTGATCTGTCACATGTG 1381
Q 1292 GATCTCATAGCAATGTTTGGCGCATATTAATCTGTGGAAGAAATGGGCGCTTGA 1351
D 1382 GATACACAGCGTGGGAGCAAGATCAAGTCCCTGTGATGAAATGGGCGCTTGA 1441
Q 1352 CTTCACTCTGGGCGCAACCTCTGTAATAATGATGTTTAAAGCACTTCAAGAA 1411
D 1442 CTTCACTCTCATGCGCATCTCCGGAATCAATGATGAAGTTTGAAGCTTCAAGAA 1501
Q 1412 TTAAAGTCAGATGAGAAAGAAATGGGCACTACAAAGGAAATCAGATGGTCCAGGG 1471
D 1502 CTCAATGTGTTGAAAGAAATGTTGCTACACAAATGAATTCAGATGGTCTCGGT 1561
Q 1472 TTTCTGAAGTAAATGACAGTTGATGCGCAACAGCTTTCTTGTGATCTTACCATC 1531
D 1562 TTACCTATGCTGCAATTAATCTATGTCACAAATCAGCTGCACTTCAAGATGATCCAGC 1621
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Q 1532 ATGATATATGATGCTAATGGAGGCTTACTGTGATCAAGTTGAAATCCAGCTT 1591
D 1622 ATCATGAGATATGACTGTGCAATGACTTCAACCACTGTCTATCAAAATTTGAATTCAGCTA 1681
Q 1592 TACAAAGCAAGAGCAACAATGACTTATGATATGAGAGAGTTACTGGACCTCAGCTG 1651
D 1682 TACAAAGCCCGGAAAGAAATGACTTGTGATATACAGAGATTAAACGTCGCGAGTTT 1741
Q 1652 CTCTCTTACCTTCTGTGTGGGCTTCTTACCAAGCTTAGGTTCTAT 1700
D 1742 CTCTTGTGATCTATGCGCGCTTCTTACAGAGCTTGTGTGATCT 1790

RESULT 12
AAL46639 standard; cDNA; 1825 BP.
ID AAL46639;
AC AAL46639;
DT 05-AUG-2002 (first entry)
DE A thaliana AKIN11 coding sequence.
DX
XX AKIN11; pathogen resistance; transgenic; plant; antibacterial; virucide;
KW fungicide; nematocide; gene; ss.
OS Arabidopsis thaliana.
FH Key Location/Qualifiers
FT CDS 1..1539
FT /*tag= a
FT /product= "AKIN11"
XX
XX WO200238780-A2.
XX
XX 16-MAY-2002.
XX
XX 07-NOV-2001; 2001MO-FR003457.
XX
XX 08-NOV-2000; 2000FR-00014354.
XX
XX (INRG ) INRA INST NAT RECH AGRONOMIQUE.
XX (CNRS ) CENT NAT RECH SCI.
XX
XX Roby D, Balague C, Godard F, Lummerzhelm M,
XX WPI: 2002-426954/45.
XX P-PSDB; AAO17663.
XX
XX Inducing or increasing resistance to pathogens in plants e.g. industrial
XX scale flowers and vegetables, by introducing a nucleic acid that encodes
XX the AKIN11 peptide.
XX
XX Claim 2; Page 67; 76pp: French.
XX
XX The present invention relates to the use of a nucleic acid that causes
XX the synthesis of the AKIN11 protein, to induce or increase the resistance
XX to pathogen attack in plants. The nucleic acid and its encoded protein
XX can be used to impart resistance to bacteria, viruses, fungi and
XX nematodes, especially necrotrophic pathogens such as Xanthomonas
XX campestris, in large-scale crops, vegetables and flowers. Probes and
XX primers that hybridise with the AKIN11 gene can be used to detect
XX resistance against pathogens, and antisense sequences can be used to
XX modulate resistance. The present sequence is the AKIN11 cDNA of the
XX invention
XX
XX Sequence 1825 BP; 525 A; 330 C; 409 G; 561 T; 0 U; 0 Other;
```

```
Query Match 40.0%; Score 778.6; DB 6; Length 1825;
Best Local Similarity 70.0%; Pred. No. 6.7e-197;
Matches 1048; Conservative 0; Mismatches 449; Indels 0; Gaps 0;
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QY	212	TTAAGGACCTAACACCTGGGAAAGACCTTACGTAATCGGTACATTTGGAAAGTAAAGTT	271
Db	49	TTACCGAATTAACAAGCTTGGTAAACCTCTTGGAATGGGTCTTTTGGGAAGTAAATA	108
QY	272	GCAGAGCACTAAGCTACTAGCACTATGCGGTGCTATTAAGATCATCACTGCGCGCAATG	331
Db	109	GCAGAGCACTGTTGTTCACAGGGCTAAAGTTGCTATCAAAATCTTAAATCGTCGTAAATC	168
QY	332	AGAAATATGAAATGGAAGAGAAGCAAAAGAGAAATTCAGAAATATTGAAGTTTCATT	391
Db	169	AAGAACATGAGATGGAAGAAAGAAATGAGAGGGAGATTAAAGATTCTACGGTTGTTATG	228
QY	392	CACCCCCATATCATTTCCGCTTTATAGAGTCATATACACCTACAGATATATATGTTGTG	451
Db	229	CATCCTCATATATATTCGGCAGATACAGTAATAGAGACCAAGATGACATTTATGTTGTG	288
QY	452	ATGGAATTGTGAATATATGAGGAGTATTTGATTAATCTGTTGAAAGGAGATTAACAG	511
Db	289	ATGGGTAATGTCMACTCTGGAGAGCTCTTTGATTTATTTGTTGAAAGGAGAGTTTACA	348
QY	512	GAAGATGAAGCTCGTCGAATCTTCCAGAGATCATATCTGCGCTGAATCTGCATAGA	571
Db	349	GAAAGTAGGGCTCGTAATCTTTTCCAGAGAAATATCTGGGTATAGATATCTGCATCGT	408
QY	572	AACATGTTGTTCACCGTCGACTTAAAGCCGGAACCTGTTACTTGATTCAAATATAT	631
Db	409	AATATGGTGTTCATAGAGACCTGAAGCCTGAGATTTACATATGATTTCAGAGTATAT	468
QY	632	GTAACACTGGCGGATTTTGGTCTGAGCAATGTCATGCATGATGGCACTTTCTGAAAGCT	691
Db	469	ATTAAAGATTGCAGACTTTGGTGTGATATGTAATCGGAGATGTCATTTTCTAAAGCG	528
QY	692	AGCTGTGGAGTCCGAACTATGCTGCTCCAGAGTAAATCTGTGTAACCTATATGCTGA	751
Db	529	AGTTGTGAAGCCCAACTAGCGTCTCCGAGGTATATACGATAAATATATATGCTGA	588
QY	752	CCTGAGGTGATGTAATGAGATTGTGGGGTGAATCTTTATGCTCTTCTTTGTGGAATCTT	811
Db	589	CCTGAAGTAGAGTATGAGATTGCCGAGTATATATGTAAGCGCTCTATATATGCGGATCTT	648
QY	812	CCATTGATGATGAAATATATCCCAATCTGTTCAAAAAATTAAAGGAGGTATCTACACA	871
Db	649	CTTTTGTGATGAAACCAATTCCTCAACCTTTTCAGAAAAATTAAAGGAGGTATCTACT	708
QY	872	CTTCCAAAGCTATTTGCTGCTTTGGCCAGGGATTTGATCCCAAGATCTTTGTTGTAG	931
Db	709	CTTCCAAAGCTATTTATCATCTGAGGCTAGAGACTGATCCCAAGAGTCTTATAGTTAC	768
QY	932	CCTATGAAGAGATCACAATTATGGGAAATTCGGGAGCATCAATGTTCCAGATTCGCTT	991
Db	769	CCGGTGAAGACGAATCACCATTCCTGAGATCCGTCAACCCGTTGGTTCACATCTCATCTC	828
QY	992	CCACGTTACTTGGCAGTGCCTCCACCAATACGACACACAACAAGCCAAATATGATGA	1051
Db	829	CCTCGTTATCTTGCTGTCTCTCCACCGGATACGTAAGAGACACTTAAAAAATCAATAG	888
QY	1052	GATACACTTCGAGATGTTGTATATATGGAATTTAACAAGAACATATGTGTGAATCATG	1111
Db	889	GAGATATGTTCAAGAAAGTGTTAACATGGGATTTGATGAACCAAGSTTTTGGAAATCTCTA	948
QY	1112	TGAGACAGACTTCAAAATATAGGCAACTGTTGCAATATTAATCTATTTGACAATCGGTTT	1171
Db	949	CGCAACAGAAACAACAAACGATGCTACTGTATCATCTACCTGTATTTGATACACGGTTC	1008
QY	1172	AGAGCAACTAGTGGCTATCTTTGGGCAATTAATCAAGAAATCAATGGAACAGAAATTAAT	1231
Db	1009	CGTGTTCACAGTGGCTATCTAATATCCAGATTCAGAGACACAAGACAGTGTTCATAT	1068
QY	1232	CAGCTGGCGTCACTGAAATCATCTATCTGTGTAAGAGAAATTAATGTTCCAGAAAGCACT	1291
Db	1069	CCTATATCGCAKACTGAAAGCGGGCCCTTACCTGTATAGCCACTGATATTCCTGCAATGTG	1128
QY	1292	GATCTCATATGACATGTTGTGGCGCAATTAATCTGTTGAAGAAAAATGGCGCTTGA	1351

Db	1129	GATACCTACCGGTTGGGAGCAAGTACACAGTCCCTGTTGATGGAAATGGGGCTTTGGA	1188
Qy	1352	CTTCAGTCTGGGGCCACCCCTCGTGAATATATGTTGAGTCTTAAAGCATTTCAAGAA	1411
Db	1189	CTTCAGTCTACATGGCGCATCTCCGGAATCATGATATMACTTTTGGAAAGCTCTTCAAGAA	1248
Qy	1412	TTAAAGCTCAGATGGAAGAAAGAAATGGGCGATCAACAGTGAATGCAAGTGTGGCCAGGG	1471
Db	1249	CTCAATGTGTTTGGAGAAAGATTTGGTCACTACACATGAAATGTCATGGGTTCTCGGT	1308
Qy	1472	TTTCCCTGAAGTTATGACACGTTAGATGCAGCACAAGCTTTCTTGGTGACTTACCATC	1531
Db	1309	TTAGCTGATGGTCCAGAAATCTATGATGTCACACATCAGCTGCATTCACAGATGATATCCAGC	1368
Qy	1532	ATGATATATGATGATGCTAATGGAGAGCTACCTATCTGTGATTCAGTTGAAATTCACACT	1591
Db	1369	ATCATTTGAGGATGACTGTGCCATACCTTCAACCCACTGTCAATCAATTTGAATTTCACTTA	1428
Qy	1592	TACAAAGACGAAGACGACAAGTACCTTCTTGATATGACAGAGATTTACTGCACTCAGCTG	1651
Db	1429	TACAAAGCCGGGAAGAAGAGTATCTGTGGATATACAGAGATTTAACGGTCGCCAGATTT	1488
Qy	1652	CTCTTCTCTGACTTCTGTGGGGCTTCTCTTACCAAGCTTAGGCTTCTATAGTGTCT	1708
Db	1489	CTCTTCTTGGATCTATAGCGCGCTTCTTTCACAGAGCTTGTGTGATCTGAATGTTT	1545

	RESULT 13
AAI46642	ID AAI46642 standard; cDNA, 1825 BP.
AC	AAL46642;
AD	05-AUG-2002 (first entry)
AE	A thaliana AKIN11 mutant coding sequence.
AF	AKIN11; pathogen resistance; transgenic; plant; antibacterial; virucide;
BG	Fungicide; nematocide; gene; mutant; ss.
CJ	Arabidopsis thaliana.
DH	Key Location/Qualifiers
EK	CDS 1..1539
FT	/tag= a
GQ	/product= "AKIN11"
HU	WO200238780-AZ.
IY	16-MAY-2002.
JL	07-NOV-2001; 2001WO-FR003457.
KP	08-NOV-2000; 2000FR-0004354.
LX	(IRRG) INRA INST NAT RECH AGRONOMIQUE.
MN	(CNRS) CENT NAT RECH SCT.
NF	Roby D, Balague C, Godard F, Lummerzheim M,
OQ	WPI; 2002-426954/45.
PB	P-Psdb; AA017664.
RD	Inducing or increasing resistance to pathogens in plants e.g. industrial
SF	scales flowers and vegetables, by introducing a nucleic acid that encodes
TG	the AKIN11 peptide.
VH	Example 4; Page 72; 76pp; French.
XE	The present invention relates to the use of a nucleic acid that causes
ZD	the synthesis of the AKIN11 protein, to induce or increase the resistance
[blank]	to pathogen attack in plants. The nucleic acid and its encoded protein

CC can be used to impart resistance to bacteria, viruses, fungi and
CC nematodes, especially necrotrophic pathogens such as Xanthomonas
CC campestris, in large-scale crops, vegetables and flowers. Probes and
CC primers that hybridise with the AKIN1 gene can be used to detect
CC resistance against pathogens, and antisense sequences can be used to
CC modulate resistance. The present sequence is a mutant version of the
CC AKIN1 cDNA of the invention

XX
SQ Sequence 1825 BP; 525 A; 329 C; 409 G; 562 T; 0 U; 0 Other;

Query Match 39.9%; Score 777; DB 6; Length 1825;
Best Local Similarity 69.9%; Pred. No. 1.8e-156;

Matches 1047; Conservative 0; Mismatches 450; Indels 0; Gaps 0;

QY 212 TTAAAGAACTTCAACCTGGGAAAGACTTTAGTATCGGTACATTTTGGAAAAGTGAAGATT 271
DB 49 TTACCGAATTAACAAGCTTGTGTAACCTCTGGAAATGGGCTTTTGGGAAAGTGAATA 108
QY 272 GCAGAGCATAGCTTACTGACATAGGGTGTCTATTAAGATCATCACTGCGCCAAATG 331
DB 109 GCAGAGCATGTGTCACAGGCGATAGAGTGTCTATCAAAATCTTAAATCGTCGTAAGTC 168
QY 332 AGAATATGAAATGAGAGAGAAAGCAAGAGATTCAGATATTCAGATTTGATTCATT 391
DB 169 AAGAATCATGAGATGAGAGAGAAAGTGAAGGAGATTAAGATTTCAAGCTTTATG 228
QY 392 CACCCCATATCATTCGGCTTTATGAGTCTATACACACTTACAGATATATATGTTG 451
DB 229 CATCTCATATATATTCGCGAGATAGAGTAAATAGAGCAAGATGACATTTATGTTG 288
QY 452 ATGGAATATGTAATGATAGGCGAGTTATTTGATTAATCATTTGTTGAAAGGAGATTAC 511
DB 289 ATGAGATATGTCAGATCTGAGAGACTTTTGATTAATTTGTTGAAAGGAGATTTACA 348
QY 512 GAAGATGAAGTCTGCGATCTTCACAGATCATATCTGCGATGAGATATCTGCATAGA 571
DB 349 GAAGATGAGGCTGTAACCTTTTCCAGAGATTAATCTGTTGTAAGTACTGCGCATG 408
QY 572 AACATGTTTCCACCGTGAATTAAGCCGAAACTTTGTTACTGTTGATCAAGATATAT 631
DB 409 AATATGTTTCTCAATAGAGACTGAGAGCTGAGAAATTTACTATTTGATTCAGAGTGT 468
QY 632 GTAAACCTTGCGGATTTTGTGCTGCAATGTCAGATGAGTGGCAATTTCTGAAGCT 691
DB 469 ATTAAGATTCAGACTTTGGGTTGATTAATTTGCGGATGCTCATTTTCTAAAGAC 528
QY 692 AGCTGTGAGAGTCCGAATATATGCTGCTCAGAGGTAATATCTGTAATATATATG 751
DB 529 AGTGTGGAAGCCCACTAGCTGCTCCGAGGTTATATCAGGTAATATATATGCTGA 588
QY 752 CTTGAGGTGATGATGAGAGTTGCGGATGATTTTATGCTCTTCTTGTGAACTCTT 811
DB 589 CTTGAGATGATGATGAGAGTTGCGGATGATTAATTTGACGCTTATTAATGCGTACT 648
QY 812 CCAATTGATGATGAGATATTTCCCAATCTGTTCAAAAAATTAGGAGGATATACACA 871
DB 649 CTTTATATGATGAAAAATTTCCCACTTTTCAAGAAATTTAAGGTTGGATTTTACCT 708
QY 872 CTTTCAAGTATTTGCTGCTTTGCGCAGAGATTTGAATCCCAAGATGCTTGTGTTGAG 931
DB 709 CTTTCAAGTATTTATCATCTGAGGCTAGAGACTGATCCCAAGATGCTTATATGTTGAC 768
QY 932 CTTATGAAGATATCAATTTAGGAAATTTGGAGATCATGATTTCCAGATTTGCGCTT 991
DB 769 CCGGTGAAGAAATCACCAATTTCCGAGATCGTCAACACCGTTGTTCCAGATCATCTC 828
QY 992 CCAAGTACTTGGAGCTGCTCCACAGATATGCAACAAAGCAAGCAAAATGATGATGAA 1051
DB 829 CTTGCTATCTTGTGCTCTCCACCGATATGAGTATGAGATTAAGATCAATGAG 888
QY 1052 GATACACTTGAAGATGTTGTTAATATGGAATTTAACAAGAACCAATGTTGATCACTG 1111
DB 889 GAGATATCTCAAGAAATGTTAATCATGGAATTTATGAAACCAAGTTTGGAAATCTCTA 948

QY 1112 TGCAGAGACTTCAAAATGAGGCACTGTTGATATATTTTACATTTGACAAATCGGTT 1171
DB 949 CGCAACGAAACACAAACGATGCTACTGTTACTACTGTTATTTGATTAACCTGTTTC 1008
QY 1172 AGAGCACTATGAGCTATCTTGGGAGAGATTAATCAAGATCAATGACAGAAATTTAAAT 1231
DB 1009 CGTGTTCAGATGGCTATCTAGATCCGAGATTTCAAGAGACCAAGAGATGTTCCAAAT 1068
QY 1232 CAGCTGCGTATCTGATATCATCTAGTCTGTGATACAGAAATTAATGTTCCAGAGACT 1291
DB 1069 CTTATGCGCACACTGAAAGGCGGCTTCACTGTAGGCCACATGATTTCTGACATATG 1128
QY 1292 GATTCCTATGACAGTGTGTTGGCCCAATTAATCTGTTGAAAGAAATGGGCGCTTGA 1351
DB 1129 GATCTACTAGCGGTTGGAGCAAGATCAAGATCCCTGTTATGAAATGGGCTTTGGA 1188
QY 1352 CTTCAAGTCTGCGGCCCACTCTGTAATATGATGAGGCTTTAAAGACATTCAGAA 1411
DB 1189 CTTCAAGTCTATGCGATCTCTGTAATATGATGAGGCTTTGAAAGCTTTCAAGAA 1248
QY 1412 TTAACGTCAGATGAAAGAAATGGGCACTACAGCTGAAATGACAGATGTCGACGG 1471
DB 1249 CTCATATGTTGTTGAAAGATTTGCTACTACAAACATGAAATGTCGATGGTTCGT 1308
QY 1472 TTTCTGAAATTAATGACAGTTTATGATGCGCAGAACAGCTTTCTGTCCTACATC 1531
DB 1309 TTAGCTGATGTCAGAAATTAATGATGTCACAAATCAGCTGACATTCAGAGTAAATCAG 1368
QY 1532 ATGGAATATGATGATGCTTAATGGAGGCTACTACTGTGATCAAGTTGAAATTCAGCTT 1591
DB 1369 ATCATGAGATGATGATGCTGATGATGATGATGATGATGATGATGATGATGATGAT 1428
QY 1592 TACAAAGCAAGACGACAAATCTCTTATGATGATGATGATGATGATGATGATGATGAT 1651
DB 1429 TACAAAGCCCGGAAAGAGATCTGCTGATATACAGAGATTAACGCTCCGAGTTT 1488
QY 1652 CTCCTCTTATGATCTGTCGCGGCTTCTTACCAAGCTTGGGTTGATGATGATGATGAT 1708
DB 1489 CTCCTCTTATGATCTGTCGCGGCTTCTTACCAAGCTTGGGTTGATGATGATGATGAT 1545

RESULT 14
AA171048 standard; cDNA; 1539 BP.
XX
AC AA171048;
DT 18-MAR-2002 (first entry)
XX
DE Arabidopsis SNF-1 protein kinase cDNA.
XX
KM SNF-1; protein kinase; transgenic plant; disease resistance; geminivirus;
XX stress resistance; crop protection; ss.
OS Arabidopsis thaliana.
XX
FH Key
FT CDS
FT 1. 1531
FT Location/Qualifiers
FT /tag= a
FT /transl_except= (pos:187..189, aa:Arg)
FT /transl_except= (pos:223..225, aa:Pro)
FT /transl_except= (pos:292..294, aa:Arg)
FT /transl_except= (pos:610..612, aa:Cys)
FT /transl_except= (pos:718..720, aa:Lys)
FT /transl_except= (pos:751..753, aa:Ala)
FT /transl_except= (pos:778..780, aa:Ala)
FT /transl_except= (pos:922..924, aa:Cly)
FT /transl_except= (pos:1108..1110, aa:His)
FT /transl_except= (pos:1177..1179, aa:Asn)
FT /transl_except= (pos:1183..1185, aa:Lys)
FT /transl_except= (pos:1192..1194, aa:Tyr)
FT /transl_except= (pos:1198..1200, aa:Lys)

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FT      /transl_except= (pos:1264, .1266, aa:Xaa)
FT      /transl_except= (pos:1486, .1488, aa:Pro)
FT      /transl_except= (pos:1492, .1494, aa:Pro)
FT      /note= "Xaa = unknown"
FT      481, .483
FT      /*tag= b
FT      /note= "encodes Asp"
FT      637, .639
FT      /*tag= c
FT      /note= "encodes Cys"

XX      WO200111036-A1.
XX      15-FEB-2001.
XX      07-AUG-2000; 2000MO-US021624.
XX      06-AUG-1999; 99US-0147613P.
XX      (OHIS ) UNIV OHIO STATE RES FOUND.
XX      Bisaro D;
XX      WPI; 2002.113778/15.
XX      P-PSDB; AAM50578.
XX      Transforming plant cell useful to prepare plants with enhanced resistance
XX      to viral pathogen, by transforming cell with exogenous DNA fragment
XX      having polynucleotide encoding SNF-1 protein kinase or its catalytic
XX      domain.
XX      Example 1; Fig 1; 36pp; English.
XX      The presence sequence is that of cDNA encoding SNF-1 protein kinase (see
XX      AAM50578) of Arabidopsis thaliana. SNF-1 is a serine/threonine kinase
XX      that plays a key role in glucose sensing and signal transduction
XX      pathways. It also regulates enzymes involved in lipid metabolism. The SNF
XX      -1 cDNA was obtained in a yeast two-hybrid screen using a truncated
XX      tomato golden mosaic virus TRAP protein as bait and an Arabidopsis cDNA
XX      library as prey. The cDNA was recognised as encoding SNF-1 by virtue of
XX      its homology to yeast and tobacco SNF-1 and by its identity to previously
XX      cloned Arabidopsis SNF-1. A method of preparing plants with enhanced
XX      resistance to infection by plant pathogens involves transforming a plant
XX      cell with a SNF-1 transgene, i.e. a DNA construct encoding SNF-1 protein
XX      kinase or its catalytic domain. The DNA construct may include an
XX      inducible, constitutive or tissue-specific promoter and the plant cell
XX      may be from a monocot or dicot. The transformed plant cell is used to
XX      generate a transgenic plant that shows enhanced resistance to plant
XX      pathogens, particularly viral pathogens (especially geminiviruses), and to
XX      abiotic stresses. In an example, transgenic Nicotiana benthamiana plants
XX      overexpressing Arabidopsis SNF-1 kinase showed increased resistance to
XX      beet curly top virus compared with control plants
XX      Sequence 1539 BP; 441 A; 289 C; 368 G; 439 T; 0 U; 2 Other;
SQ      Query Match      39.9%; Score 776.6; DB 6; Length 1539;
SQ      Best Local Similarity 70.0%; Pred. No. 2,1e-196;
SQ      Matches 1043; Conservative 0; Mismatches 446; Indels 0; Gaps 0;
QY      212 TTAAGAACTTCAACCTGGGAGAACTTTAGTATCGGTACATTGGAAAAAGTGAAGATT 271
QY      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB      49 TTACCGAATTTCAGAGCTTGTGAACCTCTTGGAAATGGGCTCTTTGGGAAAGTGAAATA 108
QY      272 GCAGAGCATAGCTTACTGACATAGGCTTCTTAAGATCATCACTGCCCAATG 331
QY      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB      109 GCAAGAGATGTTGTCCACAGGGCATTAAGTTCCTATCAAAATCCCTAATCGCTGAATC 168
QY      332 AGAATATGGAATGGAAGAAAGAAAGAGAAATTCAGATATTCAGATTGTTGATT 391
QY      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB      169 AAGAATCATGAGATGGAAGAAAGAAAGTGAAGAGAGATTAAGATTTCACGGTCTTATG 228
QY      392 CACCCCATATCATTCGGCTTATAGGCTCATATACACACTACAGATATATATGTTGTG 451
QY      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

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DB      229 CATCTCATATTAATTGCGAGATGAGTGAATAGACCAACAGATGACATTTATGTTG 288
QY      452 ATGAATATTTGTAATGATGATGCGAGATTATTTGATTAATGTTGAGAAAGCAGATTACAG 511
QY      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB      289 ATGAGATATGTCAGAGCTGGAAGAGCTTTGATTAATTTGTTGAGAAAGCAGATTACAA 348
QY      512 GAAGATGAAGCTGTCGAATCTTCCAGAGATCATATTCGGGTCGAATATGCTCCATGA 571
QY      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB      349 GAAGATGAGCTGTAATCTTTTCCAGAGATTAATTCGGTGTAGAGTACCTCCCTGCT 408
QY      572 AACATGTTGTCACCGGTACCTTAAGCCGGAAAACTTGTTCTTATTCATTAAGATTAAT 631
QY      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB      409 AATATGTTGTCATAGAGACCTGAAGCCTGAAGATTTACTATTTGATTTGAGGTTAAT 468
QY      632 GTAAACTTCGCGATTTTGGTCTGAGCAATGTCATGATGAGCCATTTTCTGAAGACT 691
QY      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB      469 ATTAAATTCAGANATTTGGGTGATTAATGTTATCGGGATGATATTTCCTAAAGAG 528
QY      692 AGCTGAGAGTCGGAATCTATGCTGCTCCAGAGTAAATCTGTTAACTATATGCTGA 751
QY      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB      529 AGTTGTGAAGCCCAACTAGACGCTGCCGAGGTATATCAGGTAAATATATGCTGA 588
QY      752 CCTGAGTGCATATAGAGTGTGGGATCTTTATGCTCTCTTTGTTGAACTCTT 811
QY      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB      589 CTGAAGTGAATGATGAGTTACGAGATTATATGACGCTCTATATATGAGTACTCTT 648
QY      812 CCATTTGATGATGAGATATTCCTCAATCTGTTCAAAAAATTAAGGAGGTATCTACAGA 871
QY      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB      649 CTTTGTGATGATGAATAAATCTTCCAACTTTTCAAGAAATTAAGGTGGATTTACACT 708
QY      872 CTTCAAGTCAATTTGCTGCTTTTGCCAGAGATTGATCCACGAATGCTTGTGTTGAG 931
QY      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB      709 CTTCAAGTCAATTTATCATCTGAGGCTAGAGACCTGATCCAAAGATGCTTAATAGTTGAC 768
QY      932 CCTATGAAGATATCAATTAAGGAAATTCGGGACATCAATGTTCCAGATTTGCCCTT 991
QY      769 CCGGTGAAGAAATCAATCTCTGATGATCCGCAACCGTTGTTCCAGACTCATCTC 828
QY      992 CCAGGTTACTTGGCACTGCTCCACAGATATGACACAACAAGCCAAATGATTTGATGA 1051
QY      829 CTCCTGTTATCTGCTCTCTCTCCACCGGATACGTTAGAGAGACTTAAGAAAGTCAATGAG 888
QY      1052 GATPACCTTGAGATGTTGTTAATATGAGATTTAACAAGAACATGTTGTGAATACATG 1111
QY      889 GAAATGTTCAAGAAATGTTTAATGAGGATTTGAATGAACCAAGGTTTGTGAATCTCA 948
QY      1112 TGAAGAGATTTGAANAATGAGCACTGTTGATATTTATTTACTATTTGCAATGAGTTT 1171
QY      949 CGCAACGAAACACAAAACGATGCTACTGTACATTAACCTGTTATTTGATACCGGTTTC 1008
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QY      1009 CGTGTTCGAAGTGGCTATCTAGAAATCCGAGTTTCAGAGAGACAAACAGTGGCTCCAA 1068
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QY      1069 CTAATGCGCACACTGAAGCGGCGCTTCACTGTAGCGCAGATGATTCCTGACATGTCG 1128
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QY      1249 CTCATATGTTGTTGAAAGAAATTTGCTACTCAATCAATGAATGATGATGATGATGATG 1308
QY      1472 TTTCTGAAATTAATGACATGTTAGATGCGAGAAACAGCTTTTGTGTGCTTACATC 1531
QY      1309 TTAGCTGATGCTGAGATTAATATATGTTCAACATCACTGCACTTCAAGATGATCCAGC 1368
DB

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Db      1205 ATCAGGGGTAGGAATGCGGACAGTTCCTGTTGAGAGAAATGGGCCCTTGGGCTTC 1264
QY      1356 AGTCTGGGGCCCAACCTCGTGAATAATGTTGAGGTCTTAAAGCACTCAAGATTAA 1415
Db      1265 AGTCTGAGGCCCAACCGTAATAATGACTGAGGTCTTAAAGCTCTACAAAGATTAA 1324
QY      1416 ACGTCAGATGGAAGAGATGGGCACTACAAAGTGAATGCAGATGGTCCCAAGGGTTTC 1475
Db      1325 ATGTTTGTGGAAGAGATTGACACTATTAACATGAAGTGCAGATGGGTGCTGGCACTG 1384
QY      1476 CT-----GAAATTAAATGACAGTTAATGCCAGCAACAGCTTTCTTGTAAT 1523
Db      1385 CTGGTCATCAATGAAGAAATGATTAACAATTCTCGCATAGTAATCATTACTTTGGAATG 1444
QY      1524 CTACCATCATGATTAATGATGATGCTAATGGAGGCTACCTACTGTGATCAAGTTGAAT 1583
Db      1445 ATTCCGGCATTAATGAAGAAATGAAGCTGTCTTAAG--TCAAATGTGTCAAGTTGAAG 1501
QY      1584 TCCAGCTTTTCAAGACGAGACGACAAGTACTCTTATGATATGACAGAGATTACTGAC 1643
Db      1502 TGCAGCTTTTCAAAACTCGTAGAGAGAAATATCTGCTGATCTTCAAGGGTCCAGGGCC 1561
QY      1644 CTCAGCTGCTCTTCTTGACTTCTGTGCGGCTTCTTACCAAGCTTAAGGTTCTATAGT 1703
Db      1562 CACAGTTTCTTTCTTGATCTGTGCGCTGTGCTTCTTTCACAGCTACGTGTTCTTAGT 1621
QY      1704 G 1704
Db      1622 G 1622

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Search completed: July 9, 2004, 11:38:16
 Job time : 841 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: July 9, 2004, 10:15:14 ; Search time 5184 Seconds
(without alignments)
11221.360 Million cell updates/sec

Title: US-09-857-522B-3
Perfect score: 1948
Sequence: 1 gtcgaccacacgctccgac.....taaaaaaaaaaaaaaaaa 1948

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues
Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
EST:
1: em_estba:*
2: em_estba:*
3: em_estba:*
4: em_estba:*
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6: em_estba:*
7: em_estba:*
8: em_estba:*
9: gb_est1:*
10: gb_est2:*
11: gb_est3:*
12: gb_est4:*
13: gb_est5:*
14: gb_est6:*
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27: em_estfun:*
28: gb_est1:*
29: gb_est2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1948	100.0	1948	11	AY107942 Zea mays
2	734	37.7	904	14	CA272308 SCVPLB208
3	634.6	32.6	690	13	CA076858 SCMCAM110
4	632.6	32.5	784	14	CB620008 OSIRIa040

5	618.6	31.8	674	13	CA077133 SCOCAM104
6	606.8	31.1	650	13	CA125391 SCRLR101
7	604.4	31.0	676	14	CF574471 MCSA115H0
8	598.8	30.7	782	14	CB659701 OSUNEC160
9	593	30.4	956	13	CA149321 SCULR2102
10	592.8	30.4	597	9	AM091047
11	589.2	30.2	863	12	B1950083 HVSWE1001
12	589	30.2	1391	11	AY112453 Zea mays
13	586.8	30.1	850	14	CB632244 OSIRIb10F
14	584.2	30.0	794	13	BQ805778 WHE3570 H
15	578	29.7	829	14	CB621531 OSIRIa07H
16	571.4	29.3	862	14	CK195998 FGAS00444
17	565.4	29.0	704	14	CF307150 HDA1--05-
18	561.2	28.8	682	14	CD232382 CCC1_30 C
19	559.8	28.7	572	9	AM018231 614070C04
20	558	28.6	736	14	CD423640 SNA1_24 D1
21	546	28.0	556	14	CA271697 SCMCUB208
22	545	28.0	733	14	CD938346 OV_109M09
23	532.6	27.3	547	9	A1740056 605070C04
24	531.2	27.3	659	14	CD223772 CCC1_30 C
25	525.8	27.0	641	12	B1292522 BJ293522
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27	522.8	26.8	675	14	CA256476 SCGFL419
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30	510.8	26.2	779	14	CB677208 OSUNEC130
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32	504.6	25.9	951	12	BM084571 PPAP_08_G
33	501.8	25.8	530	10	AM285962 LG1_255_E
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ALIGNMENTS

RESULT 1	AY107942	1948 bp	mRNA	linear	HTC 16-OCT-2002
LOCUS	AY107942				
DEFINITION	Zea mays PC0079657 mRNA sequence.				
ACCESSION	AY107942				
VERSION	AY107942.1	GI:21211020			
KEYWORDS	HTC.				
SOURCE	Zea mays				
ORGANISM	Zea mays				
REFERENCE	Haymer, C.F., Dolan, M., Miao, G.H., Vogel, J.M., Whitsitt, M.S.,				
AUTHORS	Hatney, L.W., Hanafey, M., Morgante, M., and Tinsley, S.V.				
TITLE	Maize Mapping Project/Duront Consensus Sequences for Design of				
JOURNAL	Overgo Probes				
REFERENCE	Unpublished (2002)				
AUTHORS	Coe, E.H.				
JOURNAL	Submitted (25-Apr-2002) Maize Mapping Project, University of				
TITLE	Missouri, Columbia, MO 65211, USA				
COMMENT	If you are interested in getting corresponding physical clones, these are publicly available from zmdb, www.zmdb.laestate.edu; TIGR, www.tigr.org; or NCBI, www.ncbi.nlm.nih.gov. When the source of the				

maize cDNA sequences is either Virginia Walbot, Stanford or Pat Schabale, Iowa State, then clones may be requested from ZmDB: www.zmdb.iastate.edu.

FEATURES

Source

Location/Qualifiers

1..1948
/organism="Zea mays"
/mol_type="mRNA"
/db_xref="MaizeDB:634435"
/db_xref="taxon:4577"
/clone_id="Maize Mapping Project/DuPont Consensus Library"

/note="this sequence is part of a project of EST assemblies resulting from the application of public contigs to seed DuPont contigs; this resource was assembled by DuPont as part of a collaboration for the overgo addressing of BACs in conjunction with the Maize Mapping Project"

ORIGIN

Query Match 100.0%; Score 1948; DB 11; Length 1948;

Best Local Similarity 100.0%; Pred. No. 9.2e-287; Mismatches 0; Indels 0; Gaps 0;

Matches 1948; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 1 GTGACCCACGCGTCCGACCCAAAGCCGGCATACGCCCAAGTCCAAAAGCCCTCTCC 60
Db 1 GTGACCCACGCGTCCGACCCAAAGCCGGCATACGCCCAAGTCCAAAAGCCCTCTCC 60
Qy 61 GCCCGGCTCTCCACTGCTGAGGTGTCTCCCGCTCTCCCGGCACTGCTCTCCCGCC 120
Db 61 GCCCGGCTCTCCACTGCTGAGGTGTCTCCCGCTCTCCCGGCACTGCTCTCCCGCC 120
Qy 121 GCAGGAAGTTGACCTGTCGAGGCGCGGCAACCGGTAAGTAAGATGAAGATGATG 180
Db 121 GCAGGAAGTTGACCTGTCGAGGCGCGGCAACCGGTAAGTAAGATGAAGATGATG 180
Qy 181 AAGTAGTAAGGAGGAGTGGGCACTTCTGAAGCATTAAGAACTACAACTGGAGAACTTT 240
Db 181 AAGTAGTAAGGAGGAGTGGGCACTTCTGAAGCATTAAGAACTACAACTGGAGAACTTT 240
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Db 301 TGCTATTAAGATCATCAATGCGCCCAATGAGAAATATGAAATGGAAGAAAGCAAA 360
Qy 361 GAGGAATTCAGATATTGAAGTTGTTCAATTCACCCCATATCTGCGCTTTATGAGGT 420
Db 361 GAGGAATTCAGATATTGAAGTTGTTCAATTCACCCCATATCTGCGCTTTATGAGGT 420
Qy 421 CATATACACACTCAATATATATGTTGATGATGAATATTTGTAAGTATGCGGATATT 480
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Db 721 AGAGGTAAATCTGATTAATGCTGACCTGAGGTGATGATGAGTGTGGGCT 780
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Db 841 GTTCAAAAAATTAAGGAGATATCTACACTTCCAACTCATTTGCTTTGGCCAG 900
Qy 901 GATTTGATCCCAAGATGCTTGTGAGCTTAAAGAGATACAAATTAAGGAAAT 960
Db 901 GATTTGATCCCAAGATGCTTGTGAGCTTAAAGAGATACAAATTAAGGAAAT 960
Qy 961 TCGGAGCATCAATGCTGAGATGCGCTTCCAGCTTCTTGGAGTGGCTCCACAGA 1020
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Qy 1141 TGATATTTATTTCTATTGGAACAATGCTTAAAGCAATGAGGCTATCTTGGGCA 1200
Db 1141 TGATATTTATTTCTATTGGAACAATGCTTAAAGCAATGAGGCTATCTTGGGCA 1200
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Qy 1261 TGGTACGAGAAATTAATGTTTCAGAAAGCAGTATCTCATAGAGATGTTTGGGCAATA 1320
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Qy 1321 TTATCTGTTGAAGAAATGAGGCGCTTGGACTTCAGTCTCGGCGCCACCTCTGTAAAT 1380
Db 1321 TTATCTGTTGAAGAAATGAGGCGCTTGGACTTCAGTCTCGGCGCCACCTCTGTAAAT 1380
Qy 1381 AATGTTGAGGCTTTAAAGCACTTCAAGATTTAAAGTCAAGTGAAGAGATGGCA 1440
Db 1381 AATGTTGAGGCTTTAAAGCACTTCAAGATTTAAAGTCAAGTGAAGAGATGGCA 1440
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Qy 1561 ACCTACTGATCAAGATTTGAATTCAGCTTTTCAAGACGAGAGCAAGTACTCTTT 1620
Db 1561 ACCTACTGATCAAGATTTGAATTCAGCTTTTCAAGACGAGAGCAAGTACTCTTT 1620
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Qy 1801 TGACTGCTCTTGTGAGGCGTAAAGTCAATGATATCTTAGTTAGTATTTTCTG 1860
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Dd	1861	TCTTAATATTGTCGTCTGCTAGTGATGGTTCATTTTTGAACATAAAGCATTAGCAATPA	1920
Oy	1921	AAAAAGACTAAAAAAA	1948
Dd	1921	AAAAAGACTAAAAAAA	1948
RESULT 2			
CA272308		904 bp	mRNA linear EST 26-SEP-2003
LOCUS			
DEFINITION	SCVPLB2089A09.g LB2 Saccharum officinarum cDNA clone SCVPLB2089A09		
ACCESSION	CA272308		
VERSION	CA272308.1		
KEYWORDS	EST.		
SOURCE	Saccharum officinarum		
ORGANISM	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Sacchara;		
REFERENCE	1 (bases 1 to 904)		
AUTHORS	Vettore,A.L., da Silva,F.R., Kemper,E.L. and Arruda,P.		
TITLE	The libraries that made SUCESr		
JOURNAL	Genet. Mol. Biol. 24 (1-4), 1-7 (2001)		
COMMENT	Contact: Arruda P Centro de Biologia Molecular e Engenharia Genetica Universidade Estadual de Campinas Caixa Postal 6010, 13083-970, Campinas SP, Brazil Tel.: 55 19 3788 1137 Fax: 55 19 3788 1089 Email: parnada@unicamp.br Clone distribution: clone distribution information can be found through the Brazilian Clone Collection Center (BCCC) at http://www.bcccenter.fcav.unesp.br Plate: 089 row: A column: 09 Seq primer: T7 Promoter Primer. Location/Qualifiers 1..904 /organism="Saccharum officinarum" /mol_type="mRNA" /db_xref="taxon:4547" /clone="SCVPLB2089A09" /lab_host="DH10B" /clone_id="LB2" /note="Organ: lateral buds from plants adult plants growing in greenhouse; Vector: pSport1; Site 1: SalI; Site 2: NotI; An unidirectional cDNA library generated from [lateral buds from plants adult plants growing in greenhouse]. cDNA was prepared from polyA+ mRNA using Superscript Plasmid System Kit (Invitrogen). The double-strand cDNAs were fractionated in a sepharose CL-2B 40cm-columns and fragments sizing between 0.8 and 1.5 kb were directionally cloned into the vector. Details of each source of RNA and library construction can be obtained at http://sucest.lad.ic.unicamp.br/public"		
FEATURES			
SOURCE			
Query Match	37.7%; Score 734; DB 14; Length 904;		
Best Local Similarity	91.2%; Pred. No. 3,4e-102;		
Matches 812; Conservative	0; Mismatches 75; Indels 3; Gaps 3;		
Oy	392	CACCCCATATCATTTGGCTTTATGAGTCAATATACACCTAACGATATATATGTTGTG	451
Dd	4	CACCCCATATCATTCGGCTTTATGAGTCAATATACACCAACAAGATATATATGTTGTG	63
Oy	452	ATGGAATTTTAAAGTATGCGAGTATATTTAATACATTTGTTGAGAAAGCAGATTACAG	511
Dd	64	ATGGAATTTTGGAGTATGCGAGTATTTTATTAATCATTTGTTGAGAAAGCAGATTACTA	123
Oy	512	GAAAGTAGAGTCGTGCAATCTTCACAGACATCATATCTGGCGTTCGAATATGCCATAGA	571

Accession	Gene	Protein	Accession	Gene	Protein
Db	124	GAAATGAGGCTCCGCCGATCTTCACAGATCATCTGTGTGCAATATGCGCATRGA	183		
Qy	572	AACATGGTTGTCACCGTGACCTTAAGCCGGAAACTGTGTACTGTATTCAGAGTAAAT	631		
Db	184	AACATGGTTGTCACCGTGACCTTAAGCCGGAAACTGTGTACTGTATTCAGAGTAAAT	243		
Qy	632	GTAAACCTTGGCGGATTTTGGTCTGACGATGTCTATGATGATGGCCATTTTCTGAAGACT	691		
Db	244	GTAAACCTTGGCGGATTTTGGTCTGACGATGTCTATGATGATGGCCATTTTCTGAAGACT	303		
Qy	692	AGCTGTGGAGTCCGAACTATGCTGCTCCAGGGTAAATCTGTGTAACCTATATGCTGGA	751		
Db	304	AGCTGTGGAGTCCGAACTATGCTGCTCCAGGGTAAATCTGTGTAACCTATATGCTGGA	363		
Qy	752	CCTGAGGTCGATGTATGAGAGTTTGGGGGTGATTTTATGCTCTTCTTTGTGGAACCTTT	811		
Db	364	CCTGAGGTCGATGTATGAGAGTTTGGGGGTGATTTTATGCTCTTCTTTGTGGAACCTTT	423		
Qy	812	CCATTGTGATGATGAGAAATATTTCCCAATCTGTTCAAAAAATTTAAGGAGGTATCTACACA	871		
Db	424	CCATTGTGATGATGAGAAATATTTCCCAATCTGTTCAAAAAATTTAAGGAGGTATCTACACA	483		
Qy	872	CTTCCAGTCAATTGTCTGCTTTGGCCAGGAGATTGATCCAGAACTGTGTGTGTGAG	931		
Db	484	CTTCCAGTCAATTGTCTGCTTTGGCCAGGAGATTGATCCAGAACTGTGTGTGTGAG	543		
Qy	932	CCTATGGAAGAGATACAAATTAGGGAATTTCCGAGAGATCAATGGTTCAGATTGCGCTT	991		
Db	544	CCTATGGAAGAGATACAAATTAGGGAATTTCCGAGAGATCAATGGTTCAGATTGCGCTT	603		
Qy	992	CCACGTTATCTTGGCAGTGCCCTCCACAGATACGACACACACAGCCAAATGATGTATGAA	1051		
Db	604	TCGTGTACTTGGCAGTGCCCTCCACAGATACGACACACACAGCCAAATGATGTATGAA	663		
Qy	1052	GATACACTTGGAGATGTGTTTAATATGAGATTTTAACAAGAACCAATGTGTGATCATCTG	1111		
Db	664	GATACACTTGGAGATGTGTTTAATATGAGATTTTAACAAGAACCAATGTGTGATCATCTG	720		
Qy	1112	TGCAACGAGACTTCAAAATGAGGCAACTGTGTCATATTAATTAATTAATGACAAATCGCTT	1171		
Db	721	TGCAACGAGACTTCAAAATGAGGCAACTGTGTCATATTAATTAATTAATGACAAATCGCTT	780		
Qy	1172	AGAGCAACTAGATGGCTATCTTGGGGCAGATTAATCAAGATCAATGACAGAAATTTAAAT	1231		
Db	781	AGAGCAACTAGATGGCTATCTTGGGGCAGATTAATCAAGATCAATGACAGAAATTTAAAT	840		
Qy	1232	CAGCTGGCGTCATCTGATCATCTTAATGTTCTGTGTCAGAGAAATTAATGTTCC	1281		
Db	841	TTACTGTGGCGGCGGCAATTAATTAATTTTGGGCCAAGAAATTTTTC	890		

Db 181 GAAGATGAGCTGCCGCAATCTTCACAGCAATTATCTGGGGTAGAATACTGCCACAGA 240
Qy 572 AACATGTTGTCACCGTACCTTAAGCCGGAACCTGTTACTTGAATCAAGTATAT 631
Db 241 AACATGTTGTCACCGTACCTTAAGCCGGAACCTGTTACTTGAATCAAGTATAT 300
Qy 632 GTAAATCTGGGGATTTTGTCTGAGCAATGTCATGATGATGAGCAATTTCTGAAGACT 691
Db 301 GTAAAGCTGCTGCTTGTGTTAGTACCTCAATGATGATGAGCAATTTCTGAAGCA 360
Qy 692 AGCTGTGGAGTCCGAATATATGCTGCTCAGAGGTAATATCTGTTAACTATATCTGGA 751
Db 361 AGCTGTGGAGTCCGAATATATGCTGCTCAGAGGTAATATCTGTTAACTATATCTGGA 420
Qy 752 CTTGAGTGCATGTATGAGAGTTGGGGTATCTTTATGCTCTTCTTGTGAACTCTT 811
Db 421 CTTGAGTGCATGTATGAGAGTTGGGGTATCTTTATGCTCTTCTTGTGAACTCTT 480
Qy 812 CCATTGATGATGAGATATCTCCCAATCTGTTCAAAAAATTAAGGAGGATCTACACA 871
Db 481 CCATTGATGATGAGATATCTCCCAATCTGTTCAAAAAATTAAGGAGGATCTACACT 540
Qy 872 CTTCCAGTCAATTTGCTGCTGCTTGGCCAGGATTTGATCCCAAGATGCTTGTGAG 931
Db 541 CTTCCAGTCAATTTGCTGCTGCTTGGCCAGGATTTGATCCCAAGATGCTTGTGAG 600
Qy 932 CTTATGAGAGATCAATTAAGGAAATTCGGAGCATCAATGCTTCAGATTCGCTT 991
Db 601 CCAATGAGAGATCAATTAAGGAAATTCGGAGCATCAATGCTTCAGATTCGCTT 660
Qy 992 CCAGTCAATTTGCTGCTGCTTGGCCAGGATTTGATCCCAAGATGCTTGTGAG 1051
Db 661 CTTGATCAATTTGCTGCTGCTTGGCCAGGATTTGATCCCAAGATGCTTGTGAG 720
Qy 1052 GATACACTTGCAGATGTTGTTAATGAGATTTAAACAAGAACATGCTGTGATCACTG 1111
Db 721 GATACACTTGCAGATGTTGTTAATGAGATTTAAACAAGAACATGCTGTGATCACTG 780
Qy 1112 TGCA 1115
Db 781 CGCA 784

RESULT 5
CA077133
LOCUS
DEFINITION
SCGAM1048C02.g AM1 Saccharum officinarum cDNA clone SCGAM1048C02
5', mRNA sequence.
CA077133 674 bp mRNA linear EST 23-SEP-2003
CA077133.1 GI:34929405
VERSION
KEYWORDS
SOURCE
ORGANISM
Saccharum officinarum
Saccharum officinarum
Bkaryota: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Saccharum.
1 (bases 1 to 674)
Vettore: A.L., da Silva, F.R., Kemper, E.L. and Arruda, P.
The libraries that made SUCEST
Genet. Mol. Biol. 24 (1-4), 1-7 (2001)
Contact: Arruda, P
Centro de Biologia Molecular e Engenharia Genetica
Universidade Estadual de Campinas
Caixa Postal 6010, 13083-970, Campinas SP, Brazil
Tel: 55 19 3788 1137
Fax: 55 19 3788 1089
Email: parruda@unicamp.br
Clone distribution: clone distribution information can be found
through the Brazilian Clone Collection Center (BCCC) at
http://www.bcccenter.fcav.unesp.br
Plate: 048 row: C column: 02
Seq primer: T7 Promoter Primer.

FEATURES
source
Location/Qualifiers
1..674
/organism="Saccharum officinarum"
/mol_type="mRNA"
/db_xref="taxon:4547"
/clone="SCGAM1048C02"
/lab_host="DH10B"
/clone_1lb="AM1"
/note="Organ: Apical meristem and tissues surrounding of
mature plants; Vector: pSport1; Site 1: SalI; Site 2:
NotI; An unidirectional cDNA library generated from
[Apical meristem and tissues surrounding of mature
plants]. cDNA was prepared from polyA+ mRNA using
Superscript Plasmid System Kit (Invitrogen). The
double-strand cDNAs were fractionated in a sepharose
CL-2B 40cm-columns and fragments sizing between 0.8 and
1.5 Kb were directionally cloned into the vector. Details
of each source of RNA and library construction can be
obtained at <http://sucest.lad.ic.unicamp.br/public>"

ORIGIN
Query Match 31.8%; Score 618.6; DB 13; Length 674;
Best Local Similarity 96.3%; Pred. No. 1.4e-84;
Matches 633; Conservative 0; Mismatches 24; Indels 0; Gaps 0;
Qy 899 AGGATTTGATCCCAAGATGCTGTTGTTGAGCTATGAGAGATCAAGATTTAGGGA 958
Db 1 AGGATTTGATCCCAAGATGCTGTTGTTGAGCTATGAGAGATCAAGATTTAGGGA 60
Qy 959 ATTGCGAGCATCAATGCTTCCAGATTCGCTTCCAGTATCTTGGAGTGCCTCCACA 1018
Db 61 ATTGCGAGCATCAATGCTTCCAGATTCGCTTCCAGTATCTTGGAGTGCCTCCACA 120
Qy 1019 GATACGACACACAGCAAGCCAAATGATGATGAGATCACTTGGAGTGTGTTATATG 1078
Db 121 GACACGACACAGCAAGCCAAATGATGATGAGATCACTTGGAGTGTGTTATATG 180
Qy 1079 GATTTTAAACAAGACCAATGTTGTTGATCACTGTCAGAGACTTCAAAATGAGCACT 1138
Db 181 GATTTTAAACAAGACCAATGTTGTTGATCACTGTCAGAGACTTCAAAATGAGCACT 240
Qy 1139 GTTGATATATTTACTATGATGACAATCGCTTTAGAGCACTAGTGCTATCTTGGGCA 1198
Db 241 GTTGATATATTTACTATGATGACAATCGCTTTAGAGCACTAGTGCTATCTTGGGCA 300
Qy 1199 GATTATCAAGATCAATGACAGAGATTTAATCACTGCGCTCATGATCATCTAGT 1258
Db 301 GATTATCAAGATCAATGACAGAGATTTAATCACTGCGCTCATGATCATCTAGT 360
Qy 1259 TCTGTGTCAGAGAAATTAATGTTCCAGAGAGAGATCTCATAGCACTGTTGGCGGCA 1318
Db 361 TCTGTGTCAGAGAAATTAATGTTCCAGAGAGAGATCTCATAGCACTGTTGGCGGCA 420
Qy 1319 TATTTATCTGTTAAAGAAATGAGGCGCTTGGACTTCAGTCTGCGGCCACCTCGTGA 1378
Db 421 CATTTATCTGTTAAAGAAATGAGGCGCTTGGACTTCAGTCTGCGGCCACCTCGTGA 480
Qy 1379 ATTAATGTTGAGGCTTTAAAGCACTTCAAGAAATTAACCTCAAGTGAAGAAATGGG 1438
Db 481 ATTAATGTTGAGGCTTTAAAGCACTTCAAGAAATTAACCTCAAGTGAAGAAATGGG 540
Qy 1439 CACTACAACTGAAATGCAATGCTGCGCGGCTTCCAGTGAATGACAGTTAGAT 1498
Db 541 CACTACAACTGAAATGCAATGCTGCGCGGCTTCCAGTGAATGACAGTTAGAT 600
Qy 1499 GCCAGCAACGCTTTCTTGTGACTCAACCATGATGATGATGATGATGATGATGATG 1555
Db 601 GCCAGCAACGCTTTCTTGTGACTCAACCATGATGATGATGATGATGATGATGATG 657

RESULT 6
CA125391
LOCUS
CA125391 650 bp mRNA linear EST 24-SEP-2003

DEFINITION SCRLR1016D04.g LRI Saccharum officinarum cDNA clone SCRLR1016D04
5', mRNA sequence.
ACCESSION CA125391
VERSION CA125391.1 GI:35003253
KEYWORDS EST.
SOURCE Saccharum officinarum
ORGANISM Saccharum officinarum
Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Saccharum.
REFERENCE 1 (bases 1 to 650)
Vettore, A.L., da Silva, F.R., Kemper, E.L. and Arruda, P.
The libraries that made SUCEST
Genet. Mol. Biol. 24 (1-4), 1-7 (2001)
Contact: Arruda, P
Centro de Biologia Molecular e Engenharia Genetica
Universidade Estadual de Campinas
Caixa Postal 6010, 13083-970, Campinas SP, Brazil
Tel: 55 19 3788 1137
Fax: 55 19 3788 1089
Email: parruda@unicamp.br
Clone distribution: clone distribution information can be found
through the Brazilian Clone Collection Center (BCCC) at
http://www.bcccenter.fcap.unesp.br
Plate: 016 row: D column: 04
Seq primer: T7 Promoter Primer.
Location/Qualifiers
1..650
/organism="Saccharum officinarum"
/mol_type="mRNA"
/db_xref="taxon:4547"
/clone="SCRLR1016D04"
/lab_host="DH10B"
/clone_lib="LRI"
/note="Organ: Leaf roll from field grown adult plants
(large insert library); Vector: pSPORT1; Site 1: Sali;
Site 2: NotI; An unidirectional cDNA library generated
from leaf roll from field grown adult plants (large
insert library). cDNA was prepared from poly(A+ mRNA
using Superscript Plasmid System kit (Invitrogen). The
double-strand cDNAs were fractionated in a sepharose
CL-2B 40cm-columns and fragments sizing between 0.8 and
1.5 Kb were directionally cloned into the vector. Details
of each source of RNA and library construction can be
obtained at http://sucest.lad.ic.unicamp.br/public"

ORIGIN

Query Match 31.1%; Score 606.8; DB 13; Length 650;
Best Local Similarity 95.8%; Pred. No. 8.6e-83;
Matches 623; Conservative 0; Mismatches 27; Indels 0; Gaps 0;

QY 901 GGATTATATCCAGAGATGCTGTGTTGAGCCATGAAGATCAATTTGGGGAAT 960
DB 1 GGATTATATCCAGAGATGCTGTGTTGAGCCATGAAGATCAATTTGGGGAAT 60
QY 961 TCGGAGACATCAATGTTCCAGATTCGCTTCCAGTTACTTGGCAGTCCACCGA 1020
DB 61 TCGGAGACATCAATGTTCCAGATTCGCTTCCAGTTACTTGGCAGTCCACCGA 120
QY 1021 TAGGACACAAACAGCCAAATGATTTGAATGAATACCTTGAGATGTTGTAATATG 1080
DB 121 CACGACACAGCAAGCCAAATGATTTGAATGAATACCTTGAGATGTTGTAATATG 180
QY 1081 ATTAAACAAGAACATGCTGTGATGATCACTGTGAGAGAGACTTAAATAGAGCAACTGT 1140
DB 181 ATTAAACAAGAACATGCTGTGATGATCACTGTGAGAGAGACTTAAATAGAGCAACTGT 240
QY 1141 TGCATATTAATTAATTTAGCAATCGTTTGAAGCAACTAGTGTATCTTTGGGGGAGA 1200
DB 241 TGCATATTAATTAATTTAGCAATCGTTTGAAGCAACTAGTGTATCTTTGGGGGAGA 300
QY 1201 TTATCAAGATCAATGAGACAGAAATTTAATCACTGCGCTCATCTGAATCATCTAGTTC 1260

DB 301 TTATCAAGATCAATGAGACAGAAATTTAATCACTGCGCTCATCTGAATCATCTAGTTC 360
QY 1261 TGGTACAGAAATTAATGTTCCAGAGACAGTATCTCTAATGACAGTGTGGGCGCATA 1320
DB 361 TGGTACAGAAATTAATGTTCCAGAGACAGTATCTCTAATGACAGTGTGGGCGCACA 420
QY 1321 TTATCTGTTGAAAAGAAATGGGCGCTTGACTTCAGTCTCGGGCCACCTCTGTAAT 1380
DB 421 TTATCTGTTGAAAAGAAATGGGCGCTTGACTTCAGTCTCGGGCCACCTCTGTAAT 480
QY 1381 AATGCTTGAGCTTTTAAAGACATTTCAAGATTAACCTGATGTAAGAAAGAAATGGGCA 1440
DB 481 AATGATTTAGCTTTTAAAGACATTTAAGATTTAAATGTCAGCTGGAAGAAAGATGGCA 540
QY 1441 CTACAACGTGAATGAGATGAGTGGCCAGGCTTCCGAAATTAATGACAGTTAGATGC 1500
DB 541 CTACAACGTGAATGAGATGAGTGGCCAGGCTTCCGAAATTAATGACAGTGTAGATGC 600
QY 1501 CAGCAACAGCTTCTTGCTGACTCTACATCATGATGATGATGATGCTTA 1550
DB 601 CAGCAACAGCTTCTTGCTGACTCTACATCATGATGATGATGATGCTTA 650

RESULT 7
CF574471 676 bp mRNA linear EST 24-SEP-2003
LOCUS MCSA115H01 Maturing Sugarcane Stem Lambda ZIPLOX Library (MCS)
DEFINITION Saccharum sp. cDNA clone MCSA107E09 5' similar to protein kinase,
mRNA sequence.
CF574471
CF574471
VERSION CF574471.1 GI:35205797
KEYWORDS EST.
SOURCE Saccharum sp.
ORGANISM Saccharum sp.
Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Saccharum.
REFERENCE 1 (bases 1 to 676)
Casu, R.E., Dimmock, C.M., Chapman, S.C., Grof, C.P.L., McIntyre, C.L.,
Bonnett, G.D. and Manners, J.M.
Identification of differentially expressed transcripts from
maturing stem of sugarcane by in silico analysis of stem expressed
sequence tags and gene expression profiling
Unpublished (2003)
JOURNAL
COMMENT
Contact: Rosanne E. Casu
Commonwealth Scientific and Industrial Research Organisation
Division of Plant Industry
Long Pocket Laboratories, 120 Meiers Rd, Indooroopilly, QLD, 4068,
Australia
Tel: 61 7 3214 2364
Fax: 61 7 3214 2881
Email: Rosanne.Casu@csiro.au
Bases 1-17 (GTGACCCAGCCCTCG): Sali adapter
Seq primer: T7 sequencing primer
High quality sequence stop: 676.
Location/Qualifiers
1..676
/organism="Saccharum sp."
/mol_type="mRNA"
/cultivar="Q117"
/db_xref="taxon:15819"
/clone="MCSA107E09"
/dev_stage="12 months post-planting"
/lab_host="Y1090 (ZI)"
/clone_lib="Maturing Sugarcane Stem Lambda ZIPLOX Library
(MCS)"
/note="Organ: internodes 6-11; Vector: Lambda ZIPLOX;
Site 1: Sali; Site 2: NotI; mRNA was prepared from
internodes 6-11 of the sugarcane variety Q117. cDNA was
synthesised from a NotI-oligo primer/adaptor using the
manufacture protocols (Life Technologies) and then
ligated to a Sali adapter to facilitate directional
cloning. The cDNA was cloned into the Sali and NotI sites

ORIGIN

of the lambda ZIPLOX phage vector (Life Technologies).
Constructed by Rosanne E. Casu."

Query Match 31.0%; Score 604.4; DB 14; Length 676;
Best Local Similarity 96.6%; Pred. No. 2e-82;
Matches 628; Conservative 0; Mismatches 21; Indels 1; Gaps 1;

QY 821 GATGAGATATTTCCCAATCTGTTCAAAAAATTAAAGGAGGTATCTACACCTCCAGT 880
DB 28 GGTGAGAAATTTCCCACTGTTCAAAAAATTAAAGGAGGTATCTACACCTCCAGT 87
QY 881 CATTTGCTGCTTGGCCAGGATTTGATCCCAAGAAATGCTTTGTTGAGCTTATGAG 940
DB 88 CATTTATCTGCTTTGGCTAGGGAATTTGATCCCAAGAAATGCTTTGTTGAGCTTATGAG 147
QY 941 AGAATCAAAATTAGGAAATTTGGGAGCATCAATGTTCCAGATTCGGCTTCCAGTTAC 1000
DB 148 AGAATCAAAATTCGGGAAATTCGGGAGCATCAATGTTCCAGATTCGGCTTCCAGTTAC 206
QY 1001 TTGGCAATGCTCCACAGATACAGACAAACCAAAATGATTAAGATTAATCACTT 1060
DB 207 TTGGCAATGCTCCACAGACAGACAGACAGACAGACAGACAGACAGACAGACAGACAG 266
QY 1061 CGAGATGTTGTTAATGAGATTTAAACAAGAACCATGTTGATCACTGTGACAGCA 1120
DB 267 CGAGATGTTGTTAATGAGATTTAAACAAGAACCATGTTGATCACTGTGACAGCA 326
QY 1121 CTTCAAAATGAGCACTGTTGATTAATTTACTATTGACAAATCGGTTTGAACAAT 1180
DB 327 CTTCAAAATGAGCACTGTTGATTAATTTACTATTGACAAATCGGTTTGAACAAT 386
QY 1181 AGTGGCTATCTTGGGAGGATTAACAAGAACCATGTTGATCACTGTGACAGCA 1240
DB 387 AGTGGCTATCTTGGGAGGATTTAAACAAGAACCATGTTGATCACTGTGACAGCA 446
QY 1241 TCATCTGAATCATATGATTTCTGTGACAGAGAAATTTGTTCCAGAGACAGATCTCAT 1300
DB 447 TCGTCCGAATCATATGATTTCTGTGACAGAGAAATTTGTTCCAGAGACAGATCTCAT 506
QY 1301 AGCAGTGGTTGGCGGCATATTAATCTGTTGAAAGAAATGGGCGCTTGAATCTCACT 1360
DB 507 AGCAGCGGTTGGCGGCATATTAATCTGTTGAAAGAAATGGGCGCTTGAATCTCACT 566
QY 1361 CGGGCCCACTCTGTAATTAATGTTGAGGTCTTTAAAGCACTTCAAGATTTAAAGTC 1420
DB 567 CGGGCCCACTCTGTAATTAATGTTGAGGTCTTTAAAGCACTTCAAGATTTAAAGTC 626
QY 1421 AGATGAAGAAGATGGGCACTCAACGTAATGAGATGGTCCGAGG 1470
DB 627 AGCTGAGAGAGATGGGCACTCAACGTAATGAGATGGTCCGAGG 676

RESULT 8
CB659701 782 bp mRNA linear EST 09-APR-2003
LOCUS OSJNEC16012.f OSJNEC Oryza sativa (japonica cultivar-group) cDNA
DEFINITION Oryza sativa (japonica cultivar-group)
ACCESSION CB659701
VERSION CB659701.1 GI:29663426
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Eriharotidae; Oryzaceae; Oryza.

REFERENCE 1 (bases 1 to 782)
AUTHORS Jantsuriyarat C., Lu G., Gowda M., Hatfield J., Zhou B., Mazur E.,
Kudrna D., Dean R., Soderlund C., Wang R. and Wang G.
TITLE Large-scale identification of ESTs involved in the interaction
between rice and Magnaporthe grisea
JOURNAL Unpublished (2003)
COMMENT Contact: Rod Wing

Arizona Genomics Institute
University of Arizona
Biological Sciences West, 448A, P.O. Box 210088, Tucson, AZ
85721-0088, USA
Tel: 520 626 3967
Fax: 520 621 9288
Email: <http://genome.arizona.edu>
PCR Primers
FORWARD: gta aac cga cgg cca gtc
BACKWARD: gga aac agc tat gac cat g
Plate: 16 Row: 0 Column: 12
Seq primer: gta aac cga cgg cca gtc.
Location/Qualifiers
1. .782
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/cultiar="Nipponbare"
/db_xref="taxon:39947"
/clone="OSJNEC16012"
/issue_type="Leaf"
/dev_stage="3 week"
/lab_host="DH10B"
/clone_lib="OSJNEC"
/note="Vector: Bluescript II KS +; Site 1: EcoRI; Site 2:
XhoI; 6 hrs after inoculation with Rice Blast (C9240-1)"

ORIGIN

Query Match 30.7%; Score 598.8; DB 14; Length 782;
Best Local Similarity 87.1%; Pred. No. 1.3e-81;
Matches 657; Conservative 0; Mismatches 97; Indels 0; Gaps 0;

QY 143 GGGCGGGAACCGGTAGTAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 202
DB 29 GGGCGGGAACCGGTAGTAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 88
QY 203 TCTGAACATTAAGAACTCAACCTGGAAGAACTTAACTGATTCGTAATTTGAAAA 262
DB 89 TCTGAGCACTGAAGAACTCAACCTGGAAGAACTTAACTGATTCGTAATTTGAAAA 148
QY 263 GTGAAGATTGCAAGCATTAAGCTTACTGACATTAAGCTTACTGATTAAGCTTACTGAT 322
DB 149 GTGAAGATTGCAAGCATTAAGCTTACTGACATTAAGCTTACTGATTAAGCTTACTGAT 208
QY 323 CGCAATGAAGAAATTAAGAAATGAAGAAAGCAAGAAATTAAGAAATTAAGAAATTAAG 382
DB 209 CGCAATGAAGAAATTAAGAAATGAAGAAAGCAAGAAATTAAGAAATTAAGAAATTAAG 268
QY 383 TTGTTCAATGACCCCATATCATTCGCTTATGAGGTCAATTAACACCTACAGATATA 442
DB 269 TTGTTCAATGACCCCATATCATTCGCTTATGAGGTCAATTAACACCTACAGATATA 328
QY 443 TATGTTGATGGAATTTGTAAGTATGCGAGTATTTGATTAATTAATTAATTAATTAAT 502
DB 329 TATGTTGATGGAATTTGTAAGTATGCGAGTATTTGATTAATTAATTAATTAATTAAT 388
QY 503 AGATTAAGAAAGTGAAGTCTGCGAATCTTCAGAGATTCATATGCGGTGAGATAC 562
DB 389 AGGTGAGAGAAATGAGTCTGCGAATCTTCAGAGATTCATATGCGGTGAGATAC 448
QY 563 TGCCATGAAGAAATGTTGTCACCGTGAACCTTAAGCGGAAAACTGTTACTGATTTCA 622
DB 449 TGCCACGAAAGAAATGTTGTCACCGTGAACCTTAAGCGGAAAACTGTTACTGATTTCA 508
QY 623 AAGTATATGTAAGAACTTGGGATTTGTTGCTGAGCAATGATCATGATGAGCATTTT 682
DB 509 AAGTATATGTAAGAACTTGGGATTTGTTGCTGAGCAATGATCATGATGAGCATTTT 568
QY 683 CTGAAGACTGCTGGGAGTCCGAACTATGCTGCTCCAGAGTAATATGTAAGTAACTA 742
DB 569 TTGAAGCAAGCTGTGAGATTCGAACCTATGCTGCTCCAGAGTATGCTGTAATTTA 628
QY 743 TATGCTGACCTGAGTGAATGATGAGTGTGAGGATGATTTGATTTGCTTTTGT 802

Db 629 TATGCTGACCTGAGTTGATGATGAGAGCTGTGAGTGCATCTTATGCTCTCTTTGT 688
Qy 803 GGAACCTTTCATTTGATGATGAGAAATATCCCAATGCTTCAAAAATTAAGGAGGT 862
Db 689 GGATCTCTTCATTTGATGATGAGAAATATCCCAATGCTTCAAAAATTAAGGAGGT 748
Qy 863 ATCTACACACTCCAGTCAATTTGCTGCTTTGG 896
Db 749 ATATATCTCTCCAGTCAATTTATGCTCTGG 782

RESULT 9
CA149321 956 bp mRNA linear EST 24-SEP-2003
LOCUS SCULR21025G04.g R21 Saccharum officinarum cDNA clone SCULR21025G04
DEFINITION 5', mRNA sequence.
ACCESSION CA149321
VERSION CA149321.1 GI:35051253
KEYWORDS EST.
SOURCE Saccharum officinarum
ORGANISM Saccharum officinarum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoidae; Andropogoneae; Saccharum.
1 (bases 1 to 956)
Vettore A.L., da Silva, F.R., Kemper, E.L. and Arruda, P.
The libraries that made SUCSEST
Genet. Mol. Biol. 24 (1-4), 1-7 (2001)
Contact: Arruda P
Centro de Biologia Molecular e Engenharia Genetica
Universidade Estadual de Campinas
Caixa Postal 6010, 13083-970, Campinas SP, Brazil
Tel: 55 19 3788 1137
Fax: 55 19 3788 1089
Email: parruda@unicamp.br
Clone distribution: clone distribution information can be found
through the Brazilian Clone Collection Center (BCCC) at
http://www.bcccenter.fcap.unesp.br
Plate: 025 row: G column: 04
Seq primer: T7 Promoter Primer.
Location/Qualifiers
1..956
/organism="Saccharum officinarum"
/mol_type="mRNA"
/db_xref="taxon:4547"
/clone="SCULR21025G04"
/lab_host="DH10B"
/clone_id="R21"
/note="Organ: Shoot-root transition zone from young plants
(large insert library); Vector: pSPORT1; Site 1: SalI;
Site 2: NotI. An unidirectional cDNA library generated
from [shoot-root transition zone from young plants (large
insert library)]. cDNA was prepared from polyA+ mRNA
using SuperScript Plasmid System Kit (Invitrogen). The
double-strand cDNAs were fractionated in a sepharose
CL-2B 40cm-columns and fragments sizing between 0.8 and
1.5 Kb were directionally cloned into the vector. Details
of each source of RNA and library construction can be
obtained at http://succest.lad.ic.unicamp.br/public"

ORIGIN
Query Match 30.4%; Score 593; DB 13; Length 956;
Best Local Similarity 96.1%; Pred. No. 8.7e-81;
Matches 608; Conservative 0; Mismatches 25; Indels 0; Gaps 0;

Qy 1076 ATGGGATTTTAAAGAAACCATGTGTGATCACTGTGCAGACACTTCAAAATGAGGCA 1135
Db 1 ATGGGATTTTAAAGAAACCATGTGTGATCACTGTGCAGACACTTCAAAATGAGGCA 60
Qy 1136 ACTGTTGATTTTAACTATTTGAGCAATGGTTTGAAGCAACTAGTGGCTATCTTGGG 1195
Db 61 ACTGTTGATTTTAACTATTTGAGCAATGGTTTGAAGCAACTAGTGGCTATCTTGGG 120

Qy 1196 GCAGATTATCAAGATCAATGACAGAAATTTAATCAGTGGCGTCAATGATCATCT 1255
Db 121 GCAGATTATCAAGATCAATGACAGAAATTTAATCAGTGGCGTCAATGATCATCT 180
Qy 1256 AGTTCTGATGACAGAAATTTGTTCCAGAGAGAGATCTTATGACAGTGGTTTGGCG 1315
Db 181 AGTTCTGATGACAGAAATTTGTTCCAGAGAGAGATCTTATGACAGGTTTGGCG 240
Qy 1316 CCATATTATCTGTTGAAAGAAATGAGCGCTTGAAGTTCAGTCTGAGGCGCACCTCGT 1375
Db 241 CCATATTATCTGTTGAAAGAAATGAGCGCTTGAAGTTCAGTCTGAGGCGCACCTCGT 300
Qy 1376 GAAATATGTTGATGAGTCTTTAAAGACCTTCAAGAAATTAACGTCAGATGAAGAAAT 1435
Db 301 GAAATATGATGATGAGTCTTTAAAGACCTTCAAGAAATTAACGTCAGATGAAGAAAT 360
Qy 1436 GGGCATTACAGCTGAATTCAGATGATGTCGCCAGGGTTTCTCAAGTTATGACAGTTA 1495
Db 361 GGGCATTACAGCTGAATTCAGATGATGTCGCCAGGGTTTCTCAAGTTATGACAGTTA 420
Qy 1496 GATGCCAGCAAGCTTTCTTGTGATCTTACATCATGATGATGATGATGATGATGATG 1555
Db 421 GATGCCAGCAAGCTTTCTTGTGATCTTACATCATGATGATGATGATGATGATGATGATG 480
Qy 1556 AGGCTACTACTGATGATCAAGTTGAATTCACGCTTTACAGAGCAAGAGCAAGTAC 1615
Db 481 AGGCTACTGCTGATGATCAAGTTGAATTCACGCTTTACAGAGCAAGAGCAAGTAC 540
Qy 1616 CTCTTGAATATGACAGAGATTTACTGACCTCAGCTGCTTCTTGAATCTTGTGGGCC 1675
Db 541 CTCTTGAATATGACAGAGATTTACTGACCTCAGCTGCTTCTTGAATCTTGTGGGCC 600
Qy 1676 TTCCTTACCAAGCTTAGGTTCTATAGTGTCT 1708
Db 601 TTCCTTACCAAGCTTAGGTTCTATAGAGCTCT 633

RESULT 10
AM091047 597 bp mRNA linear EST 18-OCT-1999
LOCUS 614070C04.y1 614 - root cDNA library from Walbot Lab Zea mays cDNA,
DEFINITION mRNA sequence.
ACCESSION AM091047
VERSION AM091047.1 GI:6056642
KEYWORDS EST.
SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoidae; Andropogoneae; Zea.
1 (bases 1 to 597)
REFERENCE Walbot V.
TITLE Maize ESTs from various cDNA libraries sequenced at Stanford
UNIVERSITY
JOURNAL Unpublished (1999)
COMMENT Contact: Walbot V
Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 723 8221
Email: walbot@stanford.edu
Plate: 614070 row: C column: 04.
Location/Qualifiers
1..597
/organism="Zea mays"
/mol_type="mRNA"
/cultiivar="W23"
/db_xref="taxon:4577"
/tissue_type="root"
/dev_stage="3-4 days old"
/lab_host="XL0LR"
/clone_id="614 - root cDNA library from Walbot Lab"

/note="Organ: root; Vector: pBluescriptII SK+; Site 1: EcoRI; Site 2: XhoI; 3-4 days old root tissue from Walbot Lab (LM)"

ORIGIN

Query Match 30.4%; Score 592.8; DB 9; Length 597;
Best Local Similarity 99.7%; Pred. No. 1.2e-80;
Matches 594; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1172 AGAGCAACTAGTGGCTATCTTGGGGCAGATTATCAAGAAATGACAGAAATTTAAAT 1231
DB 2 AGAGCAACTAGTGGCTATCTTGGGGCAGATTATCAAGAAATGACAGAAATTTAAAT 61
QY 1232 CAGTGGGCTATCTTGGGGCAGATTATCAAGAAATGACAGAAATTTAAAT 1231
DB 62 CAGTGGGCTATCTTGGGGCAGATTATCAAGAAATGACAGAAATTTAAAT 121
QY 1292 GATCCTCATAGCAGTGGTTTGGGGCAGATTATCTTGGGGCAGATTATCAAGAAATTTAAAT 1351
DB 122 GATCCTCATAGCAGTGGTTTGGGGCAGATTATCTTGGGGCAGATTATCAAGAAATTTAAAT 181
QY 1352 CTTGAGTCTCGGGCCACCTCTGGAATTAATGGTTGAGTCTTAAAGCACTTCAAGAA 1411
DB 182 CTTGAGTCTCGGGCCACCTCTGGAATTAATGGTTGAGTCTTAAAGCACTTCAAGAA 241
QY 1412 TTAAGCGTCAAGTGAAGAAATGGGGCAGATTATCAAGAAATGACAGAAATTTAAAT 1471
DB 242 TTAAGCGTCAAGTGAAGAAATGGGGCAGATTATCAAGAAATGACAGAAATTTAAAT 301
QY 1472 TTTCTGAGTGAATTAATGACAGTGAATGACAGAAATTTAAAGCACTTCAAGAA 1531
DB 302 TTTCTGAGTGAATTAATGACAGTGAATGACAGAAATTTAAAGCACTTCAAGAA 361
QY 1532 ATGATATATGATGATGCTTAATGAGGCTTACCTGATGATCAAGTTGAATTCAGCTT 1551
DB 362 ATGATATATGATGATGCTTAATGAGGCTTACCTGATGATCAAGTTGAATTCAGCTT 421
QY 1592 TACAAGCGAAGGAGCGAAGTACTCTTATGATGAGGCTTACCTGATGATCAAGTTGAATTCAGCTT 1651
DB 422 TACAAGCGAAGGAGCGAAGTACTCTTATGATGAGGCTTACCTGATGATCAAGTTGAATTCAGCTT 481
QY 1652 CTTCTCTGAGTGAATTAATGACAGTGAATGACAGAAATTTAAAGCACTTCAAGAA 1711
DB 482 CTTCTCTGAGTGAATTAATGACAGTGAATGACAGAAATTTAAAGCACTTCAAGAA 541
QY 1712 ATGTGCAAAATTTGATGCTGATGATGAATTAACGAAAGCATGTAATAGAACTT 1767
DB 542 ATGTGCAAAATTTGATGCTGATGATGAATTAACGAAAGCATGTAATAGAACTT 597

RESULT 11
BI950083
LOCUS 863 bp mRNA linear EST 19-OCT-2001
DEFINITION HVSM10018H14f Hordeum vulgare spike EST library HVCNDA0012
(Fusarium infected) Hordeum vulgare subsp. vulgare cDNA clone
HVSM10018H14f, mRNA sequence.
ACCESSION BI950083
VERSION BI950083.1 GI:16291889
KEYWORDS Hordeum vulgare subsp. vulgare
SOURCE Hordeum vulgare subsp. vulgare
ORGANISM Hordeum vulgare subsp. vulgare
REFERENCE 1 (bases 1 to 863)
Wing, R., Muehlbauer, G.J., Close, T.J., Kleinbols, A., Wise, R.,
Heinen, S., Begum, D., Frisch, D., Yu, Y., Henry, D., Palmer, M.,
Rambo, T., Simmons, J., Fenton, R.D., Malatrasi, M., Choi, D.W.,
Oates, R. and Main, D.
TITLE Development of a genetically and physically anchored EST resource
for barley genomics: Fusarium infected Morex spike cDNA library
JOURNAL Unpublished (2001)
COMMENT Contact: Wing RA

Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 7288
Fax: 864 656 4293
Email: rwing@clemson.edu
Total hg bases = 601
Seq primer: AATTACCTCCTCAAGGG
High quality sequence stop: 729.
Location/Qualifiers
1. 863

FEATURES

source

/organism="Hordeum vulgare subsp. vulgare"
/mol_type="mRNA"
/cultivar="Morex"
/sub_species="vulgare"
/db_xref="taxon:112509"
/clone="HVSM10018H14f"
/tissue_type="Spike"
/lab_host="TJC121"
/clone_1lb="Hordeum vulgare spike EST library HVCNDA0012
(Fusarium infected)"
/note="Vector: pBluescript SK(-); Site 1: EcoRI; Site 2:
XhoI; Plants were grown at the University of Minnesota in
the GJ Muehlbauer lab; spikes were harvested and snap
frozen at 0, 1, 2, 3, 4, 5, 6, and 8 days after Fusarium
graminearum inoculation (Heinen). In the TJ Close lab at
the University of California, Riverside, total RNA was
prepared from each sample pool, equal quantities of all
eight RNA pools were combined, poly(A) RNA was purified
from the mixture, one primary unamplified cDNA library was
made, and 1 million pfu were in vivo excised to give
pBluescript SK(-) cDNA phagemids (Choi, Fenton,
Malatrasi). Phagemids were plated and picked at the
Clemson University Genomics Institute (CUGI) (Begum,
Palmer, Frisch, Atkins and Wing). Plasmid DNA
preparations, DNA sequencing and sequence analysis were
performed at CUGI (Wing, Yu, Frisch, Henry, Simmons,
Oates, Rambo, Main). The sequence has been trimmed to
remove vector sequence and contains a minimum of 100 bases
of phred value 20 or above. For more details on library
preparation and sequence analysis see
http://www.genome.clemson.edu/projects/barley. To order
this clone see http://www.genome.clemson.edu/orders Also
see Close TJ, Wing R, Kleinbols A, Wise R (2001)
Genetically and physically anchored EST resources for
barley genomics. Barley Genetics Newsletter 31:29-30.
(http://wheat.pw.usda.gov/gnpages/bgn/31/cover.html)"

ORIGIN

Query Match 30.2%; Score 589.2; DB 12; Length 863;
Best Local Similarity 86.4%; Pred. No. 3.5e-80;
Matches 673; Conservative 0; Mismatches 104; Indels 2; Gaps 2;

QY 185 AGTAAAGGAGTGGGCTTCTGAAGCTTAAGGACATCAACCTGGAGAACTTTAGT 244
DB 5 ACTAGAGAGAGCGGGCTTCTGAAGCTTAAAGACTCAATCTGGGCAAGACTTGGT 64
QY 245 ATCGGTATTTGAAAAGTGAAGATTGACAGCATTAAGCTTACTGACATAGGTTGCT 304
DB 65 ATAGGACATTTGAAAAGTGAAGATTGACAGCATTAAGCTTACTGACATAGGTTGCT 124
QY 305 ATAAAGATCTCAACCTCCGCCAAATGAGAAATATGAAATGGAAGAAAGCAAGAGA 364
DB 125 ATAAAGATTTGAAACCGTCTCTAAATGAACTATGAACATGGAAGAAAGCAAGAGA 184
QY 365 GAATTCAGATATTTGAAGTTGTTCAATCAACCCCATATCACTTGGCTTATGAGTCATA 424
DB 185 GAGATCAAGATATTTGAAGTTGTTCAATCAACCCCATATCACTTGGCTTATGAGTCATT 244
QY 425 TACAACCTTCAAGATATTTGTTGATGAAATTTGATGATGATGATGATGATGATGAT 484
DB 245 TACAACCTTCAAGATATTTGTTGATGAAATTTGATGATGATGATGATGATGATGATGAT 304

RESULT 13	LOCUS	DEFINITION	ACCSSION	VERSION
CB632244	CB632244	850 bp mRNA linear EST 08-APR-2003		
	OS1EBD10F22.f	OS1EB Oryza sativa (indica cultivar-group) cDNA		
	clone OS1EB10F22 5', mRNA sequence.			
	CB632244			
	CB632244.1	GI:29627233		

University of Arizona
Biological Sciences West, 448A, P.O. Box 210088, Tucson, AZ
85721-0088, USA
Tel: 520 626 3967
Fax: 520 621 9288
Email: <http://genome.arizona.edu>
PCR Primers
FORWARD: gta aaa cga cgg cca gtc
BACKWARD: gga aac agc tat gac cat g
Plate: 10 row: F column: 22
Seq primer: gta aaa cga cgg cca gtc.

/note="Vector: pBluescript II KS +; Site 1: EcoRI; Site 2: XhoI; 24 hrs after inoculation with Rice Blast (PO6-6-3)"

QY	143	GGCCGGCCAAACCCGGTAAGTAAGGTGAAAAATGATATGAAAGTACTAAAGGAGTGGGCAT	202
Db	100	GGGGGGGGAGCTCCGGCGGTGCTCAGGGGAAAAATGATGGAATATCTAAAGGCGGTGGGCAT	159
QY	203	TCTGAGCATTTAAGGAATCAACCTGGGAAAGAACTTTAGGTATCGGTACATTTGGAAAA	262
Db	160	TCTGAGGCATCGAAGAACTACAACTTTGGAAAGAACTTTAGGTATATGGCTCATTTGGAAAA	219
QY	263	GTAAGATTTGAGAGCATACACTTACTGCAATAGGGGTTGCTATTAAGATCAATCAATGCG	322
Db	220	GTAAAGATTGACAGCATACAGCATTTACAGACACAGAGTTGCTATTAAGATCTCTGAACCGC	279
QY	323	CGCCAAATGAAATATATGAAATGGAAAGAGAAAGCAAGAGAAAGATTCAGATATTATTAAG	382
Db	280	CGCCAAATGAAATATATGAAATGGAGAGAAAGCAAGAGAAATCAAGATCTGAGA	339
QY	383	TTGTTCAATCCACCCCATATCATTTGCGCTTTATGAGGTCAATATACACTACAGATATA	442
Db	340	TTGTTCAATCAATCCCATATCATTTGCGCTTTATGAGGTATATATACACTCTACCGATATA	399
QY	443	TATGTTTGATGGAATATTTGTAAGTATGCGCAATTATTTGATTAATTTGTTGAGAAAGGC	502
Db	400	TATGTTTGATGAGAGTATCTGCAAGTTTGGAACATGTTGATTAATTTGTTGAGAAAGGC	459
QY	503	AGATTACAGGAAGTAAAGCTCGTGCATCTTCACAGACATCATCTCGGGGTGCATATAC	562
Db	460	AGTTTGACAGGAAGTAAAGCTCGCGCAATCTTCACAGATTAATATCTGGGGTAGAATAC	519
QY	563	TGCCATAGAAACATGTTGTTGCCACCGTACCTTAAAGCCGGAACCTTGTTACTTGATCA	622
Db	520	TGCCACAGAAACATGTTGTTCACTGTGATCTGAAGCCAGAAACCTTGTTACTTGATCA	579
QY	623	AAGTATATGTAATACTTGGGATTTTGGTCTGAGCAATGTCATGCAATGATGGCCATTTT	682
Db	580	AAGTATATGTAATACTTGGCTGATCTTGGTGTGAGTAACGTCAATGCAATGATGGCCATTTT	639
QY	683	CTGAAGACTACTGTGAGGAGTCCGAACTATGCTGTCCAGAGGTAAATATTCGTAAACTA	742
Db	640	TTGAAGACAACTGTGGAGTCCAACTATCTGTCTCCAGAGGTGATCTCTGGTATATTA	699
QY	743	TATGCTGGAACCTGAGTGCATGATATGAGATTTGGGGTGATCTTTATGCTCTTCTTGT	802
Db	700	TATGCTGGAACCTGAGTGTGATATGAGAGTCAAGAGATCTTTATGCTCTCTCTTGT	759
QY	803	GGAACCTTCCATTTGATGATGAGAAATATTCCAATCTGTTCAAAAAAATTAAGGAGGT	862
Db	760	GGCACTCTTCATATGATGATGAGAAATATCCCAACCTATTCAAAAAAGATTAAGGAGGT	819
QY	863	ATCTACACACTTCCAGATCTTTGCTGCT	892
Db	820	ATATATCTCTCCGAGTCATTTATCTGCT	849

RESULT 14					
BO805778					
LOCUS					
DEFINITION	BO805778	794 bp	mRNA	linear	EST 31-JUL-2002
ACCESSION	WH3570_H07_P14Z5	Wheat	developing grains	cDNA library	Triticum
VERSION	aestivum cDNA clone	WH3570_H07_P14	mRNA	sequence.	
KEYWORDS	BO805778				
SOURCE	BO805778.1	GI:22029987			
ORGANISM	EST.				
	Triticum aestivum (bread wheat)				
	Triticum aestivum				
	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;				
	Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;				
	Pooidae; Triticeae; Triticum.				
REFERENCE	1 (bases 1 to 794)				
AUTHORS	Altenbach,S., Anderson,O.D., Chao,S., Chin,A., Close,T.J.,				
	Cotton,K., Crossman,C., Fenton,R.D., Lazo,G.R., Pham,J.,				

TITLE
Rausch, C.J., Wilson, C. and Woo, J.
The structure and function of the expressed portion of the wheat
genomes - Developing grains cDNA library
Unpublished (2002)

JOURNAL
Contact: Olin Anderson
US Department of Agriculture, Agriculture Research Service, Pacific
West Area, Western Regional Research Center
800 Buchanan Street, Albany, CA 94710, USA
Tel: 5105595773
Fax: 5105595818

COMMENT
Email: oanderson@pw.usda.gov
Sequences have been trimmed to remove vector sequence and low
quality sequence with phred score less than 20
Seq primer: SK primer.

FEATURES

Source

location/Qualifiers
1..794
/organism="Triticum aestivum"
/mol_type="mRNA"
/cultivar="Butte 86"
/db_xref="taxon:4565"
/clone="WHE3570_H07_P14"
/rissue_type="whole grains"
/dev_stage="3-44 days post anthesis seed"
/lab_host="E. coli SOLR"
/clone_lib="wheat developing grains cDNA library"
/note="Vector: Lambda ZAP II, excised phagemid; Site 1:
EcoRI; Plants were grown under six following different
environmental regimes in greenhouse, Environment 1)
240C/170C day/night, well-watered, with post-anthesis
fertilizer, Environment 2) 240C/170C day/night,
fertilizer, Environment 3) 370C/170C day/night, well-watered,
Environment 4) 370C/170C day/night, well-watered, with
post-anthesis fertilizer, Environment 5) 370C/170C
day/night, well-watered, without post-anthesis fertilizer,
Environment 6) 370C/170C day/night plus drought, with
post-anthesis fertilizer, Environment 7) 370C/170C
day/night plus drought, without post-anthesis fertilizer,
developing wheat grains from the following were excised
and frozen in liquid nitrogen, Environment 1 at 3, 5, 7,
8, 10, 12, 16, 20, 24, 28, 32, 36, 40, 44 DPA Environment
2 at 3, 5, 7, 8, 10, 12, 16, 20, 24, 28, 32, 36, 40, 44
DPA Environment 3 at 3, 5, 7, 8, 10, 12, 16, 20, 24, 28,
32, 34 DPA Environment 4 at 3, 5, 7, 8, 10, 12, 16, 20,
24, 28, 32, 34 DPA Environment 5 at 3, 5, 7, 8, 10, 12,
16, 20, 24, 28, 30 DPA Environment 6 at 3, 5, 7, 8, 10,
12, 16, 20, 24, 28, 30 DPA and total RNA was prepared by
S. Altembach and K. Cronin at USDA-ARS, Albany, CA. A
cDNA library was made using poly (A) RNA, and the cDNA
clones were in vivo excised to give Bluescript SK(-)
phagemids in the TJ Clouse lab (Chin, Clouse, Fenton) at
the University of California, Riverside. Plasmid DNA
preparations and DNA sequencing were performed in the OD
Anderson lab (others)."

ORIGIN

Query Match
Best Local Similarity 84.7%; Pred. No. 2.1e-79;
Matches 655; Conservative 0; Mismatches 118; Indels 0; Gaps 0;

386 TTCATTCACCCCATATCATTCGGCTTTATAGAGTCATATACACCTACAGATATATAT 445
Db TTAATTCACCCCTCATATCATTCGGCTTTATAGAGTCATATACACCTACAGATATAT 81
446 GTTGAGTGAAGTATTTGAAGTGAAGTATTTGATTCATTTGAGAAAGGCGA 505
Db GTTGAGTGAAGTATTTGAAGTGAAGTATTTGATTCATTTGAGAAAGGCGG 141
506 TTACAGAGAGTGAAGTGTGCGAATCTTCCAGAGATCATATCTGGCGTAATCTGC 565
Db TTACAGAGAGTGAAGTGTGCGAATCTTCCAGAGATCATATCTGGCGTAATCTGC 201
566 CATGAAAACATGTTGTCACCGTGACCTAAAGCCGGAACCTGTACTTGATCAAG 625

Db 202 CACAGAAACATGTTGTCATCGTATCTAAACCCAGAAAACCTGTACTGTATCTAA 261
Qy TATAATGTAACATCTGGAGATTTTGGCTGAGCAATGTCATGATGGCCATTTTCG 685
Db TATAATGTAACATCTGGAGATTTTGGCTGAGCAATGTCATGATGGCCATTTTCG 321
Qy 686 AAGACTAGCTGTGGAGTCCGAATCTATGCTGCTCCAGAGTAAATCTGTAAACATAT 745
Db AAGACTAGCTGTGGAGTCCGAATCTATGCTGCTCCAGAGTAAATCTGTAAACATAT 381
Qy 746 GCTGACCTGAGTCCGATGATGATGAGTGTGGGCTGATTTTATGCTCTTTTGTGA 805
Db GCTGACCTGAGTCCGATGATGATGAGTGTGGGCTGATTTTATGCTCTTTTGTGC 441
Qy 806 ACCTTCATTTGATGATGAGTATTTCCCAATCTGTTCAAAAATTAAGGAGGTATC 865
Db AGAGTTCATTTGATGATGAGTATTTCCCAATCTGTTCAAAAATTAAGGAGGTATC 501
Qy 866 TACACATTCGCAAGTCAATTTGCTGCTTGGCCAGGATTTGATCCAGATGCTTGT 925
Db TATATCTTCGCAAGTATTTATCTGATCTTGAATGGAATTTGATCCAGATATCTTAT 561
Qy 926 GTTGAGCTTGTGAAGAGATCAATTAAGGAAATTCGGAGCATATGCTTCAGAT 965
Db GTTGATCCATGAAGAGATCAATTAAGGAAATTCGGAGCATATGCTTCAGAT 621
Qy 966 CGCCTTCACGTTACTTGGAGTGGCTCCACGATATGACACAGCAAGCAAAATGAT 1045
Db CGCCTTCCTGCTACTGAGATGCTCCAGATGCTCCGCAAAACGCAAGCAAAATGAT 681
Qy 1046 GATGAAGATACACTTGCAGATGTTGTTAATATGGAATTTAAAGAAACATGTGTGA 1105
Db GATGAAGATACACTTGCAGATGTTGTTAATATGGAATTTAAAGATCATGTGTGGA 741
Qy 1106 TCACCTGCGAGAGACTTCAAAATGAGGCACTGTGCAATTAATTAATTAAT 1158
Db TCACCTGCGAGAGACTTCAAAATGAGGCACTGTGCAATTAATTAATTAATTAAT 794

RESULT 15

LOCUS CB621531 829 bp mRNA linear EST 08-APR-2003
DEFINITION OSlIE07H13.1 f OSlIEA Oryza sativa (indica cultivar-group) cDNA
clone OSlIE07H13 5', mRNA sequence.

ACCESSION CB621531
VERSION CB621531.1 GI:29616519

KEYWORDS Oryza sativa (indica cultivar-group)
SOURCE Oryza sativa (indica cultivar-group)

ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE 1 (bases 1 to 829)
Jantasuriyarat, C., Lu, G., Gowda, M., Hatfield, J., Zhou, B., Mazur, E.,

Kudrna, D., Dean, R., Soderlund, C., Wing, R. and Wang, G.
Large-scale identification of ESTs involved in the interaction
between rice and Magnaporthe grisea

Unpublished (2003)
Contact: Rod Wing
Arizona Genomics Institute
University of Arizona
Biological Sciences West, 448A, P.O. Box 210088, Tucson, AZ
85721-0088, USA
Tel: 520 626 3967
Fax: 520 621 9288
Email: htcp://genome.arizona.edu

COMMENT

JOURNAL
Contact: Rod Wing
Arizona Genomics Institute
University of Arizona
Biological Sciences West, 448A, P.O. Box 210088, Tucson, AZ
85721-0088, USA
Tel: 520 626 3967
Fax: 520 621 9288
Email: htcp://genome.arizona.edu

PCR Primers
FORWARD: gta aac cga cgg cca gtc
BACKWARD: gga aac agc tat gac cat g
Plate: 07 row: H column: 13
Seq primer: gta aac cga cgg cca gtc.

FEATURES
Source
1..829
location/Qualifiers

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/cultivar="IR36"
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/clone="OSIIBa07H13"
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/dev_stage="3 week"
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/clone_lib="OSIIBa"
/notes="Vector: pluscript II KS +; Site_1: EcoRI; Site_2
XhoI; Vector Mimic SPL II"

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ORIGIN

Query Match	29.7%	Score 578;	DB 14;	Length 829;
Best Local Similarity	87.0%;	Pred. No. 1.8e-78;		
Matches 635;	Conservative 0;	Mismatches 95;	Indels 0;	Gaps 0;

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Qy	203	TCTGAGCATTAAAGAACTTACAACCTGGAGAGAACTTTAGTATCCGTCACTTTGGAAAA	262
Db	160	TCTGAGGCACTGAAGAACTACATCTTTGAAGAAGCTTTAGTATGGCTCATTTGGAAAA	219
Qy	263	GTGAAGATTGCAGAGCATTAAGCTTACTGGAACATAGGGTTGCTATTAAGATCATCACTGC	322
Db	220	GTGAAGATTGCAGAGCATTAAGCTTACAGAGCACAGAGTTGCTATTAAGATCCTGAAACCCG	279
Qy	323	CGCCAAATGAGAAATATGGAAATGGAAGGAAGAAAGCAAGAGAAATTCAGAAATATGGAAG	382
Db	280	CGCCAAATGAGAAATATGGAAATGGAAGGAAGAAAGCAAGAGAAATTCAGAGATCTGAAG	339
Qy	383	TTGTTTCATTCAACCCCATATCATTCCTGGCTTTATAGGTCATATACACACTACAGATATA	442
Db	340	TTGTTTCATTCAATCCCATATCATTCCTGGCTTTATAGGTTATATACACTCTACAGATATA	399
Qy	443	TATGTTTGATGGAATATTTGTAAAGTATGGCGAGTTATTTGATTAATTTGTTGGAAGGC	502
Db	400	TATGTTTGATGGAATATTTGTAAAGTATGGCGAGTTATTTGATTAATTTGTTGGAAGGC	459
Qy	503	AGATTACAGGAAGATGAAGCTGCGAATCTCCAGCAATCATATCTGGCGTCGAATAC	562
Db	460	AGTTTCAGGAAGATGAAGCTGCGAATCTTCAGCAATTAATCTGGGAGTAATAC	519
Qy	563	TGCCATAGAAACATGTTGTCCACCGTGAACCTTAAGCCGGAAAACTTGTATCTTGAATTA	622
Db	520	TGCCACAGAAACATGTTGTTCATGTGATCTGAAGCCAGAAAACTTGTCTACGTGAATTA	579
Qy	623	AAGTAAATGTAAAACTTGGGATTTTGGTCTGAGCAATGTCATGATGATGGCCATTTT	682
Db	580	AAGTAAATGTAAAACTTGGGATTTTGGTGTAGTAATGTCATGATGATGGCCATTTT	639
Qy	683	CTGAAGATTAAGTGTGGGAGTCCGAACATATGCTGCTCCAGAGTAAATATCTGTAAACTTA	742
Db	640	TTGAAGAAAGCTGTGGGAGTCCAAACATATGCTGCTCCAGAGTAAATATCTGTAAACTTA	699
Qy	743	TATGCTGACCTGAAGGTGATGTATGAGAGTTTGGGGTATATCTTTATGCTCTTCTTGT	802
Db	700	TATGCTGACCTGAAGGTGATGTATGAGAGTGTGAGATATCTTTATGCTCTTCTTGT	759
Qy	803	GGAACCTTTCATTTGATGATGAGAATATTTCCCAATCTGTTCAAAAAATTAAGGAGGT	862
Db	760	GGTACTCTTTCATTTGATGATGAGAATATTTCCCAACCTATTCAAAAAAGATTAAGGAGGT	819
Qy	863	ATCTACACAC	872
Db	820	ATATATACTC	829

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Job time : 5190 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: July 9, 2004, 11:12:59 ; Search time 917 Seconds
(Without alignments)

10353.680 Million cell updates/sec

Title: US-09-857-522B-3

Sequence: 1 gtcgaccaccagcgtccggac.....taaaaaaaaaaaaaaaaaa 1948

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 3183909 seqs, 2436941669 residues

Total number of hits satisfying chosen parameters: 6367818

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database:

Published Applications NA: *
1: /cgn2_6/prodata/1/pubpna/US07_PUBCOMB.seq: *
2: /cgn2_6/prodata/1/pubpna/PCR_NEW_PUB.seq: *
3: /cgn2_6/prodata/1/pubpna/US06_NEW_PUB.seq: *
4: /cgn2_6/prodata/1/pubpna/US06_PUBCOMB.seq: *
5: /cgn2_6/prodata/1/pubpna/US07_NEW_PUB.seq: *
6: /cgn2_6/prodata/1/pubpna/PCRUS_PUBCOMB.seq: *
7: /cgn2_6/prodata/1/pubpna/US08_NEW_PUB.seq: *
8: /cgn2_6/prodata/1/pubpna/US08_PUBCOMB.seq: *
9: /cgn2_6/prodata/1/pubpna/US09A_PUBCOMB.seq: *
10: /cgn2_6/prodata/1/pubpna/US09B_PUBCOMB.seq: *
11: /cgn2_6/prodata/1/pubpna/US09C_PUBCOMB.seq: *
12: /cgn2_6/prodata/1/pubpna/US09_NEW_PUB.seq: *
13: /cgn2_6/prodata/1/pubpna/US09_PUBCOMB.seq: *
14: /cgn2_6/prodata/1/pubpna/US10_PUBCOMB.seq: *
15: /cgn2_6/prodata/1/pubpna/US10_PUBCOMB.seq: *
16: /cgn2_6/prodata/1/pubpna/US10C_PUBCOMB.seq: *
17: /cgn2_6/prodata/1/pubpna/US10C_NEW_PUB.seq: *
18: /cgn2_6/prodata/1/pubpna/US60_NEW_PUB.seq: *
19: /cgn2_6/prodata/1/pubpna/US60_PUBCOMB.seq: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	1948	100.0	1948	13	US-10-183-687-235 Sequence 235, App
2	1907	97.9	1926	13	US-10-425-114-5805 Sequence 5805, App
3	1222.4	62.8	1300	13	US-10-425-114-5415 Sequence 5415, App
4	1195.6	61.4	1899	13	US-10-183-687-255 Sequence 255, App
5	1188.4	61.0	2119	13	US-10-425-114-22369 Sequence 22369, App
6	1188.4	61.0	2607	17	US-10-437-963-49666 Sequence 49666, App
7	848.8	43.6	2484	17	US-10-437-963-49667 Sequence 49667, App
8	817.4	42.0	2224	13	US-10-437-963-80980 Sequence 80980, App
9	814.6	41.8	1991	13	US-10-425-114-35131 Sequence 35131, App
10	807.6	41.5	1778	13	US-10-425-114-2148 Sequence 2148, App
11	804.2	41.3	2107	13	US-10-183-687-237 Sequence 237, App
12	793.4	40.7	2052	13	US-10-183-687-239 Sequence 239, App
13	793.2	40.7	1742	13	US-10-425-114-4365 Sequence 4365, App
14	782.6	40.2	2123	13	US-10-183-687-247 Sequence 247, App

15	780.2	40.1	1539	9	US-09-938-842A-162 Sequence 162, App
16	780.2	40.1	1539	11	US-09-938-842A-162 Sequence 162, App
17	763	39.2	2543	13	US-10-183-687-251 Sequence 251, App
18	755.4	38.8	1539	9	US-09-938-842A-2657 Sequence 2657, App
19	755.4	38.8	1539	11	US-09-938-842A-2657 Sequence 2657, App
20	744.4	38.2	2006	13	US-10-183-687-257 Sequence 257, App
21	639	32.8	1626	16	US-10-260-238-491 Sequence 491, App
22	582.4	29.9	1277	13	US-10-424-599-38233 Sequence 38233, App
23	522	26.8	2231	13	US-10-424-599-37563 Sequence 37563, App
24	304	15.3	3079	9	US-09-834-975-974 Sequence 974, App
25	297.8	15.3	1902	16	US-10-369-499-25383 Sequence 25383, App
26	297.8	15.3	1902	16	US-10-369-499-25383 Sequence 25383, App
27	296.8	15.2	986	9	US-09-770-445-263 Sequence 263, App
28	248.8	12.8	725	16	US-10-260-238-3050 Sequence 3050, App
29	237.8	12.2	1264	16	US-10-369-499-27551 Sequence 27551, App
30	232.4	11.9	1548	17	US-10-437-963-90028 Sequence 90028, App
31	229.2	11.8	1753	13	US-10-425-114-10423 Sequence 10423, App
32	229.2	11.8	1803	13	US-10-425-114-11678 Sequence 11678, App
33	229.2	11.8	1869	13	US-10-183-687-253 Sequence 253, App
34	229.2	11.8	2173	13	US-10-424-599-83546 Sequence 83546, App
35	229.2	11.8	2730	13	US-10-424-599-83552 Sequence 83552, App
36	229.2	11.8	4719	16	US-10-258-106-25 Sequence 25, App
37	227.6	11.7	2899	16	US-10-120-988-112 Sequence 112, App
38	224.4	11.5	1607	13	US-10-425-114-24231 Sequence 24231, App
39	224.4	11.5	1886	13	US-10-425-114-281 Sequence 281, App
40	224.4	11.5	2010	13	US-10-425-114-24620 Sequence 24620, App
41	222.2	11.4	1707	13	US-10-183-687-233 Sequence 233, App
42	219.4	11.3	2572	16	US-10-191-803-134 Sequence 134, App
43	219	11.2	1771	13	US-10-425-114-30848 Sequence 30848, App
44	219	11.2	2086	15	US-10-161-565-4 Sequence 4, App
45	219	11.2	2112	9	US-09-919-585-4 Sequence 4, App

ALIGNMENTS

RESULT 1
US-10-183-687-235
Sequence 235, Application US/10183687
Publication No. US20030204870A1
GENERAL INFORMATION:
APPLICANT: Allen, Steve
APPLICANT: Allen, William B.
APPLICANT: Cahoon, Rebecca
APPLICANT: Epelbaum, Sabine
APPLICANT: Famodu, Omolayo O.
APPLICANT: Harvell, Leslie T.
APPLICANT: Jones, Todd
APPLICANT: Kinney, Tony
APPLICANT: Klein, Ted
APPLICANT: Li, Changjiang
APPLICANT: Oliveira, Igor Cunha
APPLICANT: Sakai, Hajime
APPLICANT: Shen, Bo
APPLICANT: Tarczyński, Mitchell C.
TITLE OF INVENTION: Alteration Of Oil Traits In Plants
FILE REFERENCE: BFI458 US NA
CURRENT FILING DATE: 2002-06-27
PRIOR APPLICATION NUMBER: 60/301,913
PRIOR FILING DATE: 2001-06-29
NUMBER OF SEQ ID NOS: 532
SOFTWARE: Microsoft Office 97
SEQ ID NO 235
LENGTH: 1948
TYPE: DNA
ORGANISM: Zea mays
US-10-183-687-235
Query Match 100.0%; Score 1948; DB 13; Length 1948;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1948; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTGACCCAGCGGTCGGACCAAGCCGGGCAATACGCCCCCAAGTCCAAAGCCCTCTCC 60
DB 1 GTGACCCAGCGGTCGGACCAAGCCGGGCAATACGCCCCCAAGTCCAAAGCCCTCTCC 60
QY 61 GCCCGGCTCTCCCACTGTAAGTGTCTCCCGCTCTCCCGCCGCACTGCTGTCCGCGC 120
DB 61 GCCCGGCTCTCCCACTGTAAGTGTCTCCCGCTCTCCCGCCGCACTGCTGTCCGCGC 120
QY 121 GCAGGAAGGTGACCTGTCCAGGGCCCGGCAACCCCGTAAAGTAAGTAAATGATGG 180
DB 121 GCAGGAAGGTGACCTGTCCAGGGCCCGGCAACCCCGTAAAGTAAGTAAATGATGG 180
QY 181 AAGTAAGAAAGGAGTGGGCACTTGAAGCACTTAAGGAACAACCTGGGAAGAACTTT 240
DB 181 AAGTAAGAAAGGAGTGGGCACTTGAAGCACTTAAGGAACAACCTGGGAAGAACTTT 240
QY 241 AGGTATCGGTACATTTGAAAAAGTGAAGATTGACAGCATTAAGCTTACTGACATAGGGT 300
DB 241 AGGTATCGGTACATTTGAAAAAGTGAAGATTGACAGCATTAAGCTTACTGACATAGGGT 300
QY 301 TGCCTATAAATCATCACTGCCGCCCAATGAGAAATATGAAATGGAAGAAAGCAAA 360
DB 301 TGCCTATAAATCATCACTGCCGCCCAATGAGAAATATGAAATGGAAGAAAGCAAA 360
QY 361 GAGGAATTCAGATATTGAAGTGTTCATTCACTCCCATATCATCTGCGCTTTATAGGT 420
DB 361 GAGGAATTCAGATATTGAAGTGTTCATTCACTCCCATATCATCTGCGCTTTATAGGT 420
QY 421 CATATACACACTTACAGATATATATGTTGTGATGAATATTGTAAGTATGCGCAATATT 480
DB 421 CATATACACACTTACAGATATATATGTTGTGATGAATATTGTAAGTATGCGCAATATT 480
QY 481 TGAATTAATGTTGAAGAAAGGAGATTAAGGAAGAGAGAGCTGTGAAATCTTCCAGCA 540
DB 481 TGAATTAATGTTGAAGAAAGGAGATTAAGGAAGAGAGAGCTGTGAAATCTTCCAGCA 540
QY 541 GATCATATCTGCGCTCGAATATCTGCCAATAGAAACATGTTGTCCACGCTTAAGGCC 600
DB 541 GATCATATCTGCGCTCGAATATCTGCCAATAGAAACATGTTGTCCACGCTTAAGGCC 600
QY 601 GAAAACTTGTACTTGAATCAAAAGTATATATGTAATAAATCTGCGGATTTGGTCTGAGCA 660
DB 601 GAAAACTTGTACTTGAATCAAAAGTATATATGTAATAAATCTGCGGATTTGGTCTGAGCA 660
QY 661 TGTATGATGATGAGGCACTTTTGAAGACTAGCTGAGGAGTCCGAATATGCTGCTCC 720
DB 661 TGTATGATGATGAGGCACTTTTGAAGACTAGCTGAGGAGTCCGAATATGCTGCTCC 720
QY 721 AGAGTAATATCTGTGTAACATAATGCTGACCTGAGGTGATATGATGAGTGTGGGT 780
DB 721 AGAGTAATATCTGTGTAACATAATGCTGACCTGAGGTGATATGATGAGTGTGGGT 780
QY 781 GATTCTTATGCTCTTCTTGTGGAATCTTCCATTTGATGATGAGAAATATCCCAATCT 840
DB 781 GATTCTTATGCTCTTCTTGTGGAATCTTCCATTTGATGATGAGAAATATCCCAATCT 840
QY 841 GTTCAAAAAAATTAAGGAGGATCTACACACTTCAAGTCAATTTGCTGTTGGCCAG 900
DB 841 GTTCAAAAAAATTAAGGAGGATCTACACACTTCAAGTCAATTTGCTGTTGGCCAG 900
QY 901 GGAATTTGATCCAGAAATGCTTGTGTTGAGCTTATGAGCAATCAAAATTAAGGGAAT 960
DB 901 GGAATTTGATCCAGAAATGCTTGTGTTGAGCTTATGAGCAATCAAAATTAAGGGAAT 960
QY 961 TCGGAGACATCATGTTTCCAGATTCGCTTCCAGTTACTTGGCAATGCTCCACAGCA 1020
DB 961 TCGGAGACATCATGTTTCCAGATTCGCTTCCAGTTACTTGGCAATGCTCCACAGCA 1020
QY 1021 TAGGACCAACAAGCAAAATGATGATGAGATACACTTGAATGTTTAAATATGGG 1080
DB 1021 TAGGACCAACAAGCAAAATGATGATGAGATACACTTGAATGTTTAAATATGGG 1080
QY 1081 ATTTAACAAGAACCATGTGTGTGAATCATGTGTGACAGCACTTCAAAATGAGCAACTGT 1140

DB 1081 ATTTAACAAGAACCATGTGTGTGAATCATGTGTGACAGCACTTCAAAATGAGCAACTGT 1140
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DB 1141 TGCATATTATTTACTATTGGAACAATGCTTTAGAGCAACTAGTGGCTATCTTGGGCAAA 1200
QY 1201 TTATCAAGATCAATGAGCAGGAATTTAATACAGTGGGCTCATCTGAATCATCTAGTT 1260
DB 1201 TTATCAAGATCAATGAGCAGGAATTTAATACAGTGGGCTCATCTGAATCATCTAGTT 1260
QY 1261 TGGTACAGGAATTAATGTTTCCAGAGCAAGTATCTCTCATAGCAGTGTGTTGGCCATA 1320
DB 1261 TGGTACAGGAATTAATGTTTCCAGAGCAAGTATCTCTCATAGCAGTGTGTTGGCCATA 1320
QY 1321 TTATCTGTTGAAAGAAATGGGCGCTTGGACTTCACTGAGTCTGCGGCCACCTGTGAAT 1380
DB 1321 TTATCTGTTGAAAGAAATGGGCGCTTGGACTTCACTGAGTCTGCGGCCACCTGTGAAT 1380
QY 1381 AATGTTGAGGTCTTAAAGCACTTCAAGAAATTAACGTACAGATGGAAGAAATGGCA 1440
DB 1381 AATGTTGAGGTCTTAAAGCACTTCAAGAAATTAACGTACAGATGGAAGAAATGGCA 1440
QY 1441 CTACAAAGTGAATGAGATGAGTGTGCGCAGGGTTCTGAAATTAATGACAGTTAGATGC 1500
DB 1441 CTACAAAGTGAATGAGATGAGTGTGCGCAGGGTTCTGAAATTAATGACAGTTAGATGC 1500
QY 1501 CAGCAACAGCTTCTTGTGATCTCTACCATCAATGATGATGATGATGATGATGATGATG 1560
DB 1501 CAGCAACAGCTTCTTGTGATCTCTACCATCAATGATGATGATGATGATGATGATGATG 1560
QY 1561 ACCTACTGATCAAGTGTGAATTTCCAGCTTTTCAAGACGAGAGCAGCAAGTACTCTT 1620
DB 1561 ACCTACTGATCAAGTGTGAATTTCCAGCTTTTCAAGACGAGAGCAGCAAGTACTCTT 1620
QY 1621 AGATATGACAGAGATTAATGAGACCTGACCTGCTCTTGAATCTTGTGCGGCTTCT 1680
DB 1621 AGATATGACAGAGATTAATGAGACCTGACCTGCTCTTGAATCTTGTGCGGCTTCT 1680
QY 1681 TACCAAGCTTGGGTTCTATAGTGTCTACCATGATGATGATGATGATGATGATGATG 1740
DB 1681 TACCAAGCTTGGGTTCTATAGTGTCTACCATGATGATGATGATGATGATGATGATG 1740
QY 1741 AACGGAAGCATTAATGAGAACTTGTCTGCTTTTGAAGCAAGCAATGTTGAG 1800
DB 1741 AACGGAAGCATTAATGAGAACTTGTCTGCTTTTGAAGCAAGCAATGTTGAG 1800
QY 1801 TGACTGCTTGTGTGAGCGGCTTAAGGTATGATTAATCTTAGGTTAGTATTTTCTG 1860
DB 1801 TGACTGCTTGTGTGAGCGGCTTAAGGTATGATTAATCTTAGGTTAGTATTTTCTG 1860
QY 1861 TCTTAATATTTGCGTCTGCTAGTATGTTCAATTTTGAAGCAAGTATGAGATTA 1920
DB 1861 TCTTAATATTTGCGTCTGCTAGTATGTTCAATTTTGAAGCAAGTATGAGATTA 1920
QY 1921 AAAAAGGTAAAAAATTTTAAAAA 1948
DB 1921 AAAAAGGTAAAAAATTTTAAAAA 1948

RESULT 2
US-10-425-114-5805
; Sequence 5805, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaka, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

FILE REFERENCE: 38-21(5313)B
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 5805
LENGTH: 1926
TYPE: DNA
ORGANISM: Zee maye
FEATURE:
OTHER INFORMATION: Clone ID: 700473306_FLI
US-10-425-114-5805

Query Match 97.9%; Score 1907; DB 13; Length 1926;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 1910; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

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DB 1 GACCAAGCCGGGATACGCCCCCAAGTCCAAAGCCCTCTCCGCCGCTCCCACTC 60
QY 78 GTAGTGTCTCCCGTCTCCGCCGCTCCGCCGCTCCGCCGCTCCGCCGCTCCGCCG 137
DB 61 GTAGTGTCTCCCGTCTCCGCCGCTCCGCCGCTCCGCCGCTCCGCCGCTCCGCCG 120
QY 138 TCGAGGCGCCGGCGAACCCTGTAAGTAAGTAAGTAAGTAAGTAAGTAAGTAAG 197
DB 121 TCGGGGGCGCCGCGAACCCTGTAAGTAAGTAAGTAAGTAAGTAAGTAAGTAAG 180
QY 198 GGCATCTGAAAGCATTAAGAACTAACCTGGGAAAGCTTTAGTATCGGTACATTTG 257
DB 181 GGCATCTGAAAGCATTAAGAACTAACCTGGGAAAGCTTTAGTATCGGTACATTTG 240
QY 258 GAAAGGTAAGTTCGCAAGCATTAAGCTTACTGCAATAGGCTTCTTAAGATCATCA 317
DB 241 GAAAGGTAAGTTCGCAAGCATTAAGCTTACTGCAATAGGCTTCTTAAGATCATCA 300
QY 318 ACTGCCCGCAATGAAATATGAAATGAAAGAAAGAAAGAAAGAAATTCAGATAT 377
DB 301 ACTGCCCGCAATGAAATATGAAATGAAAGAAAGAAAGAAAGAAATTCAGATAT 360
QY 378 TGAAGTGTTCATTCACCCCATATCATTCGGCTTTATGAGTCAATATACACCTTAC 437
DB 361 TGAAGTGTTCATTCACCCCATATCATTCGGCTTTATGAGTCAATATACACCTTAC 420
QY 438 ATATATATGTTGTAAGTAATATGTAATGTCGAGATTTTATGATACATTTGTTAGA 497
DB 421 ATATATATGTTGTAAGTAATATGTAATGTCGAGATTTTATGATACATTTGTTAGA 480
QY 498 AAGCAGATTCAGAGATGAGCTCGATCTTCACAGATCATCTGAGCGCTG 557
DB 481 AAGCAGATTCAGAGATGAGCTCGATCTTCACAGATCATCTGAGCGCTG 540
QY 558 AATACTGCGATAGAAACATGCTGTCCACCGTGAACCTTAAGCCGAAAACTTTTACT 617
DB 541 AATACTGCGATAGAAACATGCTGTCCACCGTGAACCTTAAGCCGAAAACTTTTACT 600
QY 618 ATTAAAGTATATGTAATAAATCTGCGATTTTGTGTCGACAAATGTCATGATGATGCC 677
DB 601 ATTAAAGTATATGTAATAAATCTGCGATTTTGTGTCGACAAATGTCATGATGATGCC 660
QY 678 ATTTTCTGAAGACTGCTGGAGTCCGAACCTAGTCTCCAGAGGTAATATCTGGTA 737
DB 661 ATTTTCTGAAGACTGCTGGAGTCCGAACCTAGTCTCCAGAGGTAATATCTGGTA 720
QY 738 AACTATATGCTGACCTGAGGTCATGATGATGAGGTTGAGGTTGATCTTATGCTCTC 797
DB 721 AACTATATGCTGACCTGAGGTCATGATGATGAGGTTGAGGTTGATCTTATGCTCTC 780
QY 798 TTTTGTGAACCTCTTCATTTGATGATGATGATGATGATGATGATGATGATGATGAT 857
DB 781 TTTTGTGAACCTCTTCATTTGATGATGATGATGATGATGATGATGATGATGATGAT 840
QY 858 GAGGTATCTACACATTCCTCAAGTCAATTTGCTGCTTTGGCAGGATTTGATCCACGAA 917

DB 841 GAGGTATCTACACATTCCTCAAGTCAATTTGCTGCTTTGGCAGGATTTGATCCACGAA 900
QY 918 TGTCTGTTGTTGAGCCCTATGAGAGATTCACATTTAGGAAATTCGGAGCTAATGCT 977
DB 901 TGTCTGTTGTTGAGCCCTATGAGAGATTCACATTTAGGAAATTCGGAGCTAATGCT 960
QY 978 TCCAGATTCGCTCCAGGTTAATCTGGCAGTCCCTCCAGAGATTCAGAACCAACGCA 1037
DB 961 TCCAGATTCGCTCCAGGTTAATCTGGCAGTCCCTCCAGAGATTCAGAACCAACGCA 1020
QY 1038 AATATGTTGATGAGATACCTTCGAGATGTTGTTAATATGAGATTTAACAAGAACCAT 1097
DB 1021 AATATGTTGATGAGATACCTTCGAGATGTTGTTAATATGAGATTTAACAAGAACCAT 1080
QY 1098 TGTGTGAATCCTGTGACAGACACTTCAAAATGAGCAACTGTTGATATTTACTAT 1157
DB 1081 TGTGTGAATCCTGTGACAGACACTTCAAAATGAGCAACTGTTGATATTTACTAT 1140
QY 1158 TGGACATTCGCTTGAAGCACTAGTGGCTATCTTGGGGAGATTCAGAAATCAATG 1217
DB 1141 TGGACATTCGCTTGAAGCACTAGTGGCTATCTTGGGGAGATTCAGAAATCAATG 1200
QY 1218 ACAGAAATTTAATCACTGCGCTCATCTGATCATCTAGTCTGTAACAGAAATTAAG 1277
DB 1201 ACAGAAATTTAATCACTGCGCTCATCTGATCATCTAGTCTGTAACAGAAATTAAG 1260
QY 1278 TCCAGAGAGATGATCTCTCATAGCATGAGTTTGGCCCAATTAATCTGTTGAAGAA 1337
DB 1261 TCCAGAGAGAGATGATCTCTCATAGCATGAGTTTGGCCCAATTAATCTGTTGAAGAA 1320
QY 1338 AATGGGCTTGAATCACTGATCTGGGCTCCACCTCGTGAATTAATGTTGAGGCTTAA 1397
DB 1321 AATGGGCTTGAATCACTGATCTGGGCTCCACCTCGTGAATTAATGTTGAGGCTTAA 1380
QY 1398 AAGCATTCAGAAATTTAAAGCTCAGATGAGAAAGAAATGGGCACTAACAGTGAATGCA 1457
DB 1381 AAGCATTCAGAAATTTAAAGCTCAGATGAGAAAGAAATGGGCACTAACAGTGAATGCA 1440
QY 1458 GATGTCGCCAGGTTCTCTGAGTTATGACACGTTAGATGCCAGAACACTTCTTG 1517
DB 1441 GATGTCGCCAGGTTCTCTGAGTTATGACACGTTAGATGCCAGAACACTTCTTG 1500
QY 1518 GTGACTTACCATCATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1577
DB 1501 GTGACTTACCATCATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1560
QY 1578 TTGAATTCAGACTTTTAAACAGACGACGACAAAGTACTCTTATGATGACAGAGATTA 1637
DB 1561 TTGAATTCAGACTTTTAAACAGACGACGACGACAAAGTACTCTTATGATGACAGAGATTA 1620
QY 1638 CTGACCTCAGCTGCTCTCTCTTGAATCTTGTGGGCTCTCTTACCAAGCTTAGGGTTC 1697
DB 1621 CTGACCTCAGCTGCTCTCTCTTGAATCTTGTGGGCTCTCTTACCAAGCTTAGGGTTC 1680
QY 1698 TATATGCTCTACCATCATGATGATGATGATGATGATGATGATGATGATGATGAT 1757
DB 1681 TATATGCTCTACCATCATGATGATGATGATGATGATGATGATGATGATGATGAT 1740
QY 1758 TAGGAACCTTGTCTCTCTCTTGGACAAAGCAATGTTGAGTGAATGCTTGTGTTG 1817
DB 1741 TAGGAACCTTGTCTCTCTCTTGGACAAAGCAATGTTGAGTGAATGCTTGTGTTG 1800
QY 1818 AGGCGTAAAGTATGATATTAAGTTAGTATCTATTTTCTTAAATATTTGTCGT 1877
DB 1801 AGGCGTAAAGTATGATATTAAGTTAGTATCTATTTTCTTAAATATTTGTCGT 1860
QY 1878 CTGCTAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1932
DB 1861 CTGCTAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1915

RESULT 3

US-10-425-114-5415
; Sequence 5415, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(5313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 5415
; LENGTH: 1300
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: 700454849_FLI
US-10-425-114-5415
Query Match 62.8%; Score 1222.4; DB 13; Length 1300;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1223; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 709 CTATGCTGCTCCAGAGTAATATCTGTAATCTATGCTGAGACTGAGTCCATGTAATG 768
DB 1 CTATGCTGCTCCAGAGTAATATCTGTAATCTATGCTGAGACTGAGTCCATGTAATG 60
QY 769 GAGTTGGGGTGATCTTTATGCTCTTCTTGTGGAAGTCTTCCATTTGATGATGAA 828
DB 61 GAGTTGGGGTGATCTTTATGCTCTTCTTGTGGAAGTCTTCCATTTGATGATGAA 120
QY 829 TATTCCTCAATCTGTTCAAAAAATTAAGGAGGTATCTACACCTTCCAGTCAATTTGTC 888
DB 121 TATTCCTCAATCTGTTCAAAAAATTAAGGAGGTATCTACACCTTCCAGTCAATTTGTC 180
QY 889 TGCTTTGGCCAGGATTTGATCCCAAGATGCTTGTGAGCTTATGAGAGAAATCAC 948
DB 181 TGCTTTGGCCAGGATTTGATCCCAAGATGCTTGTGAGCTTATGAGAGAAATCAC 240
QY 949 AATTAGGGAAATTCGGGAGCATCATGTTCCAGATTCGCTTCCAGTTACTTGGCAGT 1008
DB 241 AATTAGGGAAATTCGGGAGCATCATGTTCCAGATTCGCTTCCAGTTACTTGGCAGT 300
QY 1009 GCCTCCACAGATACGACACAAAGCCAAATGATGATGAGATACCTTCGAGATGT 1068
DB 301 GCCTCCACAGATACGACACAAAGCCAAATGATGATGAGATACCTTCGAGATGT 360
QY 1069 TGTTAATATGGGATTTTAACAAGAACCATGTGTGTAATCACTGTGACGACATTTCAAAA 1128
DB 361 TGTTAATATGGGATTTTAACAAGAACCATGTGTGTAATCACTGTGACGACATTTCAAAA 420
QY 1129 TGAGGCAACTGTTGCTATATTTACTATTGGAACATCGTTTGAAGCAACTAGTGTGCTA 1188
DB 421 TGAGGCAACTGTTGCTATATTTACTATTGGAACATCGTTTGAAGCAACTAGTGTGCTA 480
QY 1189 TCTTGGGGCAGATTAATCAAGATCAATGACAGGAATTTTAATCAGCTGGCGTCAATGTA 1248
DB 481 TCTTGGGGCAGATTAATCAAGATCAATGACAGGAATTTTAATCAGCTGGCGTCAATGTA 540
QY 1249 ATCATCTAGTTCTGTGACAGGAATTAATGTTCCAGGAAGCATGATCTCTATAGCAATGG 1308
DB 541 ATCATCTAGTTCTGTGACAGGAATTAATGTTCCAGGAAGCATGATCTCTATAGCAATGG 600
QY 1309 TTGCGGCCCATATATCTCTGTTGAAAGAAATGGCCCTTGGACTTCAGTCTCGGGCCCA 1368
DB 601 TTGCGGCCCATATATCTCTGTTGAAAGAAATGGCCCTTGGACTTCAGTCTCGGGCCCA 660
QY 1369 CCTCGTGAATAATATGTTGAGTCTTAAAGCACTTCAAGATTTAAACGTCAAGATGAA 1428

DB 661 CCTCGTGAATAATATGTTGAGTCTTAAAGCACTTCAAGATTTAAACGTCAAGATGAA 720
QY 1429 GAGGAATGGGCACTTACAGGTGAATGAGATGTTGGCCAGGGTTCTGGAATTAATGA 1488
DB 721 GAGGAATGGGCACTTACAGGTGAATGAGATGTTGGCCAGGGTTCTGGAATTAATGA 780
QY 1489 CAGTTAGATCCAGCAACAGCTTCTGTGTGACTCTACCATCATGATGATGATGTC 1548
DB 781 CAGTTAGATCCAGCAACAGCTTCTGTGTGACTCTACCATCATGATGATGATGTC 840
QY 1549 TAATGGAGGCTTACTCTGTGATCAAGTTGAATTCAGCTTTACAGAGCAAGACGA 1608
DB 841 TAATGGAGGCTTACTCTGTGATCAAGTTGAATTCAGCTTTACAGAGCAAGACGA 900
QY 1609 CAAGTACCTTGTGATATGACAGAGATCTGAGACCTCAGCTGCTCTTCCTGACTTCTG 1668
DB 901 CAAGTACCTTGTGATATGACAGAGATCTGAGACCTCAGCTGCTCTTCCTGACTTCTG 960
QY 1669 TGGGCTTCTTACCAAGCTTACAGGTTCTATAGTGTCTACCATGTCAGAAATTTTCACT 1728
DB 961 TGGGCTTCTTCTTACCAAGCTTACAGGTTCTATAGTGTCTACCATGTCAGAAATTTTCACT 1020
QY 1729 GTGCTGATGAATACCGAAAGCATGTAAATGAGAACTTGTCTCGTTTGGACAACG 1788
DB 1021 GTGCTGATGAATACCGAAAGCATGTAAATGAGAACTTGTCTCGTTTGGACAACG 1080
QY 1789 AACATGTTGAGGATCGGCTGTGTGAGCGGTAAAGGTATGATATCTTAAAGTTAG 1848
DB 1081 AACATGTTGAGGATCGGCTGTGTGAGCGGTAAAGGTATGATATCTTAAAGTTAG 1140
QY 1849 TACTATTTTCTGTTCTTAATATTTGTGCTGTCTGATGATGATGATTTTGAACATAAA 1908
DB 1141 TACTATTTTCTGTTCTTAATATTTGTGCTGTCTGATGATGATGATTTTGAACATAAA 1200
QY 1909 CGTTAGCAATTAATAAAGAGTAAA 1932
DB 1201 CGTTAGCAATTAATAAAGAGTATA 1224
RESULT 4
US-10-183-687-255
; Sequence 255, Application US/10183687
; Publication No. US20030204870A1
; GENERAL INFORMATION:
; APPLICANT: Allen, Steve
; APPLICANT: Allen, William B.
; APPLICANT: Canoon, Rebecca
; APPLICANT: Ebelbaum, Sabine
; APPLICANT: Famodu, Omolayo O.
; APPLICANT: Harvell, Leslie T.
; APPLICANT: Jones, Todd
; APPLICANT: Kinney, Tony
; APPLICANT: Klein, Ted
; APPLICANT: Li, Changjiang
; APPLICANT: Oliveira, Igor Cunha
; APPLICANT: Sakai, Hajime
; APPLICANT: Shen, Bo
; APPLICANT: Tarczyński, Mitchell C.
; TITLE OF INVENTION: Alteration Of Oil Traits In Plants
; FILE REFERENCE: B01458 US NA
; CURRENT APPLICATION NUMBER: US/10/183,687
; CURRENT FILING DATE: 2002-06-27
; PRIOR APPLICATION NUMBER: 60/301,913
; NUMBER OF SEQ ID NOS: 532
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 255
; LENGTH: 1899
; TYPE: DNA
; ORGANISM: Trifolium aestivum
US-10-183-687-255

[illegible]

Db	1080	CTATTGGGGCTGACCTAATCTACATCAATGGTAGAGATTATATACGTTTACTTCA	1139
Qy	1246	TGAATCATCTAGTCTGGTACGAGAAATTATGTTCCAGAAAGCATGATCCTCATACAG	1305
Db	1140	GGAATCAGCAAGCCCAAGTACCAAGGAGTATCTTCCAGCAAGCAATGATTTCTCAAGCAG	1199
Qy	1306	TGTTTTCGGGCAATTTATCTCTGTTGAAAGAAAATGGGCGCTTGACATTCAGTCTGGGC	1365
Db	1200	TGGCTTGGGCGCAATTTAACCCCGTTGAAGAAAATGGGCTCTTGAGGCTCCAGTCTCAGC	1259
Qy	1366	CCACCTCGTAAATTAATGTTGAGGCTTTAAAGCACTTCAAGATTTAAAGTCAGATG	1425
Db	1260	TCAACTCTGTAGATTAATGATCGAGGTTCTTAAGGCATTTCAAGAAATTTAAATGCTGCTG	1319
Qy	1426	GAAGAGAAATGGGACCTACAAAGTAAATGCAATGGTGGCCAGGTTTCTCGAAGTTAA	1485
Db	1320	GAGAGAGAAATGGAACCTACAAATGAATGAATGCAAGTGGGCGCTTGAGTTCTCGAGTCAG	1379
Qy	1486	TGACACGTTAATGTCAGCAACACGCTTCTTGATGACTTACATCATGATTAATGATGA	1545
Db	1380	TGATTAATGTTAATGCCAACCAACACGCTTGTGATGACTTACATCATGATTAACGGCGA	1439
Qy	1546	TGCTAATGGAGGCTACCTACCTGATCAAGTTTGAATTCAGGCTTTACAAAGACGAAGA	1605
Db	1440	TGCTTAATGGAGGCTACCTCGCGATCAAGTTTGAATTCAGGCTTTTACAAAGACGAAGA	1499
Qy	1606	CGACAGTACTCTTAAGATATGCAAGAGATTACTGACCTCAGCTGCTCTTCTTGAATT	1665
Db	1500	TGACAGATCACTGCTAGATATGACAGAGAGTTACTGACACTCAGCTCTCTCTCGAGATT	1559
Qy	1666	CTGTCGGGCTTCTCTTACCAAGCTTAGGGTCTTAATAGTGTCTAAC	1711
Db	1560	TTGGCGGCTTCTCTTACCAACTTAGGGTCTTAATAGATGCTCC	1605

```

      RESULT 5
      US-10-425-114-22369
      ; Sequence 22369, Application US/10425114
      ; Publication NO. US2004003488A1
      ; GENERAL INFORMATION:
      ; APPLICANT: Liu, Jingdong
      ; APPLICANT: Zhou, Yihua
      ; APPLICANT: Kovalic, David K.
      ; APPLICANT: Screen, Steven E
      ; APPLICANT: Tabaska, Jack E
      ; APPLICANT: Cao, Yongwei
      ; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
      ; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
      ; FILE REFERENCE: 38-21(53313)B
      ; CURRENT APPLICATION NUMBER: US/10/425,114
      ; CURRENT FILING DATE: 2003-04-28
      ; NUMBER OF SEQ ID NOS: 73128
      ; SEQ ID NO 22369
      ; LENGTH: 2119
      ; TYPE: DNA
      ; ORGANISM: Oryza sativa japonbare
      ; FEATURE:
      ; OTHER INFORMATION: Clone ID: LIB3477-009-G7_FLI
      US-10-425-114-22369
    
```

Query Match	Similarity	61.0%	Score 1188.4	DB 13	Length 2119
Best Local	Similarity	85.4%	Pred. No. 0		
Matches 1337	Conservative	0	Mismatches 226	Indels 3	Gaps 1
QY	143	GGCGCGGCAACCGGTAGTAAAGCATGATGTAAGGAGTGGGCAT	202		
Db	100	GGCGGGGAGCTCGGGTGCTCAGTAAATGATGTAAGTAAAGCGGTGGCAT	159		
QY	203	TCTGAGCATTAAGAACTACAACTCTGGGAAAGACTTTAGGTATCGGTACATTTGGAAA	262		
Db	160	TTTAGGCACTGAAGAACTACAACTTTGGAAAGACTTTAGGTATGGCTCATTTTGGAAA	219		

Db 1883 CGCCAAATGAAATATATGAAATGAGAGAAACCAAGAGAAATCAAGATCTGAGA 1824
 Qy 383 TTGTTCAATGACCCCATATCATTCGGCTTATAGAGTCATATACACCTACAGATATA 442
 Db 1823 TTGTTCAATGACCCCATATCATTCGGCTTATAGAGTCATATACACCTACAGATATA 1764
 Qy 443 TATGTTGATGAGATATATGATATAGCGAGTATATTTGATATCATTTGTTGAGAAAGG 502
 Db 1763 TATGTTGATGAGATATATGATATAGCGAGTATATTTGATATCATTTGTTGAGAAAGG 1704
 Qy 503 AGATTAACAGAAAGATGAGAGTCTGTCGAACTTCCAGAGATCATATCTGCGTGAATAC 562
 Db 1703 AGGTTGACAGAAAGATGAGAGTCTGCGCAATCTTCCAGAGATCATATCTGCGGTTGAATAC 1644
 Qy 563 TGGCATAGAAACATGTTGTCACCGTGAACCTTAAGCCGAAACCTTGTAATTGATTA 622
 Db 1643 TGGCAGAGAAACATGTTGTCACCGTGAACCTTAAGCCGAAACCTTGTAATTGATTA 1584
 Qy 623 AAGTATATGTAATTAATTTGCGGATTTTGTCTGAGCAATGTCATGATGAGCCATTTT 682
 Db 1583 AAGTATATGTAATTAATTTGCGGATTTTGTCTGAGCAATGTCATGATGAGCCATTTT 1524
 Qy 683 CTGAAAGCTAGCTGTGAGAGTCCGAACTATGCTCTCCAGAGTAAATATCTGTAATCTA 742
 Db 1523 TTGAAAGCAAGCTGTGAGAGTCCGAACTATGCTCTCCAGAGTAAATATCTGTAATCTA 1464
 Qy 743 TATGCTGAGCTGAGTGTGATATGAGTGTGGGATGATCTTTATGCTCTCTTCTTGT 802
 Db 1463 TATGCTGAGCTGAGTGTGATATGAGTGTGGGATGATCTTTATGCTCTCTTCTTGT 1404
 Qy 803 GGAATCTTCCATTTGATGATGAGAAATATTTCCCAATCTGTTCAAAAAATTAAGGAGAT 862
 Db 1403 GGAATCTTCCATTTGATGATGAGAAATATTTCCCAATCTGTTCAAAAAATTAAGGAGAT 1344
 Qy 863 ATCTACACACTTCCAACTATGTTGCTGTGTCGCAAGGATTTGATCCACGAAATCTT 922
 Db 1343 ATATATCTCTCCAACTATGTTGCTGTGTCGCAAGGATTTGATCCACGAAATCTT 1284
 Qy 923 GTTGTGAGCTTATGAGAGAAATCAAAATTAAGGAAATTTGGGAGCATCAATGTTTCAG 982
 Db 1283 GTTGTGATCAAGAAAGAAATCAAAATTAAGGAAATTTGGGAGCATCAATGTTTCAG 1224
 Qy 983 ATTGCGCTTCCAGCTTACTTGTGCGAGTCTCTCCACAGATACGACAAACCAAGCAATATG 1042
 Db 1223 ATTGCGCTTCCAGCTTACTTGTGCGAGTCTCTCCACAGATACGACAAACCAAGCAATATG 1164
 Qy 1043 ATTGATGAGATACCTTCAAGATGTGTAACTTGGGTTATGGAAGACCAATGTGTGT 1102
 Db 1103 ATTGATGAGATACCTTCAAGATGTGTAACTTGGGTTATGGAAGACCAATGTGTGT 1104
 Qy 1103 GAATCTCTGCGCAATATGAGAGAAATGAGCAACTGTGCAATATTTAACTCTTGGAC 1044
 Db 1103 GAATCTCTGCGCAATATGAGAGAAATGAGCAACTGTGCAATATTTAACTCTTGGAC 1044
 Qy 1163 AATCGTTTATGAGCACTAGTGTATCTTGGGCGAGATTAATCAAGATCAATGAGCAGG 1222
 Db 1043 AATCGATTCGAGATACCAAGTGTATTTGGGAGCAGATATCAAGAAATCTTGGAGAGG 984
 Qy 1223 AATTTAATCAGCTGCGGTCACTGAAATCTAATGTTCTGGTACGAGAAATTAATGTTCCA 1282
 Db 983 AATTTAATCAGCTGCGGTCACTGAAATCTAATGTTCTGGTACGAGAAATTAATGTTCCA 924
 Qy 1283 GGAAGCAGTATCTCTATGAGAGTGTGCGGCAATTAATCTGTTGAAAAGAAATG 1342
 Db 923 GGAAGCAGTATCTCTATGAGAGTGTGCGGCAATTAATCTGTTGAAAAGAAATG 864
 Qy 1343 GCGCTTGAATCTGAGTCTGCGGCGCACTCTGTAAGAAATTAATGTTGAGCTTTAAAGCA 1402
 Db 863 GCTCTTGAATCTGAGTCTGAGTCTGCGGCGCACTCTGTAAGAAATTAATGTTGAGCTTTAAAGCA 804
 Qy 1403 CTTCAGAAATTAATGCTGAGTGAAGAAATGAGGCACTACCAAGTGAATGAGATG 1462
 Db 803 CTTCAGAAATTAATGCTGAGTGAAGAAATGAGGCACTACCAAGTGAATGAGATG 744

Qy 1463 TGGCAGGCTTCTGAGTATGACAGGTGATGCGCAGAAAGCTTCTTGGTAC 1522
 Db 743 AGGTTGGG--ACTAGGCACTGATATGATTAAGTATTAACAACGCTTGTGATAC 687
 Qy 1523 TCTACATCATGATATGATATGATATGATATGAGAGGCTACCTGATCAAGTTTGA 1582
 Db 686 TCATCATATATGATATGATATGATATGATATGATATGAGAGGCTACCTGATCAAGTTTGA 627
 Qy 1583 TTCCAGCTTATCAAGAGAGAGAGAGAGAGTACCTCTTATATATGAGAGATTAAGTGA 1642
 Db 626 ATCCAGCTTATCAAGAGAGAGAGAGAGAGTATCTGATATGAGAGATTAAGTGA 567
 Qy 1643 CTTAGCTGCTCTCTGATCTCTGAGGCGCTTCTTCAAGAGCTTAGGTTCTATAG 1702
 Db 566 CTTAGCTCTCTTCTGAGCTTCTGAGCTTCTGAGCTTCTTCAAGAGCTTAGGTTCTATAG 507
 Qy 1703 TGGTCT 1708
 Db 506 TACCT 501

RESULT 7
 US-10-437-963-49667
 : Sequence 49667, Application US/10437963
 : Publication No. US2004012343A1
 : GENERAL INFORMATION:
 : APPLICANT: La Rosa, Thomas J.
 : APPLICANT: Kovacic, David K.
 : APPLICANT: Zhou, Yihua
 : APPLICANT: Cao, Yongwei
 : APPLICANT: Wu, Wei
 : APPLICANT: Boukharov, Andrey A.
 : APPLICANT: Barbazuk, Brad
 : APPLICANT: Li, Ping
 : TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated with
 : TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
 : FILE REFERENCE: 38-21 (53221) B
 : CURRENT APPLICATION NUMBER: US/10/437, 963
 : CURRENT FILING DATE: 2003-05-14
 : NUMBER OF SEQ ID NOS: 204966
 : SEQ ID NO 49667
 : LENGTH: 2484
 : TYPE: DNA
 : ORGANISM: *Oryza sativa*
 : FEATURE:
 : OTHER INFORMATION: Clone ID: PAT_MRT4530_52229C.1
 : US-10-437-963-49667

Query Match 43.6%; Score 848.8; DB 17; Length 2484;
 Best Local Similarity 70.5%; Pred. No. 5.9e-232;
 Matches 1326; Conservative 0; Mismatches 217; Indels 337; Gaps 1;
 Qy 161 GTAAGAGTGAATATGATGAGTGAATGAAAGGAGTGGGATTTCTGAGCATTAAGGAAAC 220
 Db 150 GTCACTGTGAATATGAGGAAATGCTAGAGGGGGGATTTCTGAGCATTAAGGAAAC 209
 Qy 221 TACAACTGGGAAATCTTGAATGCTGATCTGATCTTGGAAAGTGAAGTTCAGAGCAT 280
 Db 210 TACAACTGAGGAAATCTTGAATGCTGATCTTGGAAAGTGAAGTTCAGAGCAT 269
 Qy 281 AAGCTTACGAGATATGAGGTTGCTATTAAGATCATCACTGCGGCAATTAAGAAATATG 340
 Db 270 AAGCTTACGAGGAGAGAGTGTCTATTAAGATCTCAACCGTGCCTGCAATTAAGAAATATG 329
 Qy 341 GAAATGAGAGAGAGAGAGAGAGATTAAGATATTAAGATTTGATTTCAATCCCAT 400
 Db 330 GAATGAGAGAGAGAGAGAGAGATTAAGATATTAAGATTTGATTTCAATCCCAT 389
 Qy 401 ATCATTCGGCTTATGAGTCAATATACACCTTACAGATATATATTTGATGAGATAT 460
 Db 390 ATCATTCGGCTTATGAGTCAATATACACCTTACAGATATATATTTGATGAGATAT 449

Db 298 ATATTGACTGTGCAAGAATGTCATCAAGATCTCAATCCCGTAAGATCAAGAGCATG 357
Qy 341 GAATGGAAGAAAGAGAAATTCAGAAATTTGAAGTTGTTCAATTCACCCCAT 400
Db 358 GAGATGGAAGAAAGTTAAAGAAATCAAGATCTTAAGATTTATATGACCACAT 417
Qy 401 ATCATTCGGCTTTATGAGTCATATACACCTTACAGATATATATGTTGATGAAATAT 460
Db 418 ATCATTCGGCTTTATGAGTCATATACACCTTACAGATATATATGTTGATGAAATAT 477
Qy 461 TGTAAATGTCGAGGTTATTTGATTAATCTTTGAGAAAGCAAGATTAACAGAAATGAA 520
Db 478 GTCAAAATCTGGAAGTTGTTGATTAATCTTTGAGAAAGCAAGATTAACAGAAATGAA 537
Qy 521 GCTGTCGAATCTTCAGAGATCATATCTGCGTCGAATCTGCGATGAAAGATGTT 580
Db 538 GCTGAGCCTTTTTCAGAGATCATATCTGCGTCGAATCTGCGATGAAAGATGTT 597
Qy 581 GTCCACCGTGAACCTAAAGCCGGAATCTTTGATCTTGAATCAAGATTAATGAAATCTT 640
Db 598 GTTCATGTCATCTTAAGCCAGAACCTCTTTTGAATCAAGATGAAATGTTAATGTT 657
Qy 641 GCGGATTTTGTCTGAGCAATGTCATGATGAGCCATTTTCTGAAGACTGCTGCGG 700
Db 658 GCAGACTTGTGCTGAGTAATGTTATGCGTATGCTCACTTCTGAAGCAAGTTGTTGTT 717
Qy 701 AGTCGAACCTATGCTGCTCCAGAGTAATCTGCTGAATCTATATGCTGAGCCTGAGGTC 760
Db 718 AGCCAAATTAATGAGCACTGAGAGTATCTGCTGAATCTATATGCTGAGCCTGAGGTC 777
Qy 761 GATGATGAGTTGTTGAGGTTATCTTTATGCTCTTTTGAATCACTTCCATTTGAT 820
Db 778 GATGATGAGTTGTTGAGGTTATCTTTATGCTCTTTTGAATCACTTCCATTTGAT 837
Qy 821 GATGAGAAATTTCCCAATCTGCTCAAAAAATTAAGGAGATCTACACTTCCAGT 880
Db 838 GACGAGAAATTTCCCAATCTGCTCAAAAAATTAAGGAGATCTACACTTCCAGT 897
Qy 881 CATTTGCTGCTTGGGCAAGGATTTGATCCAGAAATGCTTGTGTTGAGCCTGATGAG 940
Db 898 CATTTGCTGCTTGGGCAAGGATTTGATCCAGAAATGCTTGTGTTGAGCCTGATGAG 957
Qy 941 AGAATCAAAATTAAGGAAATTCGGAGATCAATGTTTCCAGATTCGCTTCCAGTTAC 1000
Db 958 AGAATCAAAATTAAGGAAATTCGGAGATCAATGTTTCCAGATTCGCTTCCAGTTAC 1017
Qy 1001 TTGSCAGTCTCTCCACAGATAGACACACACCAAGATGATGAAATGAAATCACTT 1060
Db 1018 TTGSCAGTCTCTCTCCACAGATAGACACACCAAGATGATGAAATGAAATCACTT 1077
Qy 1061 CGAGATGTTGTTATATGAGATTTTAAGAAACCATGTTGATCACTGTCAGAGAGA 1120
Db 1078 AATGATGTTATCAATATGAGGTTTGAACAAAGATCACTTATGCAATCACTTCAAGAGA 1137
Qy 1121 CTTCAAAATGAGCACTGTTGCAATTTATTTATTTGCAATCGGTTTGAAGCACT 1180
Db 1138 CTTCAAAATGAGCACTGTTGCAATTTATTTATTTGCAATCGGTTTGAAGCACT 1197
Qy 1181 AGTGGCTATCTTGGGAGATTTATCAAGATCAATGAGCAAGAAATTTAAATCACTGCGG 1240
Db 1198 AGTGGCTATCTTGGGAGATTTATCAAGATCAATGAGCAAGAAATTTAAATCACTGCGG 1257
Qy 1241 TCATCTGAATCAATTAATGTTCTGTTAGAGAAATTTATGTTTCAAGAGACATGATCTCAT 1300
Db 1258 CCAAGTGAACACCAAACTCAGCAGATCATGAGAGATGAGGATGAGATCTCTCT 1317
Qy 1301 AGCAGTGGTTTGGCGCATATTTATCTGTTGAAGAAATGGCGCTTGAAGTCACTGCT 1360
Db 1318 GCGTTTGGCTTGAAGCATTTTGAAGTGAAGAAATGGCGCTTGAAGTCACTGCT 1377
Qy 1361 GCGGCGCACTCTGTTGAATTAATGAGTTGAGGTTTAAAGCACTTCAAGAAATTAAGCTC 1420
Db 1378 CGAGCATCTCCACGAGAAATTAATGAGTTCTTAAAGCTTGAAGAGCTTAAAGTT 1437

Qy 1421 AGATGGAAGAAATGGGCACTAACGTTGAATGAGATGTTGCCAGGTTTCTGAA 1480
Db 1438 TGCTGGAAGAAATGGGCACTAACGTTGAATGAGATGTTGCCAGGTTTCTGAA 1497
Qy 1481 GTTAATGACAGTTTGAATGTCAGCAAGCTTTCTTGTGATCTTACATCATGATTAAT 1540
Db 1498 CATGAGATGATGATGATTAACCAAGCTTTGTGTGATGATGATGATTAATGAAAT 1557
Qy 1541 GATGATCTTAATGGAGGCTTACCTGATGATCAAGTTTGAATTCAGCTTTTACAAAGC 1600
Db 1558 GATGACAGTGAAGAAATCAACCAAGCTGTC---AAATTTAAATTCAGCTTTTACAAACA 1614
Qy 1601 AAGGACAGATGATCTCTTGAATGATGAGATGATGATGATGATGATGATGATGATGAT 1660
Db 1615 AAGGATGAAATTAATCTTCTTGAATGATGATGATGATGATGATGATGATGATGATGAT 1674
Qy 1661 GACTTCTGTGCGGCTTCTTACCAAGCTTGAAGTTTGAATGAT 1703
Db 1675 GACTTCTGTGCGGCTTCTTACCAAGCTTGAAGTTTGAATGAT 1717

RESULT 9
US-10-425-114-35131
; Sequence 35131, Application US/10425114
; Publication No. US20040034888A1
GENERAL INFORMATION:
; APPLICANT: Liu, Jindong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
TITLE OR INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
FILE REFERENCE: 38-21(5313)B
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ. ID NOS: 73128
SEQ. ID NO 35131
LENGTH: 1991
TYPE: DNA
ORGANISM: Zea mays subsp. mexicana
OTHER INFORMATION: Clone ID: UC-ZMFLTEOSINTB089A07_FLI
US-10-425-114-35131

Query Match 41.8%; Score 814.6; DB 13; Length 1991;
Best Local Similarity 69.7%; Pred. No. 3,je-222;
Matches 1150; Conservative 0; Mismatches 489; Indels 12; Gaps 3;
Qy 53 CCTCTCGCCGCTCTCTCCACTGTAAGTGTCTCCGCTCTCCGCGCACTGCTC 112
Db 9 CCTCTCGCCGCTCTCTCCACTGTAAGTGTCTCCGCTCTCCGCGCACTGCTC 68
Qy 113 GTCGCGCGGAGAAAGTTGACCTGTGCAAGGCGCGGAAACCGGTAAGT---AAGAGT 169
Db 69 GCGCGCGCGCGCGCTGCTCTCGGCGGCGGAGAACCTGCAAGCTGCAAGCTCTCCCTGCG 128
Qy 170 AAAATGATGGAATGTAAGTAAGGAGTGGCATTTGTAAGCATTTAAGAACTTACCACTG 229
Db 129 GCGAGTACACAGATGAGGAGGCGGAGAGATGCGCAACCTTTGAGCGGTTACAGAAAT 168
Qy 230 GGAAGAACTTTAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 289
Db 189 GCGCAAAACCTTGGGAAATTTGGGTGTTGCTGTAAGTGAAGATCCAGAACTATATTGACT 248
Qy 290 GGAATGAGTGTGCTTAAAGATCATCACTGCGGCAATGGAATTAAGAAATGGAATGGA 349
Db 249 GGTATGAGTGTGCGATCAAGATTTCTAATCGCAAGAGATGGAAGATGATGATGAG 308
Qy 350 GAGAAAGCAAGAGAAATTAAGATTAAGATTTGATTTGATTTGATTTGATTTGATTTGAT 409
Db 1378 CGAGCATCTCCACGAGAAATTAATGAGTTCTTAAAGCTTGAAGAGCTTAAAGTT 1437

Db 309 GAGAAATTAGAGAAATCAAGATCTGAGATTATTCATCTCATATCATAGC 368
Qy 410 CTTATGAGGTCATATACACCTACAGATATATATGTTGATGAAATATGTAAT 469
Db 369 CTTATGAGGTCATATACACCTGCTGATATATATGTTATGAGATATGTTAA 428
Qy 470 GGGAGTTATTTGATTCATTTGTAAGAAAGCAGATTACAGAAAGTAACTCTG 529
Db 429 GAGAGTTGTTGATTCATGTTGAGAAAGGCTACACGAAAGAGAGCCGAC 488
Qy 530 ATCTTCAGAGATCATATCTGCGTGAATCTCCATGAAACATGTTCTCACCT 589
Db 489 TTTTTCAGAGATCATATCTGCGTGAATATGTCATAGAACATGTTCTCACCT 548
Qy 590 GACCTAAGCCGAAACTGTTACTGATTCAAGATATATGTAACCTTGGAGATT 649
Db 549 GATTAAAGCCAGAAATCTTCTTTGATTCAAATACATATTAAGATGCGGATT 608
Qy 650 GGTCTGAGCAATGTCATGATGATGCGCATTTTCTGAAGCTAGCTGAGAGTCC 709
Db 609 GGTATGATGATGTTATGCGTATGTCATCTTCTTAAGACAGTTGTGGAGCCG 668
Qy 710 TATCTGCTCCAGAGTATATCTGTTAACTATATGCTGACCTGAGTCTGATG 769
Db 669 TATGACACCTGAGTATATCTGTTAACTATATGCTGAGTCTGATGATGCT 728
Qy 770 AGTTGTGGGATGTTCTTTATGCTCTTCTTTGGAATCTCTCATTTGATGAT 829
Db 729 AGCTGTGAGTATCTTTACGCTCTTCTTTGAGCATCTCCATTTGATGATG 788
Qy 830 ATTCCCAATCTGTCAAAAAAATTAGAGAGTATCTACACATCTCCAGCTATT 889
Db 789 ATTCCAACCTTTCAAAAAATAAGGAGTATATATACCTTCTCACTGATTTG 848
Qy 890 GCTTGGCCAGAGTTGATCCACGAATGTTGTTGAGCTTAAAGAAAGTACA 949
Db 849 CCTTCACGAGGACTTGATTCACGAATGCTGTTGTTATTCAAAGAAAGATTA 908
Qy 950 ATTAGGAAATTTGGGAGCATCAATGTTCCAGATTGCGCTCCAGCTTCTTGG 1009
Db 909 ATAGCTAAATCTGTGAACATGTGTGTTCAAGATCCGATTCACCTTATTTG 968
Qy 1010 CCTCCACAGATACGACACAAAGCAAAATGATGATGATGATGATGATGAT 1069
Db 969 CCGCTCCAGACACTGCTCAACAAAGTTAAAGGTCGACGAGAACTTTAATG 1028
Qy 1070 GTTATATGAGATTAACAGAACCATGTGTGATCACTGTGACAGACATTTCA 1129
Db 1029 ATTAAATGAGTGTGTTGACAAAGATCAGCTAATTAATCTGCAAAAAGA 1088
Qy 1130 GAGGCACTGTGATTTATTTTCTATTTGACAAATGCTTTAGAGCAATAGTGC 1189
Db 1089 GAGGCACTGTGATTTATTTTCTATTTGACAAATGCTTTAGAGCAATAGTGC 1148
Qy 1190 CTTGGGCAATTTTCAAGATCAATGACAGAAATTTAAATGCTGGGCTCAT 1249
Db 1149 CTTGGGCAATTTTCAAGATCAATGACAGAAATTTAAATGCTGGGCTCAT 1205
Qy 1250 TCAATGATTTCTGTGACAGAAATTAATGTTCCAGAAAGCAGTATCTCTAG 1309
Db 1206 ACACCACTTCAAGAACTGAACTTGTGACAGATGCTTTCAAGATCTCGGG 1265
Qy 1310 TTTGGGCAATTTTCTGTGAAAGAAATGCGGCTGGAATCTTCAAGTCTCGG 1369
Db 1266 TTTGGGCAATTTTCTGTGAAAGAAATGCGGCTTGTCTTCAAGTCTCGG 1325
Qy 1370 CTTGTAATTAATGTTGAGGCTTTAAAGCACTTCAAGATTTAAAGTCAAG 1429
Db 1326 CCAAGAAATTAATTAAGTAAAGTCTTAAAGCTTCAAGAACTGAAATTTAA 1385
Qy 1430 AAGAAATGAGCACTTCAAGTGAATGCAATGTCAGGCTTCTGAAATTTAA 1489
Db 1386 AAGATTTGGCACTTCAAGTGAATGCAATGTCAGGCTTCTGAAATTTAA 1439

Qy 1490 ACCTTAGATCCAGCAACGCTTTCTTGATGACTTACATCATGATATGATGCT 1549
Db 1440 ATGATGATTAACAGTATATGCTTCACTGAGGAGTCTGATATATGAACTGAT 1499
Qy 1550 AATGGAGGCTTACTTCTGATCAAGTTGAAATTCAGCTTTTCAAGAGAGCAG 1609
Db 1500 ATGAGAAATCAACCCCTTCAAGTGAAGTTGAGATTCAGCTTTTCAAAA 1559
Qy 1610 AAGTACCTCTTATATGAGAGATTAATGAGAGTCAAGCTCAGCTGCTTCTG 1669
Db 1560 AAGTACCTCTTATACCTGCAAGAGGTCAGTGAATCAATCTTCTTCTGAG 1619
Qy 1670 GCGGCTTCTTACCAAGCTTAAAGTTCTAT 1700
Db 1620 TCGGCTTCTTACTGAGCTGAGAGTTCTTT 1650

RESULT 10
US-10-425-114-2148
; Sequence 2148, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jindong
; APPLICANT: Zhou, Yahua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaka, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(5313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 2148
; LENGTH: 1778
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: 700204782_FLI
US-10-425-114-2148

Query Match 41.5%; Score 807.6; DB 13; Length 1778;
Best Local Similarity 72.1%; Pred. No. 3.1e-220;
Matches 1082; Conservative 0; Mismatches 409; Indels 9; Gaps 2;

Qy 201 ATTCTGAAGCATTAAGAACTACACCTGGAAAGAACTTTAGTATCGTACATT 260
Db 147 ATGCCAACCTTTGGGCGGTTACCGAATTGGCAAAACCTAGGAATTTGGGT 206
Qy 261 AAGTGAAGATGAGAGCATTAAGCTTACGAGATTAAGGTTGCTATTAAGATCAT 320
Db 207 AAGTGAAGATGAGAGCATTAATTAAGCTGAGCCATTAAGGTCATTAAGATCT 266
Qy 321 GCGGCAATGAGAAATATGAAATGAAAGAGAAAGCAAGAGATTTCAAGATTTGA 380
Db 267 GCGGCAATGAGAAATGAGAAATGAAAGAGAAAGAGAAAGAGAAATCAAGATCT 326
Qy 381 AGTTGTCATTCACCCCATATCATTTGCTTTATAGGTCATATACACCTTACAG 440
Db 327 GATTATTTATGACATCTCATATCATAGCGCTTTATAGGTCATATACACCTT 386
Qy 441 TATATGTTGATGATATATGTAAGTATGAGGCTTATTTGATTCATTTGAGAA 500
Db 387 TTTATGTTGATGATATATGTAAGTATGAGGCTTATTTGATTCATTTGAGAA 446
Qy 501 GCAGATTACAGAAAGTGAAGCTGTGAAATCTTCAGAGATCATATCTGCGTGA 560
Db 447 GAAGACTACATGAAGAAAGCCGCGCTTTTTCAGAGATCATATCTGCGTGA 506
Qy 561 ACTGCCATGAACATGCTTTGTCACCGTGAACCTTAAAGCCGAAACTTGTACT 620

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Db      507 ATTGCATAGGACATGCTGCTCCCGTGAATTAAAGCCAGAAATCTTTTGATT 566
Qy      621 CAAGATTAATATGTAAGCTTGGATTTGGTCTGAGCAATGTCAGTATGAGCCATT 680
Db      567 CGAATATGCAATTAAGATTGCTGATTTTGGCTTAAGTAATGTAATGCGATGCTCT 626
Qy      681 TTCTGAAGACTAGCTGTGGAGTCCGAATATGCTGTCCAGAGTAATATCTGTAAAC 740
Db      627 TTCTTAAGAGAGTGTGTATGCCGAATTATGAGACCTGAGAGTCATATCTGTAAAC 686
Qy      741 TATATGCTGACCTGAGGTGATATGAGTGTGGGTGATTTCTTATGCTCTTCTT 800
Db      687 TATATGCTGCTCGAAGTGTATGCTGAGCTGCGCGTATTTCTTATGCTCTTCTT 746
Qy      801 GTGGAATCTTCTTCTTATGATGATGATAATATCCCAATCTGTTCAAAAAATTAAGGAG 860
Db      747 GTGCACTCTTCTTCAATTTGACATGATGAAATATTTCAACCTTTTAAAGAAATTAAGGAG 806
Qy      861 GTATCTACACACTTCCAAAGTCAATTTGTCTGTGGCCAGGGATTTGATCCCAAGATGC 920
Db      807 GAATATATACCTTCTTCTTATGCTGATTTGATCACTTCAAGAGGAGACTTGTATCTTGAATGC 866
Qy      921 TTGTGTGTAAGCTTATGAGAAATCAATTAAGGAAATTTGGAGCATCATGTTCC 980
Db      867 TGTGTGTGTAATCCGATGAAAAGATTAATCAATGTAATCCGTGAACATGTGTGTTCA 926
Qy      981 AGATTCCCTTCCAGCTTACTTGGCAGTGCCTCCACAGATATGACACACAAACCCAAA 1040
Db      927 AAATTCACCTTCCGCTTATTTACTGTATCCGCTCCGGAACATGCAACAAATTTAGA 986
Qy      1041 TGATTGTAAGATACACTTGCAGATGTTGTTAATATGGAATTAACAGAACCATGTGT 1100
Db      987 AGCTGACAGAGAAACCTTTAATATGATGTTAATGATGAGTTTGAAGATGAGCTTA 1046
Qy      1101 GTGATCACTGTGACAGACACTTCAAAATGAGGCACTGTTGATTTATTTACTATTGG 1160
Db      1047 TTGAATCTTGCACAAAGATGAGATGAGAGCAAGTGTGCTAATTTACTCATGG 1106
Qy      1161 ACATATGCTTGAAGCAATGATGCTATCTTGGGAGATTAACAGAAATCATATGACA 1220
Db      1107 ACATATGCTTGCACAAAGATGAGATGAGAGCAAGTGTGCTAATTTACTCATGG 1166
Qy      1221 GGAATTAATTAAGCTGAGCTGCTCATATGATCATATGATTTCTGTGAGAGAAATATGTC 1280
Db      1167 CATCTTCTCTCA---AGTACATGCTGAACCAACCACTTCAAGCACTGAACTGACACAC 1223
Qy      1281 CAGAGACAGTATCTCATAGCAGTGTGCGGCAATATTTCTGTTGAAAAAAT 1340
Db      1224 ATGTGTTACAGAAATCTCCGGGGTCTGTTTGAAGGACATTTTGCATCTGAAGAAAT 1283
Qy      1341 GGGGCGTTGACTTCACTTCTGAGCCCACTCTGTAATTAATGTTGAGTCTTAAAG 1400
Db      1284 GGGGCGTTGACTTCACTTCTGAGCCCACTCTGTAATTAATGTTGAGTCTTAAAG 1343
Qy      1401 CACTTCAAGATTAAGCTGATGATGAGAAAGATGAGCACTCAAGAGTGAATGCAAT 1460
Db      1344 CACTGCAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1403
Qy      1461 GGTGCCAGAGGTTTCTGAAGTTATGACAGTTATGATGATGATGATGATGATGATGATGAT 1520
Db      1404 GGAATCTGCTGCTGCTGAGAGT-----ATGATGCAATTAATGATGATGATGATGATGATGAT 1457
Qy      1521 ACTTCACTATCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1580
Db      1458 AGCTGTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1517
Qy      1581 AATTCAGCTTTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1640
Db      1518 AGATTCAGCTTTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1577
Qy      1641 GACCTAGCTGCTTCTTCTTGAATCTGTGCGGCTTCTTCAAGAGAGAGAGAGAGAGAGAGAGAG 1700
Db      1578 GACCACAACTCTCTTCTTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1637

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RESULT 11
US-10-183-687-237
; Sequence 237, Application US/10183687
; Publication No. US20030204870A1
; GENERAL INFORMATION:
; APPLICANT: Allen, Steve
; APPLICANT: Allen, William B.
; APPLICANT: Cahoon, Rebecca
; APPLICANT: Epelbaum, Sabine
; APPLICANT: Famodu, Omolayo O.
; APPLICANT: Harvell, Leslie T.
; APPLICANT: Jones, Todd
; APPLICANT: Kinney, Tony
; APPLICANT: Klein, Ted
; APPLICANT: Li, Changliang
; APPLICANT: Oliveira, Igor Cunha
; APPLICANT: Sakai, Hajime
; APPLICANT: Shen, Bo
; APPLICANT: Tarczyński, Mitchell C.
; TITLE OF INVENTION: Alteration Of Oil Traits In Plants
; FILE REFERENCE: BBI458 US NA
; CURRENT APPLICATION NUMBER: US/10/183,687
; PRIOR FILING DATE: 2002-06-27
; PRIOR APPLICATION NUMBER: 60/301,913
; NUMBER OF SEQ ID NOS: 532
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 237
; LENGTH: 2107
; TYPE: DNA
; ORGANISM: Zea mays
US-10-183-687-237

Query Match      41.3%; Score 804.2; DB 13; Length 2107;
Best Local Similarity 71.7%; Pred. No. 3.3e-219;
Matches 1084; Conservative 0; Mismatches 418; Indels 9; Gaps 2;

Qy      190 AGGAGTGGCAGATTTGAGCACTTAAGAACTACACCTGGAGAAAGCTTATGATCGG 249
Db      238 AGCGGAGAGAGATGCCAACCTTTGAGCGGTACAGAAATGGCAAAACCTGGGAATTCG 297
Qy      250 TACATTTGAAAGTGAAGATTCAGAGCATAGCTTACGATCATGAGTGTGCTATATAA 309
Db      298 GTGCTGGAAGTGAAGATTCGGAACATATATGATGCTATGATGAGTGTGATCAA 357
Qy      310 GATCATCACTGCGCCAAATGAGAAATATGAGAAATGAGAGAGAGAGAGAGAGAGAT 369
Db      358 GATTCATACGCAAGAGATGAGAGAGATGAGATGAGAGAGAGAGAGAGAGAGAT 417
Qy      370 CAAGATTAAGAGTGTTCATTCACCCCAATCATTCGCTTTATGAGTCAATATAC 429
Db      418 CAAGATTAAGAGTATTTATGATCATTCATCATCATGCTTTATGAGTGAATAC 477
Qy      430 ACCTACGATATATATGTTGTGATGATATTTGTAAGTATGAGAGATTTATGATTCAT 489
Db      478 ACCTGATATATGTTGTGATGATATTTGTAAGTATGAGAGATTTGTAATATCAT 537
Qy      490 TGTGAAAGAGAGATTAACAGAGATGAGAGTCTGTCGATCTTCAGAGATCATATAC 549
Db      538 CTTTGAAGAGAGAGAGATTAACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGATC 597
Qy      550 TGGCGTGAATTAATGCTTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 609
Db      598 TGTGTGTAATTAATGCTTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGATC 657
Qy      610 GTTACTGATTAAGATTAATGTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 669
Db      658 TCTTTGATTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 717
Qy      670 TGATGGCAATTTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAT 729

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Db 718 TGAATGCTACCTTTCTTAAAGACGAGTTGGTAGCCCAATTATAGACACCTGAGTCAAT 777
Qy 730 ATCTGGTAACCTATATCTGAGACCTGAGTGCATGATATGAGATTTGGGGTGAATCTTTA 789
Db 778 ATCTGGTAACCTATATCTGAGACCTGAGTGCATGATATGAGATTTGGGGTGAATCTTTA 837
Qy 790 TGGCTCTTTTGGAACTCTTCCATTTGATGATGAGATATTTCCAACTCTTTCAAAA 849
Db 838 TGGCTCTTTTGGAACTCTTCCATTTGATGATGAGATATTTCCAACTCTTTCAAAA 897
Qy 850 AATTAGGAGATCTACACACTTCCAACTATTTGTCTGCTTTGGCCAGGATTTGAT 909
Db 898 AATTAGGAGATCTACACACTTCCAACTATTTGTCTGCTTTGGCCAGGATTTGAT 957
Qy 910 CCAACGATCTGTTGTTGAGCCTATGAGAGATCAATTAAGGAAATTTGGGAGCA 969
Db 958 TCCAGATCTGTTGTTGAGCCTATGAGAGATCAATTAAGGAAATTTGGGAGCA 1017
Qy 970 TCAATGTTCCAGATTTGCTTCCAGCTTACCTTGGCAGTCCCTCCACAGATACGACACA 1029
Db 1018 TGTGTGTTCAAGATCCGACTTCCGCGCTATTTGGCTGTGCGCGCTCCAGACACTGCTCA 1077
Qy 1030 ACAAGCCAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1089
Db 1078 ACAAGTTAAAGGTCGACGAGGAACTCTTAATGATGATGATGATGATGATGATGATGAT 1137
Qy 1090 GAACCATGTTGTTGATCACTGTCGACAGACTTCAAAATGAGGCACTGTGATATTA 1149
Db 1138 GAATCAGCTATTAATCTCTGCAAAAAGATTCGAAATGAGGCAAGTTGCTATTA 1197
Qy 1150 TTTACTATTTGACATCGTTTAAAGCACTAGTGGCTATCTTGGGCGAGATTAACA 1209
Db 1198 TTTACTATTTGACATCGTTTAAAGCACTAGTGGCTATCTTGGGCGAGATTAACA 1257
Qy 1210 ATCAATGACAGATTTAAATCACTGCGCTATCTGATCATCTTGTCTGTACAG 1269
Db 1258 ATCAATGACAGCTCTTGTCTCA---AGTAATGCTGAAACACCACTTCAGCACTGA 1314
Qy 1270 GAATTAATTTCCAGAGAGAGATGATCTCAGATGAGGTTTGGGCGATATTAATCTGT 1329
Db 1315 ACTTCGTCAGATGAGTTTTCAGATCTCCAGTCTGCTGCTGAGGCACTTTTGAC 1374
Qy 1330 TGAAGAAATGAGGCGCTTGAATCTTCACTCGGCGCCACCTCTGTAATGATGAT 1389
Db 1375 TGAAGAAATGAGGCGCTTGAATCTTCACTCGGCGCCACCTCTGTAATGATGAT 1434
Qy 1390 GGTCTTAAAGCACTTCAAGATTTAAAGCTCAGATGAGAGAGATGAGGCACTACAGCT 1449
Db 1435 AGTCTTAAAGCTCTGCAAGAACTGAATGTTTACTGAAAAAGATGAGCACTACAGCT 1494
Qy 1450 GAAATGAGATGAGGCGCGCTTGAATCTTCACTCGGCGCCACCTCTGTAATGATGATGAT 1509
Db 1495 GAAATGAGATGAGGCGCGCTTGAATCTTCACTCGGCGCCACCTCTGTAATGATGATGAT 1548
Qy 1510 CTTCCTTGTGACCTTCAATCATGATGATGATGATGATGATGATGATGATGATGATGAT 1569
Db 1549 CTTCCTTGTGACCTTCAATCATGATGATGATGATGATGATGATGATGATGATGATGAT 1608
Qy 1570 GATCAAGTTGAATTCAGCTTTTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1629
Db 1609 AGTCAGATTTGAATTCAGCTTTTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1668
Qy 1630 GAGAGTACAGAGCTGAGCTCTCTTCACTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1689
Db 1669 AAGGAG 1728
Qy 1690 TAGGCTTCTAT 1700
Db 1729 GAGAGTCTTT 1739

RESULT 12
US-10-183-687-239

Sequence 239, Application US/10183687
Publication No. US20030204870A1
GENERAL INFORMATION:
APPLICANT: Allen, Steve
APPLICANT: Allen, William B.
APPLICANT: Cahoon, Rebecca
APPLICANT: Epelbaum, Sabine
APPLICANT: Famodu, Omolayo O.
APPLICANT: Harvell, Leslie T.
APPLICANT: Jones, Todd
APPLICANT: Kinney, Tony
APPLICANT: Klein, Ted
APPLICANT: Li, Changliang
APPLICANT: Oliveira, Igor Cunha
APPLICANT: Sakai, Hajime
APPLICANT: Shen, Bo
APPLICANT: Tarczyński, Mitchell C.
TITLE OF INVENTION: Alteration Of Oil Traits In Plants
FILE REFERENCE: B1458 US NA
CURRENT APPLICATION NUMBER: US/10/183,687
CURRENT FILING DATE: 2002-06-27
PRIOR APPLICATION NUMBER: 60/301,913
PRIOR FILING DATE: 2001-06-29
NUMBER OF SEQ ID NOS: 532
SOFTWARE: Microsoft Office 97
SEQ ID NO 239
LENGTH: 2052
TYPE: DNA
ORGANISM: Zea mays
US-10-183-687-239

Query Match 40.7%; Score 793.4; DB 13; Length 2052;
Best Local Similarity 72.4%; Pred. No. 4e-216;
Matches 1079; Conservative 0; Mismatches 391; Indels 21; Gaps 3;

Qy 210 CATTAAGAACTACAACTGCGAAGAACTTTAGCTATCGCTATTTGGAAAAAGTGAAGA 269
Db 244 CGTTGAGAAATTAATGCGATTTGCGAAGATTCGGAATTTGGCTATTCGGAAGGTAAAA 303
Qy 270 TTGCGAGCATTAAGCTTTACGACATAGGTTGCTTAAGATCATCACTGCGCAAA 329
Db 304 TTGCGAGCATTAAGCTTTACGACATAGGTTGCTTAAGATCATCACTGCGCAAA 363
Qy 330 TGAAGAAATGAGAAATGAG 389
Db 364 TGAAG 423
Qy 390 TTCACTTCAATCATTTGCTTTATGAGTCAATACACACTTACAGATATATGTTG 449
Db 424 TGCATCACAATTAATCCGCTCTATGAGGTTATGACACACCGCTGATATTTATGTTG 483
Qy 450 TGAATGATTTGATGATGAGGAGTTATTTGATTAATGATTAATGTAAGAGAGAGATTAC 509
Db 484 TTAATGAGATTTGATGATGAGGAGTTATTTGATTAATGATTAATGTAAGAGAGAGATTAC 543
Qy 510 AGGAAGATGAGAGCTGCTGCAATCTTCAGAGATCATATCTGCGTGAATATGCGCAT 569
Db 544 AAGGAAGAGAGAGCTGCGCTTTCTTCCACAGATTAATCCGCTGTAATATGCGCAT 603
Qy 570 GAAACATGTTGTCACCGTACCTTAAAGCGGAAAACTTTGTAATCTTGAATCAAGTATA 629
Db 604 GAAACATGTTGTCACCGTACCTTAAAGCGGAAAACTTTGTAATCTTGAATCAAGTATA 663
Qy 630 ATGTAATACTTGGGAGTTTGGCTGAGCAATGTCATGATGATGATGATGATGATGATGATGAT 689
Db 664 ATGTAATACTTGGGAGTTTGGCTGAGCAATGTCATGATGATGATGATGATGATGATGATGAT 723
Qy 690 CTAGCTGTGAGAGTCCGAATATATGCTCTCAGAGGTAATATCTGTAATATATGCTG 749
Db 724 CAAGTGTGTACCCAAATATATGCTGCTCAGAGGTAATATCTGTAATATATGCTG 783
Qy 750 GACCTGAGTGCATGATGAGAGTTGAGGTTCTTATGCTCTTCTTGTGAACTC 809


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Db 784 GACGTGAAGTGAATGTGTGAGGCTGTGGGGTATTCTTTATGCTTTTATGTGTACTC 843
Qy 810 TTCCATTGATGATGAGATATATCCCATCTGTTCAAAAAATTAAGGAGATCTACA 869
Db 844 TGCCATTGATGAGAGAAATCAAAACCTTTTAAAGAAATTAAGGGGATATATA 903
Qy 870 CACTCCAAATGCTTGTCTGTGGCCAGGGATTGATCCCAAGAACTTGTGTG 929
Db 904 CCTTCCAGCCATTTGTGTGTGAGAGGAGTTGATTCAGAAATGCTAGTGTGCG 963
Qy 930 AGCCTAAGAGAGATCAATTAAGGAAATTCGGAGCATCATAGTGTGCAATTCGCC 989
Db 964 ATCTTAAGAGCGGATACCATTCGTGAATTCGGAACATGATGTTGTTCAAAATCTTC 1023
Qy 990 TTCCAGCTTACTTGGCAGTGTCTTCCAGATACGACAAACAAGCCAAATGATGATG 1049
Db 1024 TCCCGCCCTTATGATGCTGTCTCTCAGATAGTGGCAACAAGTCAAAAAGTTGATG 1083
Qy 1050 AAGATACCTGAGATGTTGTTAATATGGATTTAACAAGACATGTGTGATCAC 1109
Db 1084 AGGAACTTCCGAGGTTTATAGTATGGATATGACAGAACTGTGTGATCAAA 1143
Qy 1110 TGTGACAGACATTCAAATAGAGCACTGTGATATTTACTATTTGACATACGT 1169
Db 1144 TCCAAAAAGGCTGCAAAATGAGGCACTGTGATATTTACTTGTGACATAGGC 1203
Qy 1170 TTAGAGCACTAGTGTCTATCTTGGGCAATTAACAAGATCAATGACAGAAATTA 1229
Db 1204 TCCGTAACACAGGCTATCTTGTGAGCTGAATGCAAGAGCTATGACCTCTCATCT 1263
Qy 1230 ATGAGCTGGGCTATCTGAATCATCTAGTCTGTGATAGAGAAATATGTTCCAGAGCA 1289
Db 1264 CAACATGATCATATGAAACCAAGTTGACAGCTGGAAATGACAGCAATATTTA 1323
Qy 1290 GTATCTCTAGCAGTGTGTGGCCATATTTCTGTGAAAGAAATGGGCGCTTG 1349
Db 1324 TGAAGTCTC---CAGTTGGCTTGAAGACATCTTCCAGCTGAGAGAAATGGGCTTG 1380
Qy 1350 GACTTCAGTCTGGGCCCCCCTCGTGAATATATGTTGAGTCTTAAGCACTTCAAG 1409
Db 1381 GTCTTCAGTCTGAGCAGCATCCAAAGAAATATATGTGAAAGTCTGAAAGCTCTGCAAG 1440
Qy 1410 AATTAACGTCAGATGGAAGAAATGGGCACTACAGGTGAATGAGATGGGCCAG 1469
Db 1441 AATTAATGTTTACTGAAAAAAGATAGTCACTATAATCATGATGAGATGAGTCTG 1500
Qy 1470 GGTTCCTGAAGTTAATGACACGTTAGATCCAGCAACAGCTTCTGTGACTCTACCA 1529
Db 1501 GCTTCTCTGCTCAAAATTCATTAACAATCATTAACCTCA-----GTGCAAGGT 1545
Qy 1530 TCATGATTAATGATGATCTTAATGGAGCTACCTACTGTGATCAAGTTGAATTCAGC 1589
Db 1546 CCAATGAACTGATAGCCTGAGTGAAGGTTA--ACTTTAATTAATTTGAATTCAGC 1602
Qy 1590 TTTAACAAGAGAGAGAGACAGAACTCTTAGATAGAGAGAGTACTAGCCTCAGC 1649
Db 1603 TGTAACAAAACAAGAGAGAAATATCTCTCAGATTTGCAAAAGATGAGTGGCACAGC 1662
Qy 1650 TGCTCTCTTGAATCTGTGTGGGCTTCTCTTACCAAGCTTAGGGTTCTAT 1700
Db 1663 TCTCTTTCTGGAATGTGTGGGCGCTTTCTAATCTCAAGAGATCTTT 1713
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RESULT 13

US-10-425-114-4365
; Sequence 4365, Application US/10425114
; Publication No. US20040034888A1

; GENERAL INFORMATION:

; APPLICANT: Liu, Jindong

; APPLICANT: Zhou, Yihua

; APPLICANT: Kovalic, David K.

; APPLICANT: Screen, Steven E

; APPLICANT: Tabaska, Jack E

```
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(5313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 7128
; SEQ ID NO 4365
; LENGTH: 1742
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: 70035426_FLI
US-10-425-114-4365
```

Query Match 40.7%; Score 793.2; DB 13; Length 1742;
Best Local Similarity 72.9%; Pred. No. 4.1e-216;
Matches 1071; Conservative 0; Mismatches 378; Indels 21; Gaps 3;

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Qy 231 GAGAACTTATGATTCGATACATTTGGAAAGTGAAGTGAAGCATTAACCTTACTG 290
Db 1 GCAAGACTCTGGAAATTTGCTCATTCGGAGGTAAGTTCGGAGCATATCAGACCTG 60
Qy 291 GACATAGGTTGCTATTAAGATCATCACTGCCCAATGAGAAATGAGAAATGGAAG 350
Db 61 GACCAAGGTGGCAATCAAGATTTCTACCGCCGTAAATCAGAGGCAATGAGATGGAAG 120
Qy 351 AGAAGCAAGAGAGATTCAGATTAATGAATTTGATTCACCCCATATCATTTGGC 410
Db 121 AGAAGTTAAAGAGATTAAGATTAATGAGTTATTTATGATCATCAATATATCCGCC 180
Qy 411 TTATAGGTCATATACACCTACAGATTAATATGTTGATGAGAAATATGATATAG 470
Db 181 TCTATGAGTTATAGACACCGCGTATATTTATGTTATGATGATGATTAAGTGTG 240
Qy 471 GCGAGTTATTTGATTCATTTGTTGAGAAAGCAGATTAACAAGATGAGAGTCTGCA 530
Db 241 GGAATATTTATTTATCATTTGTTGAGAAAGTATGCTGACAGAGAGAGAGGCTGCC 300
Qy 531 TCTTCAGCAGATCATATCTGGCGTCAATCTGCAATAGCAATGATGTTGTCACCGTG 590
Db 301 TCTTCCAAAGATTAATATCCGGGTGTAATATGTCATAGAAACATATGTTGTCATCGTG 360
Qy 591 ACCTAAAGCCGGAACCTGTACTTGTATCAAGATTAATGTAATTAACCTTGGCGATTTTG 650
Db 361 ATCTAAAGCCGGAACCTGTACTTGTATCAAGATTAATGTAATTAACCTTGGCGATTTTG 420
Qy 651 GTCTGAGCAATGTCATGATGATGCGCATTTTGTGAAGACTAGCTGTGGAGTCCGAAT 710
Db 421 GCTTAAGTATGTTATGCGGAGATGTCATTTTCTGAAGACATGTTGTAGCCCAATT 480
Qy 711 ATGCTGCTCAAGGATTAATCTGTAACTATATATGCTGACCTGAGAGTGAATGGA 770
Db 481 ATGCTGCTCAAGGATTAATCTGTAACTATATGCTGACCTGAGAGTGAATGGA 540
Qy 771 GTTGTGGGATGATTTCTTTATGCTCTTGTGTGAAGTCTTCCATTTGATGAGAAATA 830
Db 541 GCTGTGGGATTAATCTTTATGCTCTTGTGTGAAGTCTTCCATTTGATGAGAAATA 600
Qy 831 TTCCCATCTGTTCAAAAAATTAAGGAGATTAACACATTTCCAAAGCATTTGTCTG 890
Db 601 TACCAAACTTTTAAAGAAATTAAGGAGATTAATATATACCTTCCAGCATTTGTCTG 660
Qy 891 CTTTGGCAAGGATTTGATCCACGATGCTTGTGTGAGCTTATGAAGAGATCAAA 950
Db 661 GTCCACAGAGGATTTGATTCAAAGATGCTATGTCATCTTATGAAGCGGATCAACA 720
Qy 951 TTAGGAAATTCGGAGCATCAATGTTCCAGATTTGCTTCCAGCTTACTTGGCAGTGC 1010
Db 721 TTGTGAAATTCGCGAAGATGATGTTCAAAATTTCTCCCGCCCTATTTGAGCTGTGC 780
Qy 1011 CTCACAGATACGACAAACAAGCCAAATGATGATGAGATTAACCTTGCAGATGTTG 1070
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Db      781 CTCCTCCAGATAGTGCACAAGTCAAAAAGTTGATGAGAACTCTCCGTGAGGTTT 840
Qy      1071 TTAAATATGGATTTAAACAAAGACATGTGTGAAATACCTGTGACAGACCTTCAAAATG 1130
Db      841 TAGGTATGGAGATATGACAAAGACCTGTGTGATGATCAATCAAAAAGGCTGCAAAATG 900
Qy      1131 AGGCACTGTGTTGATATTTATTTACTATATGCAATCGGTTTAGAGCAACTAGTGCTATC 1190
Db      901 AGGCACTGTGTTGATATTTACTATATGCAATCGGTTTAGAGCAACTAGTGCTATC 960
Qy      1191 TTGGGGCAGATTTACAGAAATCAATGACAGAAATTTAAATCAGCTGGCTCATCTGAT 1250
Db      961 TTGGAGCTGATGTCAGAAAGCTATGAGCTCTCATCTCAAAATGCTCATATATATAA 1020
Qy      1251 CATCTAGTTCTGACAGAAATTAATGTTCCAGGAACAGTGAATCCCTCATAGAGGTT 1310
Db      1021 CACCAATTTAGACAGCTGGGAATGACAGCAAAATATTTATGAGTCTC---CAGTTGGCT 1077
Qy      1311 TGGCGCATATTTATCTGTGAAAGAAATGGCGCTTGGACCTTCAGTCTGGGCCACC 1370
Db      1078 TGAGACCAATCTTCCAGCTGAGAGAAATGGGCTCTTGGCTTCAGTCTGAGCATC 1137
Qy      1371 CTCGTGAATTAATGTTGAGGCTTTAAAGACCTTCAAGATTAACGTGATGAGA 1430
Db      1138 CAAAAGAAATTAATGTTGAGGCTTTAAAGACCTTCAAGATTAATGTTACTGAGAAA 1197
Qy      1431 AGAATGGGCACTACAGGTAAATGACAGATGCTGCCAGGTTTCCGAAAGTTAATGACA 1490
Db      1198 AGATAGGCTACTAATACATGAGAGAGATGAGTCTGCTTCCGCTCAAAATTAATA 1257
Qy      1491 CGTTAGAGCCAGCAAGAGCTTTCTGTGACTTACATCATGATATGATGATGCTA 1550
Db      1258 ACATCATTAATCTCA-----GTGAGGGTTCATTTGAATGATGATGCTGA 1302
Qy      1551 ATGGAGGCTACTACTGTTGATCAAGTTGATTCAGCTTACAGACGAAAGACACA 1610
Db      1303 GTGAGAGGTTA---AGTTTAATTAAGTTTGAATTCAGCTGTACAAAACAGAGACAGA 1359
Qy      1611 AGTACCTCTAGATGATGAGAGGTTACTGGACCTCAGCTGCTCTTCTGACTTCTG 1670
Db      1360 AATACCTCTGATTTGCAAGAGATGAGTGGGCGACAGCTCTCTTCTGACTTGTGCG 1419
Qy      1671 CGGCTTCTTACCAAGCTTATAGGTTCTAT 1700
Db      1420 CGGCTTCTTACCAAGCTTATAGGTTCTT 1449

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; SOFTWARE: Microsoft Office 97
; SEQ ID NO 247
; LENGTH: 2123
; TYPE: DNA
; ORGANISM: Glycine max
; US-10-183-687-247

Query Match      40.2%; Score 782.6; DB 13; Length 2123;
Best Local Similarity 71.1%; Pred. No. 5,2e-213;
Matches 1072; Conservative 0; Mismatches 414; Indels 21; Gaps 2;

Qy      213 TAAGAACTACAACTGGGAGAACTTTAGATGCTATCATTTGAAAGAAAGTGAATTG 272
Db      169 TACCAATTAATTAATTTGGGAAAAACATCGGGATTTGATCTTTTGGCAAGTAAAAATTG 228
Qy      273 CAGAGATAGACTTACTGACATAGAGGTTGCTTAAGATCATCACTGCGGCAATGA 332
Db      229 CAGACATGTTGACTGCGCATAGGTTGCGATCAAGATCTTAACCGACGAAATTA 288
Qy      333 GAATATGAAATGAGAAAGAAAGCAAAAGAAATTTCAAGATTTGAATTGTTGTTTC 392
Db      289 AGAATGAGAAATGAGAAAGAAAGTGAAGAAATCAAAATTTTAAGTTGTTGATGC 348
Qy      393 ACCCCATATCATTTGGCTTTATGAGTCAATATACACCTACAGATATATGTTGTA 452
Db      349 ATCTCATATTTTCACTTATGAAATCATAGAACTCCAACTGACATATATGTTGTA 408
Qy      453 TGAATTTTGTATGATGAGGACTTATTTGATTAATTAATGTTGAGAAAGCAATTAAG 512
Db      409 TGAAGTATGAAAGTCTGAGAGCTTTTGTATTAATGAGAAAGGTTAGGTTGAGG 468
Qy      513 AAGATGAGCTGCTGCAATCTTCACAGATCATATCTGGCGTGAATCTGCCATAGAA 572
Db      469 AAGATGAGCTGCTTAATTTTTCACAGATTAATCTCTGGGTTGAGTATGTCACAGGA 528
Qy      573 ACATGTTTTCACCGTACCTTAAGCCGAAACTTTGTTATCTTGAATTCAGATATATG 632
Db      529 ATATGTTGTTCAATGAGATTTGAAGCTGAGAAATTTACTTTTGAGCTCCAAATGTAATG 588
Qy      633 TAAAGCTGGGATTTTGTCTGACAGATGTCAGATGATGATGAGCAATTTCTGAAGCTA 692
Db      589 TCAAGATGCTGATTTTGTCTGACAGATGTCAGATGATGATGAGCAATTTCTGAAGCTA 648
Qy      693 GCTGTGGAGTCCGAATATGCTGCTCAAGAGTAAATCTGTAAATCTATATGCTGAGAC 752
Db      649 GTTGTGAAACCTTAATCTATGAGCTCTGAGTTATCTCTGGAAATGTATGCTGAGAC 708
Qy      753 CTGAGTGCATGATGAGAGTTGTTGGGTTATCTTTATGCTCTTCTTTTGTGAACTTTC 812
Db      709 CTGAGTGCATGATGAGAGTTGTTGGGTTATCTTTATGCTCTTCTTTTGTGAACTTTC 768
Qy      813 CATTTGATGATGAGATATTTCCCAATCTGTTCAAAAATTTAAGGAGGATCTACACAC 872
Db      769 CTTTGTATGATGAGATATTTCCCAATCTCTTCAAGAAATTAAGGAGGATTTACACTC 828
Qy      873 TTCCAAATCATTTGTCTGCTTTTGGCCAGAGATTTGATCCCAAGATGTTGTTGAGC 932
Db      829 TTCCAAATCATTTATACCCGGTGTAGAGATTTGATACAGAGATGCTTGTGTTGAGC 888
Qy      933 CTATGAGAGATCACAATTTAGGAAATTTGGAGATCAATGTTTCCAGATTTGCTTTC 992
Db      889 CTATGAGAGATCACAATTTAGGAAATTTGGAGATCAATGTTTCCAGATTTGCTTTC 948
Qy      993 CAGTTACTTTGGAGTGGCTCCACAGATTCGACACAAAGCAAGCCAAATGATGATGAG 1052
Db      949 CAGTTACTTTAGTGTGTCACACAGATTCGACACAGCCGCAAGCAAGATGATGAGG 1008
Qy      1053 ATACACTTCAGATGTTGTTAATATGAGATTTAACAAGAACATGTTGTGAATCACTGT 1112
Db      1009 AGATCTTTCAGAGATGTTGAAATGAGATTTGACAGAGATCAATGTTGATGATCTTTC 1068
Qy      1113 GCAGCAGACTTCAAAATGAGCAACTGTTGATATTTATTTACTATTTGACAAATGCGTTTA 1172

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Db 1069 GGAACAGATACAAATGAGGGTACTGTGCATCTATTGTTATTGGACAACCGATTTC 1128
Qy 1173 GAGACATAGTGGCTATCTTGGGCGAGTTATCAAGATCATGACAGAAATTAAATC 1232
Db 1129 GTGTTTCCAGGCTATCTTGGAGCTGAGTTCAAGACATGATTCGGTTTAAATC 1188
Qy 1233 AGCTGGCGTCACTGAATCATCTATGTTCTGTACAGAGAAATTATGTTCCAGAAAGCATG 1292
Db 1189 AATAGCATTCAGAGAACTGCTCTTCAAGTTGTTGAAACCGCTTCCAGGCTACATNG 1248
Qy 1293 ATCTCATAGCAGTGTGTTGCGGCCATATATCTCTTTGAAAGAAATGSGCGCTTGAC 1352
Db 1249 AATATCCAGAGTGAATCGAGCAACAGTTCCTGTTGAAAGAAATGSGCCCTTGCGC 1308
Qy 1353 TTCACTCGGCGCCACCCCTGTGAAATATGTTGAGGCTTTAAAGCATTTCAAGAT 1412
Db 1309 TTCACTCGAGCCATCTCTGTGAAATATGACATGAGGTTCTTAAAGCTTTGCAAGAT 1368
Qy 1413 TAAACGTACATGAGAGAGATGGGCACTACAAAGTAAATGACATGATGTCGCCAGGT 1472
Db 1369 TAAATGTTGTTGAGAGAGATGGTCACTACATGATGATGATGATGATGATGATG 1428
Qy 1473 TTCTGT-----AGTTAATGACAGTTAATGATGCAAGCAAGCTTTCTTG 1517
Db 1429 TTCTGTGTCACGAGAGATGTTAATATGATGATGATGATGATGATGATGATGATG 1488
Qy 1518 GTGACTCTACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1577
Db 1489 ATGATTCATCATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1542
Qy 1578 TTGAATTCAGCTTACAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAT 1637
Db 1543 TTGAATTCAGCTTACAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAT 1602
Qy 1638 CTGACCTCAGCTCTCTCTCTGATCTTCTGATCTTCTGATCTTCTGATCTTCTGATCT 1697
Db 1603 AGGCTCCAGAGTTCTTCTTCTGATCTGATCTGATCTTCTGATCTTCTGATCTTCTG 1662
Qy 1698 TATGCTG 1704
Db 1663 TCTAGAG 1669

RESULT 15
US-09-938-842A-162
; Sequence 162, Application US/0993842A
; Patent No. US20020160378A1
; GENERAL INFORMATION:
; APPLICANT: Harper, Jeff
; APPLICANT: Kreps, Joel
; APPLICANT: Wang, Xun
; APPLICANT: Zhu, Tong
; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
; FILE REFERENCE: SCRIPI300-3
; CURRENT APPLICATION NUMBER: US/09/938,842A
; CURRENT FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: US 60/227,866
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: US 60/264,647
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/300,111
; PRIOR FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 5379
; SEQ ID NO 162
; LENGTH: 1539
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-938-842A-162

Query Match 40.1%; Score 780.2; DB 9; Length 1539;
Best Local Similarity 70.2%; Pred. No. 2e-212;
Matches 1046; Conservative 0; Mismatches 443; Indels 0; Gaps 0;

Qy 212 TTAAAGACTACAACTGGGAGAACTTTAGGTATCGGTACATTTGGAAAAGTGAAGATT 271
Db 49 TTACCGAATTAACAGCTTGGTAAACTCTTGAATTTGGGCTTTTGGAAAGTGAAATA 108
Qy 272 GCAGAGCATTAAGCTTACTGACATAGGGTGTCTATAAAGATCATCAACCTGCCCAATG 331
Db 109 GCAGAGCATGTGTCAAGGGCATTAAGTGTCTATCAAAATCTTAAATCGTCGTAAGATC 168
Qy 332 AGAAATATGAAATGAAAGAGAAAGCAAGAGAAATTCAGATATTGAAGTTGTCAAT 391
Db 169 AAGAACTGAG 228
Qy 392 CACCCCATATCATTCGCTTTATAGAGATATACACACCTACAGATATATATGTTGTG 451
Db 229 CATCTCATATTATTCGCGAGTATGAGATATATAGACACAGAGTCAATTTATGTTGTG 288
Qy 452 ATGAAATATGTAATGATGAGCGAGTTATTTGATTACATTTGTTGAAAGAGAGATTAAG 511
Db 289 ATGAGATATGCAAGCTTGGAGAGCTCTTGAATATTTGTTGAAAGAGAGATTAAG 348
Qy 512 GAAGATGAAGCTGCTGCAATCTTCAGCAAGATCATATCTGCGATGCAATCTGCCATAGA 571
Db 349 GAAGATGAGCTGCTGCAATCTTTTCAGCAAGATCATATCTGCGATGCAATCTGCCATAG 408
Qy 572 AAGATGTTGTCACCGGTGACCTTAAAGCCGAAACCTTGTATCTGATCAAGATTAAT 631
Db 409 AATATGTTGTCATTAAGAGCTGAGAGCTGAGAGATTTACTATTTGATGAGTGTATAT 468
Qy 632 GTAATCTGCGATTTTGTGCTGAGCAATGTCATGATGAGGCAATTTTCTGAAAGCT 691
Db 469 ATTAAGATTCAGAGCTTTGGTGAATGATGATGATGATGATGATGATGATGATGATGATG 528
Qy 692 AGCTGGAGTCCGAATCTATGCTGCTCAGAGGTAATATCTGTAATATATGCTGGA 751
Db 529 AGTGTGGAAGCCCACTAGCTGCTCCGAGGTTATATCAGGTAATATATATGCTGGA 588
Qy 752 CCGAGGTGATGATGAGAGTGTGAGGTTGATCTTATGCTCTTGTGGAAGCTT 811
Db 589 CCGAGGTGATGATGAGAGTGTGAGGTTGATGATGATGATGATGATGATGATGATGATGATG 648
Qy 812 CCATTTGATGATGAGATATTTCCCAATCTGTCCAAAAATTAAGGAGGATCTACACA 871
Db 649 CTTTGTATGATGAGAAACATTTCCCACTTTTCAAGAAATTAAGGATGATTAACACT 708
Qy 872 CTTCCAAAGTATTTGCTGCTTGGCCAGGATTTGATCCACAGATGCTTTGTTGAG 931
Db 709 CTTCCAAAGTATTTATCATCTGAGGCTAGAGACCTGATCCCAAGAGATGCTTAATGTTGAC 768
Qy 932 CTTATGAAGAGATCAACATTAAGGAAATTCGGAAGATCAATGTTCCAGATTCGCTT 991
Db 769 CCGGTGAAGAGATCAACATTTCCGATCCGTCMAACCGGTGTTCCAGACTCATCTC 828
Qy 992 CCAAGTACTTGGAGAGCTCCACAGATAGACACACAAAGCCAAATGATGATGA 1051
Db 829 CTTGTTATCTTGTGCTGCTCTCCACGAGATACAGTACAGAGCTAAAGATCAATGAG 888
Qy 1052 GATACACTTGAGATGTTGTTAATATGAGATTTAACAAGAACATGTTGTGATCACTG 1111
Db 889 GAGATAGTTCAAGAGAGGTTAATCATGAGATTTGATGAACACGTTTGGAAATCTCTA 948
Qy 1112 TGACAGCAGCTTCAAAATGAGCAACCTTGTCATATTTATTTACATTTGCAATCGGTTT 1171
Db 949 CGCAACAGAACACAAACGATGCTACGTTACATCTGTTATTTGGAATACCGGTTTC 1008
Qy 1172 AGAGCACTAGTGGCTATCTTGGGCGAGTTATCAAGATCAATGACAGAAATTTAAAT 1231
Db 1009 CGTGTTCAGAGTGGCTATCTAGAAATCGAGTTTCAAGAGCAACAGACATGTTCCAAAT 1068
Qy 1232 CAGCTGCGTATCTGATCATCTAGTTCTGTGTAACAGAAATTAATGTTCCAGAAAGCAGT 1291
Db 1069 CTAATGCGCACACCTGAAGGCGGCTTCACTGTAGGCGACATGAGATTCCTGACATGTTG 1128

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Qy 1292 GATCCTCATAGCAGTGGTTTCCGGCCATATTAATCTGTGAAAGAAAATGGCGCTTGA 1351
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 1129 GATCAGCTACGGGTTGGAGCAAGATCAAGTCCCTGTGATGGAATAATGGGCTTTGGA 1188
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Qy 1352 CTTGAGTCTGGGGCCCACTCTGTGAATAATGTTGAGGCTTTAAAGCACTTCAAGAA 1411
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 1189 CTTGAGTCTGATGGGCATCTCTCGGAATCATGAAATGAAAGTTTGAAGCTCTTCAAGAA 1248
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Qy 1412 TTAAAGCTCAGATGAGAGAAATGGGCATCAAGCGTGAATGCAAGATGAGTGCCAGGG 1471
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 1249 CTCATGTGTGTGAAGAAATGTTGTCACTACACAAATGAATGCGATGGGTTCTGTGT 1308
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Qy 1472 TTTCCTGAAGTTAATGACAGTTAGATCCAGCAACAGCTTCTTGTGTGACTTACCATC 1531
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 1309 TTAGCTGATGGTCAGAAATCACTATGTCAACAAATCAGCTGCACCTTCAAGATGAATCCAGC 1368
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Qy 1532 ATGGAATATGATGATGCTAAATGGAGGCTTACTAGTATCAAGTTGAATTCAGCTT 1591
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 1369 ATCATTTGAGATGACTGTGCCATGACTTCAACCCACTGTCAATCAAAATTTGAACCTTCAAGCTA 1428
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Qy 1592 TACAGAGCAAGAGCAAGTACCTTTAGATATGAGAGAGTTACTGAGACCTCAGCTG 1651
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 1429 TACAAAGCCCGGAGAGAAATCTTGTGATATACAGAGAGTTAACGGTCCGAGGTTT 1488
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Qy 1652 CTTTCTTGAATCTTGTGGGCGCTTCTTACCAAGCTTAGGGTTCTAT 1700
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 1489 CTCTTCTTGGATCTATGCGCGGCTTCTTACAGAGCTTGTGTGATCT 1537
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||

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Search completed: July 9, 2004, 15:28:10
 Job time : 926 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 7, 2004, 17:50:54 ; Search time 59 Seconds
(without alignments)
2437.571 Million cell updates/sec

Title: US-09-857-522B-4

Perfect score: 2693
Sequence: 1 MDGSSKSGCHSEALRNVLG.....GPELLFDCAFLTKLRVL 509

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database :

A.GeneSeq_29Jan04:*
1: GeneSeq1980s:*
2: GeneSeq1990s:*
3: GeneSeq2000s:*
4: GeneSeq2001s:*
5: GeneSeq2002s:*
6: GeneSeq2003as:*
7: GeneSeq2003bs:*
8: GeneSeq2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2693	100.0	509	3 AAB03416	AAB03416 Corn puta
2	2693	100.0	509	6 ABR40708	ABr40708 Zea mays
3	2422	89.9	509	6 ABR40809	ABr40809 Oryza sat
4	2378	88.3	531	6 ABR40718	ABr40718 Trilicium
5	1977	73.4	505	6 ABR40810	ABr40810 Oryza sat
6	1974.5	73.3	514	6 AAB03420	AAB03420 Soybean p
7	1974.5	73.3	514	6 ABR40714	ABr40714 Glycine m
8	1969.5	73.1	512	6 ABR44015	ABr44015 Human SNF
9	1963	72.9	504	6 ABR40815	ABr40815 Cucumis s
10	1958	72.7	570	6 ABR40710	ABr40710 Zea mays
11	1939	72.0	515	6 AAB03422	AAB03422 Soybean p
12	1939	72.0	515	6 ABR40716	ABr40716 Glycine m
13	1931	71.7	579	6 AAB03417	AAB03417 Corn puta
14	1931	71.7	579	6 ABR40709	ABr40709 Zea mays
15	1923	71.4	511	2 ABR40842	ABr40842 SHP. 8/2
16	1903.5	70.7	512	3 AAG36157	AAG36157 Arabidops
17	1899.5	70.5	512	5 AAO17663	AAO17663 A thalian
18	1891.5	70.2	512	5 AAO17664	AAO17664 A thalian
19	1890.5	70.2	523	3 AAB03425	AAB03425 Wheat put
20	1890.5	70.2	523	6 ABR40719	ABr40719 Trilicium
21	1881.5	69.9	514	6 ABR40816	ABr40816 Glycine m
22	1809.5	67.2	512	5 AAM50578	AAM50578 Arabidops
23	1734	64.4	454	3 AAG36158	AAG36158 Arabidops
24	1724	64.0	452	3 AAG36159	AAG36159 Arabidops
25	1545.5	57.4	494	3 AAG39432	AAG39432 Arabidops

26	1405.5	52.2	437	3 AAG39433	AAG39433 Arabidops
27	1368.5	50.8	420	3 AAG39434	AAG39434 Arabidops
28	1184	44.0	244	3 AAB03424	AAB03424 Wheat put
29	1144	42.5	552	2 AAR64312	AAR64312 Rat liver
30	1119	41.6	548	7 ADD48046	Add48046 Rat Prote
31	1115	41.4	550	7 ADD48048	Add48048 Human Pro
32	1109	41.2	582	4 ABB59603	ABB59603 Drosophi1
33	1101.5	40.9	565	7 ADB61363	ADB61363 Protein o
34	1015.5	37.7	345	2 AAM29894	AAM29894 Mammalian
35	1013.5	37.6	633	6 ABR52941	ABR52941 Protein s
36	971	36.1	304	7 ADC07762	ADC07762 Rice prot
37	940	34.9	257	2 AAM29899	AAM29899 Mammalian
38	861.5	32.0	257	2 AAY43926	Aay43926 Yeast pro
39	749	27.8	783	4 AAG65764	AAG65764 Human pro
40	749	27.8	783	4 AAB85786	AAB85786 Human kin
41	746	27.7	744	5 AAE19049	AAE19049 Human PAR
42	746	27.7	823	3 AAW90879	AAW90879 Human ker
43	745	27.7	729	2 AAW37158	AAW37158 Human Twe
44	745	27.7	729	4 AAB65628	AAB65628 Novel pro
45	745	27.7	729	6 AAE33552	AAE33552 Human mic

ALIGNMENTS

RESULT 1
ID AAB03416 standard; protein; 509 AA.
XX AAB03416;
AC AAB03416;
XX 03-JAN-2001 (first entry)
DT
XX
DE Corn putative carbon catabolite repression protein SNF1 #2.
XX Corn; carbon catabolite repression; sucrose non-fermenting protein 1;
KW SNF1; plant growth.
XX
XX Zea mays.
OS
XX
XX WO200036115-A2.
XX
XX 22-JUN-2000.
XX
XX 15-DEC-1999; 99WO-US029824.
XX
XX 16-DEC-1998; 98US-0112563P.
XX
XX (DUPO) DU PONT DE NEMOURS & CO E. I.
XX
XX Allen SM, Heppard EP, Sakai H, Weng Z, Helentjaris TG, Macool DJ;
XX Miao G;
XX WPI; 2000-431593/37.
XX N-PSDB; AAS52768.
XX
XX New nucleic acids encoding sucrose non-fermenting 1 (SNF1) proteins
XX involved in carbon catabolite repression in plants and seeds, useful for
XX controlling carbon and nitrogen partitioning pathways during plant growth
XX and development.
XX
XX Claim 10; Page 35-36; 59pp; English.
XX
XX The present sequence is a putative sucrose non-fermenting protein SNF1
XX protein sequence from corn. Its coding sequence was isolated by searching
XX a corn cassel shoot cDNA library for sequences similar to those encoding
XX SNF1 in Arabidopsis thaliana, Cucumis sativus, Glycine max and Oryza
XX sativa. The protein is involved in carbon catabolite repression, and so
XX the gene and protein can be used in plants to control the nitrogen and
XX carbon partitioning pathways during plant growth and development. They
XX can also be used to alter the accumulation of carbohydrates, lipids and
XX proteins during plant growth

Sequence 509 AA;

Query Match 100.0%; Score 2693; DB 3; Length 509;
Best Local Similarity 100.0%; Pred. No. 1e-246;
Matches 509; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDGSSKSGHSEALRNVLGRITLIGTFGKVKIAEHKLTGHRVAIKIINCROMNMEME 60
DB 1 MDGSSKSGHSEALRNVLGRITLIGTFGKVKIAEHKLTGHRVAIKIINCROMNMEME 60

QY 61 KAKREFKILKLFHPHIIIRLYEVIYPTDIYVMEYCKYGELEFYIYEKRLQDEARRI 120
DB 61 KAKREFKILKLFHPHIIIRLYEVIYPTDIYVMEYCKYGELEFYIYEKRLQDEARRI 120

QY 121 FQOIIISGEYCHRMVVRHDKPENLLDSKYNVKLADFGLSNMHGHFLKTS CGSPNY 180
DB 121 FQOIIISGEYCHRMVVRHDKPENLLDSKYNVKLADFGLSNMHGHFLKTS CGSPNY 180

QY 181 AAPVTSGLKYAGEVDVWSCGVLLYALLCGTLPPDDENIPNLFKIKGIIYTLPSHLSA 240
DB 181 AAPVTSGLKYAGEVDVWSCGVLLYALLCGTLPPDDENIPNLFKIKGIIYTLPSHLSA 240

QY 241 LARDLIPRMVVEPMKRIITIREIREHQMFOIRLPRYLAAPPDITQAKMIDEDTLADV 300
DB 241 LARDLIPRMVVEPMKRIITIREIREHQMFOIRLPRYLAAPPDITQAKMIDEDTLADV 300

QY 301 NMGRNKNHVCESLCSRLQNEATVAYLLDNRFRAATSGYLGAQVQESMDRLNQLASSES 360
DB 301 NMGRNKNHVCESLCSRLQNEATVAYLLDNRFRAATSGYLGAQVQESMDRLNQLASSES 360

QY 361 SSSGTRNVVPGSSDPHSSGRLPYYPVERKVALGLOSRAHPREIWEVYKALQELNVWKK 420
DB 361 SSSGTRNVVPGSSDPHSSGRLPYYPVERKVALGLOSRAHPREIWEVYKALQELNVWKK 420

QY 421 NGHYNVKCRWCPGPEVNDTLDASNSFLGSDTIMDNNDANGRLPTVIKFEFOLYKTXDK 480
DB 421 NGHYNVKCRWCPGPEVNDTLDASNSFLGSDTIMDNNDANGRLPTVIKFEFOLYKTXDK 480

QY 481 YLLDMQRTGPOLLFLDFCAAFITKRLV 509
DB 481 YLLDMQRTGPOLLFLDFCAAFITKRLV 509

RESULT 2
ABR40708 standard; procein; 509 AA.
ABR40708;
16-MAY-2003 (first entry)
Zea mays oil trait related protein sequence SEQ ID NO:236.
Plant; oil trait; oil phenotype; altered lipid profile; MAP kinase; receptor-like protein kinase; mitogen activated protein kinase; oil; LIP15-like transcription factor caleosin; ATP citrate lyase; SMT1; CMC-like transcription factor; antisense inhibition; co-suppression; transgenic plant.
Zea mays.
MO200302751-A2.
09-JAN-2003.
27-JUN-2002; 2002WO-US020152.
29-JUN-2001; 2001US-0301913P.
(DUPO) DU PONT DE NEMOURS & CO E I.
(PION-) PIONEER HI-BRED INT INC.
Allen SM, Allen WB, Cahoon RE, Epelbaum S, Famodu OO, Harvell LT;

PI Jones TJ, Kinney AJ, Klein TM, Li C, Oliveira IC, Sakai H, Shen B;
PI Tarczyński MC;
XX WPI: 2003-201509/19.
DR N-PSDB; ACC00743.
XX Novel nucleotide fragment encoding polypeptides having receptor-like
PT protein kinase activity, caleosin-like activity, useful for altering oil
PT phenotypes in plants such as sunflower, coconut, soybean, wheat and rice.
XX Claim 12; Page 273-274; 542pp; English.

PS The present invention describes an isolated nucleotide fragment (I)
XX comprising a nucleic acid sequence (NS) chosen from a NS encoding a
CC polypeptide (p) having receptor-like protein kinase activity, mitogen
CC activated protein (MAP)-kinase activity, LIP15-like transcription factor
CC activity, caleosin-like activity, ATP citrate lyase activity, SMT1-like
CC activity and CMC-like transcription factor activity. Also described: (I)
CC complement (II) of (I); (2) a chimeric construct (III) comprising (I) or
CC (II), operably linked to a regulatory sequence; (3) a plant (IV)
CC comprising (III) in its genome; (4) seeds (V) obtained from (IV); and (5)
CC oil obtained from (V). (I) or its part can be used in antisense
CC inhibition or co-suppression in a transformed plant. (III) is useful for
CC altering the oil phenotype in a plant such as corn, soybean, wheat, rice,
CC canola, Brassica, sorghum, sunflower or coconut. (III) is also useful for
CC creating transgenic plants having altered lipid profiles. (I) can also be
CC used as a hybridisation probe. ACC00626 to ACC00668 and ABR40591 to
CC ABR40879 represent sequences used in the exemplification of the present
CC invention
XX

Sequence 509 AA;

Query Match 100.0%; Score 2693; DB 6; Length 509;
Best Local Similarity 100.0%; Pred. No. 1e-246;
Matches 509; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDGSSKSGHSEALRNVLGRITLIGTFGKVKIAEHKLTGHRVAIKIINCROMNMEME 60
DB 1 MDGSSKSGHSEALRNVLGRITLIGTFGKVKIAEHKLTGHRVAIKIINCROMNMEME 60

QY 61 KAKREFKILKLFHPHIIIRLYEVIYPTDIYVMEYCKYGELEFYIYEKRLQDEARRI 120
DB 61 KAKREFKILKLFHPHIIIRLYEVIYPTDIYVMEYCKYGELEFYIYEKRLQDEARRI 120

QY 121 FQOIIISGEYCHRMVVRHDKPENLLDSKYNVKLADFGLSNMHGHFLKTS CGSPNY 180
DB 121 FQOIIISGEYCHRMVVRHDKPENLLDSKYNVKLADFGLSNMHGHFLKTS CGSPNY 180

QY 181 AAPVTSGLKYAGEVDVWSCGVLLYALLCGTLPPDDENIPNLFKIKGIIYTLPSHLSA 240
DB 181 AAPVTSGLKYAGEVDVWSCGVLLYALLCGTLPPDDENIPNLFKIKGIIYTLPSHLSA 240

QY 241 LARDLIPRMVVEPMKRIITIREIREHQMFOIRLPRYLAAPPDITQAKMIDEDTLADV 300
DB 241 LARDLIPRMVVEPMKRIITIREIREHQMFOIRLPRYLAAPPDITQAKMIDEDTLADV 300

QY 301 NMGRNKNHVCESLCSRLQNEATVAYLLDNRFRAATSGYLGAQVQESMDRLNQLASSES 360
DB 301 NMGRNKNHVCESLCSRLQNEATVAYLLDNRFRAATSGYLGAQVQESMDRLNQLASSES 360

QY 361 SSSGTRNVVPGSSDPHSSGRLPYYPVERKVALGLOSRAHPREIWEVYKALQELNVWKK 420
DB 361 SSSGTRNVVPGSSDPHSSGRLPYYPVERKVALGLOSRAHPREIWEVYKALQELNVWKK 420

QY 421 NGHYNVKCRWCPGPEVNDTLDASNSFLGSDTIMDNNDANGRLPTVIKFEFOLYKTXDK 480
DB 421 NGHYNVKCRWCPGPEVNDTLDASNSFLGSDTIMDNNDANGRLPTVIKFEFOLYKTXDK 480

QY 481 YLLDMQRTGPOLLFLDFCAAFITKRLV 509
DB 481 YLLDMQRTGPOLLFLDFCAAFITKRLV 509

Query Match	Best Local Similarity	89.9%	Score 2422	DB 6	Length 509
Matches	451	Conservative 35	Mismatches 23	Indels 0	Gaps 0
1	MDGSSKSGGSHSALNNYNGRTLTIGTFEGKVIAEHLTGHRVAIKIINCROWNNMEME	60			
1	MEGNARCGGSHSALNNYNGRTLTIGTFEGKVIAEHLTGHRVAIKIINCROWNNMEME	60			
61	KAKREFKILKILFIHHIIRLVYEVITPTDIIYVMECKRGELFDYIVYEGRIQOEDBARI	120			
61	KAKREFKILKILFIHHIIRLVYEVITPTDIIYVMECKRGELFDYIVYEGRIQOEDBARI	120			

Qy	121	FOQIISGVEYCHNNVYHGDLPENLLDSDKNNYCLADPGLSNMHGHFLKTS	CGSPNY	180
Db	121	FOQIISGVEYCHNNVYHVDLPENLLDSDKNNYCLADFGLSNMHGHFLKTS	CGSPNY	180
Qy	181	AAPEVISGKLYAPEVDVWVSCGVIYYALLCGTLPPDDENINPLPKKIKGGLYTLPSHLSA	240	
Db	181	AAPEVISGKLYAPEVDVWVSCGVIYYALLCGTLPPDDENINPLPKKIKGGLYTLPSHLSA	240	
Qy	241	LAARDLPRMLVPEPMKRITIREIREHOWFOIRLPEVYLAVPPDDTTOAKMIDEDTLDDV	300	
Db	241	LARDLPRMLVVDPMKRITIREIREHOWFOIRLPEVYLAVPPDDTTOAKMIDEDTLDDV	300	
Qy	301	NMGFNKRVHVESICSLQLEAVAYLLLDNFRFATSGYLGADYQESMDRLNOLASSES	360	
Db	301	NMGFNKRVHVESICSLQLEAVAYLLLDNFRFATSGYLGADYQESMDRLNOLASSES	360	
Qy	361	SSSGTNRVYVGGSSDPHSGSLRPYPERKMALGLOSRAPEIRIWEVYLKALQELNFWKK	420	
Db	361	ASSSTRVYLDGSSDPHSGSLRPYPERKMALGLOSRAPEIRIWEVYLKALQELNFWKK	420	
Qy	421	NGHYNVKCRWCPGFPPEVNDTLDPASNSFLGDSYTIMONDANGRLPTVKKFEFQLYKTKDDK	480	
Db	421	NGQYNNKCRMSVGPQATMDLVNHSFVDDSTIMONDGVNORLPAVIKFELQLYKSRDK	480	
Qy	481	YLLDMQRTGPPQLFLTFDPCAAFLTKRLVL	509	
Db	481	YLLDMQRTGPPQLFLTFDPCAAFLTKRLVL	509	
RESULT 4				
ABR40718	ID	ABR40718	standard; proteoin; 531 AA.	
AC	ABR40718;			
XX	16-MAY-2003	(first entry)		
DT	Triticum aestivum oil trait related protein sequence SEQ ID NO:256.			
DE	Plant; oil trait; oil phenotype; altered lipid profile; MAP kinase; oil; receptor-like protein kinase; mitogen activated protein kinase; oil; LIP15-like transcription factor caleosin; ATP citrate lyase; SNF1; CKC-like transcription factor; antisense inhibition; co-suppression; transgenic plant.			
KW	Triticum aestivum.			
XX	MO2003002751-A2.			
FN	09-JAN-2003.			
PD	27-JUN-2002; 2002MO-US020152.			
PE	29-JUN-2001; 2001US-0301913P.			
XX	(DUPO) DU PONT DE NEMOURS & CO E I.			
PA	(PION-) PIONEER HI-BRED INT INC.			
XX	Allen SM, Allen WB, Cahoon RE, Epeibaum S, Famodu OO, Harvell LT, Jones TJ, Kinney AJ, Klein TW, Li C, Oliveira IC, Sakai H, Shen B, Taczynski MC;			
XX	WPI: 2003-201509/19.			
DR	N-PSDB; ACC00753.			
XX	Novel nucleotide fragment encoding polypeptides having receptor-like protein kinase activity, caleosin-like activity, useful for altering oil phenotypes in plants such as sunflower, coconut, soybean, wheat and rice.			
PS	Claim 12; Page 296-298; 542bp; English.			
XX	The present invention describes an isolated nucleotide fragment (I) comprising a nucleic acid sequence (NS) chosen from a NS encoding a			

CC	polypeptide (pp) having receptor-like protein kinase activity; mitogen
CC	activated protein (MAP)-kinase activity; LIP15-like transcription factor
CC	activity; calceosin-like activity; ATP citrate lyase activity; SNF1-like
CC	activity and CCK-1-like transcription factor activity. Also described: (1)
CC	complement (II) of (I); (2) a chimeric construct (III) comprising (I) or
CC	(II), operably linked to a regulatory sequence; (3) a plant (IV)
CC	comprising (III) in its genome; (4) seeds (V) obtained from (IV); and (5)
CC	oil obtained from (V). (I) or its part can be used in antisense
CC	inhibition or co-suppression in a transformed plant. (III) is useful for
CC	altering the oil phenotype in a plant such as corn, soybean, wheat, rice,
CC	canola, Brassica, sorghum, sunflower or coconut. (III) is also useful for
CC	creating transgenic plants having altered lipid profiles. (I) can also be
CC	used as a hybridisation probe. ACC00626 to ACC00868 and ABR40591 to
CC	ABR40879 represent sequences used in the exemplification of the present
CC	invention
CX	
XX	Sequence 531 AA;
SQ	
Query Match	88.3%; Score 2378; DB 6; Length 531;
Best Local Similarity	86.8%; Pred. No. 9.9e-211;
Matches 442; Conservative	34; Mismatches 33; Indels 0; Gaps 0;
OY	1 MDGSSKSGSHSPALNNYLIGRTLTGCTGGKVIAEHKLTGHRVAIKINCROMRMMEEE 60
DB	23 MEGNTRGGGHSDALKNNVGNVGRITLGCTGGKRIAHAKHTGKHVALKIINRORMRMEME 82
OY	61 KAKREFKILKLFIHPIIRLVEVIYTPTDIYVMEEKYGELEFDYIEVKRGLOEDBARI 120
DB	83 KAKRKIKILRLFIHPIIRLVEVIYTPDIFVWMEYCKKGELFDICVEKRGLOEDBARI 142
OY	121 FOQIIISGVGYCHRRMNVVRHDLPKEULLDDSKNVYGLADPGLSNWHDGHFLTKSCGSRY 180
DB	143 FOOIIISGVGYCHRRMNVVHRDLKPENMLLDISKNVYGLADPGLSNWHDGHFLTKSCGSRY 202
OY	181 AAPEVISGKLYAAGPEVDVWMSGVLLYALLCGTLPPDENIPVLFKKIKGTTLPSHLSA 240
DB	203 AAPEVISGKLYAAGPEVDVWMSGVLLYALLCGTLPPDDDNIPVLFKKIKGTIILPSHLSA 262
OY	241 LARDLIPLMLVPEPMKRITTIRESIREHOWFOIRLPRYLAVPREDTIOAKMIDEDTLRDV 300
DB	263 LARDLIPLMLVDPMKRITTIRESIRHPMFQRNLPRYLAVPREDTIOAKMIDEDTLKEIV 322
OY	301 NMGFKNHVCESLCSRLONEATVAYLLLDNRFRATSGTIGADYOESMDRNLNQLASSE 360
DB	323 NLGYDKDHVCESLCNRLONEATVAYLLLDNRFRASTGIGADYIQSMGRSFNOFTLES 382
OY	361 SSSGGRANVPGSSDDSHSLGRPYEVEREKMAJGLSRAPREIMVEYKALOELNVRWKK 420
DB	383 ASPSTRQYULPASNDQSGSLRPYYVERKMAJGLOSRAQPREIMTEVLAKEDELNVCMKK 442
OY	421 NGHYNVKCRMGCPPEPVNDTLDASNSFLGDSITIMDNDANGRLPTVIKREFOLYXTXDK 480
DB	443 NGHYNMKCRMCGFPQVSMDLANHSFVDDSTITMDNGANGRLPAVIKFEIQLYXTXDK 502
OY	481 YLLDMQRTYGPOLLFLDFCAALTLTGRLV 509
DB	503 YLLDMQRTVGPOLLFLDFCAALTLMLRVLV 531
RESULT 5	
ID	ABR40810 standard; protein; 505 AA.
AC	ABR40810;
XX	
DT	16-MAY-2003 (first entry)
XX	
DE	Oryza sativa oil trait related protein sequence SEQ ID NO:402.
KW	Plant; oil trait; oil phenotype; altered lipid profile; MAP kinase;
KW	receptor-like protein kinase; mitogen activated protein kinase; oil;
KW	LIP15-like transcription factor; calceosin; ATP citrate lyase; SNF1;
KW	CCK-1-like transcription factor; antisense inhibition; co-suppression;

[illegible]

PS Claim 12; Page 287-289; 542pp; English.

XX The present invention describes an isolated nucleotide fragment (1)

CC comprising a nucleic acid sequence (NS) chosen from a NS encoding a

CC polypeptide (PP) having receptor-like protein kinase activity, mitogen

CC activated protein (MAP)-kinase activity, LIP5-like transcription factor

CC activity, calcosin-like activity, ATP citrate lyase activity, SNF1-like

CC activity and CXC-like transcription factor activity. Also described: (1)

CC complement (II) of (I); (2) a chimeric construct (III) comprising (I) or

CC (II), operably linked to a regulatory sequence; (3) a plant (IV) or

CC comprising (III) in its genome; (4) seeds (V) obtained from (IV); and (5)

CC oil obtained from (V). (I) or its part can be used in antisense

CC inhibition or co-suppression in a transformed plant. (III) is useful for

CC altering the oil phenotype in a plant such as corn, soybean, wheat, rice,

CC canola, Brassica, sorghum, sunflower or coconut. (III) is also useful for

CC creating transgenic plants having altered lipid profiles. (I) can also be

CC used as a hybridisation probe. ACC00626 to ACC00868 and ABR40591 to

CC ABR40879 represent sequences used in the exemplification of the present

CC invention

XX

XX Sequence 514 AA;

XX

Query Match 73.3%; Score 1974.5; DB 6; Length 514;

Best Local Similarity 74.0%; Pred. No. 2.2e-178;

Matches 382; Conservative 49; Mismatches 76; Indels 9; Gaps 3;

QY 1 MDGSS--KSGSEALRYNYLGRITLGITGPKVKIAEHKLTGHRVAIKIINCGRMNMEM 58

DB 1 MDGPRGCGAGLDLDFPKYKLGITLGISFGKVKIAEHVLTGHRVAIKILRRKIKNMEM 60

QY 59 EEKAKREFKILKFIHPHIIIRLYEVITYPTDIYVMEYCKYGLFDYIVKGRLOEDBEAR 118

DB 61 EEKVRREIKILRLFMHPHIIIRLYEVITYPTDIYVMEYCKYGLFDYIVKGRLOEDBEAR 120

QY 119 RIFQOIIISGVYCHRNMYVHRDLKPEMLLDISKYNYVLADFGLSNVWHDGFLTKSCGSP 178

DB 121 NFFQOIIISGVYCHRNMYVHRDLKPEMLLDISKYNYVLADFGLSNVWHDGFLTKSCGSP 180

QY 179 NYAAPEVISGKLYAGPEVDVMSGCVIYALCGLTPDDENINPLFKIKIGIYTLPSHL 238

DB 181 NYAAPEVISGKLYAGPEVDVMSGCVIYALCGLTPDDENINPLFKIKIGIYTLPSHL 240

QY 239 SALARDLIPMLVVEPMKRTITIREIHEQWFOIRLPRYLAVPPDDTQOAKMIDEDTLRD 298

DB 241 SPGARLDLIPMLVVDPMKRMRTIPEIRQHPMFQARLPRYLAVPPDDTQOAKMIDEDTLRD 300

QY 239 VVNMGFNKNHVCESLCSRLQNEATVAYYLLDNRFRASGYLGADYQESMDRNLNQLASS 358

DB 301 VVNMGFNKNHVCESLCSRLQNEATVAYYLLDNRFRASGYLGADYQESMDRNLNQLASS 360

QY 359 ESSSSGTRNYPVPGSSDPHSSGLRPYVVERKMAIGOSRAHPREIMTEVULKALQELNVW 418

DB 361 ELASSVGNRRPFGIMEYGVGLSRQFVERKMAIGOSRAHPREIMTEVULKALQELNVW 420

QY 419 KKNGHYNVCRCWCPGFP-----EYNDTLDASNSFLGDSITMNDNDANGRLPTVIKFEFOL 473

DB 421 KKIGHYNNKCRWVAGIPGHHEGMVNNVHNSHYFGDSITMNDNDANGRLPTVIKFEFOL 474

QY 474 YKTKDDKYLDMORVITGPOLLFLDPCAFPLTKLARVL 509

DB 479 YKTRBEKYLTLDRVQGFPLDLCAAFPLAQLARVL 514

RESULT 8

ABR44015

ABR44015 standard; protein; 512 AA.

XX ABR44015;

XX

XX 04-AUG-2003 (first entry)

XX DT

XX Human SNF1-related protein kinase KIN10.

XX

KW Serine/threonine kinase; cytosolic; neuroprotective; antidiabetic;

KW gene therapy; cancer; chronic obstructive pulmonary disease; COPD; human;

KW SNF1-related protein kinase KIN10; EC 2.7.1; enzyme.

XX

XX Homo sapiens.

XX

XX WO2003035859-A2.

XX

XX 01-MAY-2003.

XX

XX 17-OCT-2002; 2002MO-EP011615.

XX

XX 19-OCT-2001; 2001US-0330077P.

XX

XX (FAR) BAYER AG.

XX

XX Liou J;

XX

XX WPI; 2003-421421/39.

XX

XX

XX New serine/threonine kinase polypeptide or polynucleotide, useful for

PT preparing a composition for treating cancer, diabetes, CNS disorder or

PT Chronic Obstructive Pulmonary Disease (COPD).

XX

XX Disclosure; Fig 3; 109pp; English.

XX

XX The invention relates to a human serine/threonine kinase polypeptide and

CC encoding polynucleotide. The polynucleotide can be expressed by standard

CC recombinant methodology. The polynucleotide is useful for preparing a

CC composition for treating cancer, diabetes, CNS disorder or Chronic

CC Obstructive Pulmonary Disease (COPD). The present sequence represents a

CC human SNF1-related protein kinase KIN10 identified by swisnew/Q38997/

CC K110 ARARH used in alignment studies with the human serine/threonine

CC kinase

XX

XX Sequence 512 AA;

XX

Query Match 73.4%; Score 1969.5; DB 6; Length 512;

Best Local Similarity 72.8%; Pred. No. 6.5e-178;

Matches 377; Conservative 52; Mismatches 74; Indels 15; Gaps 4;

QY 1 MDGSSK--SGSEALRYNYLGRITLGITGPKVKIAEHKLTGHRVAIKIINCGRMNMEM 58

DB 1 MDGSGTSRSGVSSILPNYKLGITLGISFGKVKIAEHVLTGHRVAIKILRRKIKNMEM 60

QY 59 EEKAKREFKILKFIHPHIIIRLYEVITYPTDIYVMEYCKYGLFDYIVKGRLOEDBEAR 118

DB 61 EEKVRREIKILRLFMHPHIIIRLYEVITYPTDIYVMEYCKYGLFDYIVKGRLOEDBEAR 120

QY 119 RIFQOIIISGVYCHRNMYVHRDLKPEMLLDISKYNYVLADFGLSNVWHDGFLTKSCGSP 178

DB 121 NFFQOIIISGVYCHRNMYVHRDLKPEMLLDISKYNYVLADFGLSNVWHDGFLTKSCGSP 180

QY 179 NYAAPEVISGKLYAGPEVDVMSGCVIYALCGLTPDDENINPLFKIKIGIYTLPSHL 238

DB 181 NYAAPEVISGKLYAGPEVDVMSGCVIYALCGLTPDDENINPLFKIKIGIYTLPSHL 240

QY 239 SALARDLIPMLVVEPMKRTITIREIHEQWFOIRLPRYLAVPPDDTQOAKMIDEDTLRD 298

DB 241 SPGARLDLIPMLVVDPMKRMRTIPEIRQHPMFQARLPRYLAVPPDDTQOAKMIDEDTLRD 300

QY 239 VVNMGFNKNHVCESLCSRLQNEATVAYYLLDNRFRASGYLGADYQESMDRNLNQLASS 358

DB 301 VVNMGFNKNHVCESLCSRLQNEATVAYYLLDNRFRASGYLGADYQESMDRNLNQLASS 359

QY 359 ESSSSGTRNYPVPGSSDPHSSGLRPYVVERKMAIGOSRAHPREIMTEVULKALQELNVW 418

DB 360 ESVAASPVSHRLFGIMEYGVGLSRQFVERKMAIGOSRAHPREIMTEVULKALQELNVW 419

QY 419 KKNGHYNVCRCWCPGFPFVNDTLDA-----NSNFGDSITMNDNDANGRLPTVIKFEF 471

DB 420 KKIGHYNNKCRWV-----NSADGMLSNMMDNNVNGDESSITENEAAYKSPVNVVFEI 474

XX PS Claim 12; Page 278-280; 542pp; English.

XX CC The present invention describes an isolated nucleotide fragment (1)

XX CC comprising a nucleic acid sequence (NS) chosen from a NS encoding a

XX CC polypeptide (P) having receptor-like protein kinase activity, mitogen

XX CC activated protein (MAP)-kinase activity, lipid-like transcription factor

XX CC activity, calcosin-like activity, ATP citrate lyase activity, SNF1-like

XX CC activity and CLK-like transcription factor activity. Also described: (1)

XX CC complement (II) of (I); (2) a chimeric construct (III) comprising (I) or

XX CC (II), operably linked to a regulatory sequence; (3) a plant (IV)

XX CC comprising (III) in its genome; (4) seeds (V) obtained from (IV); and (5)

XX CC oil obtained from (V). (I) or its part can be used in antisense

XX CC inhibition or co-suppression in a transformed plant. (III) is useful for

XX CC altering the oil phenotype in a plant such as corn, soybean, wheat, rice,

XX CC canola, Brassica, sorghum, sunflower or coconut. (II) is also useful for

XX CC creating transgenic plants having altered lipid profiles. (I) can also be

XX CC used as a hybridisation probe. ACC00626 to ACC00868 and ABR40591 to

XX CC ABR40879 represent sequences used in the exemplification of the present

XX CC invention

XX SQ Sequence 570 AA:

Query Match 72.7%; Score 1958; DB 6; Length 570;

Best Local Similarity 74.8%; Pred. No. 9.5e-177;

Matches 382; Conservative 48; Mismatches 67; Indels 14; Gaps 6;

QY 1 MDGSSKSGHSEALRNVLGRTLGITGFGKVKIAEHKLTGHRVAIKILNCKRMNMEME 60

DB 72 MEGAGK--DGNPLRNRYIGKTIGISFGKVKIAEHSTGKVAIKILNRKIKGMEE 128

QY 61 KAKEPKILKLFIPHIIRLYEVITYPTDIYVMEYCKYGLFDYIEKRLQDEAR 120

DB 129 KVKKEIKILRFPMPIIRLYEVITDTPADYVMEYCKYGLFDYIEKRLQDEAR 188

QY 121 FQGIISGEYCHRMNVVHRDLKPENLILDSKYNKVLADFGLSNVMDHGLFKTSCG 180

DB 189 FQGIISGEYCHRMNVVHRDLKPENLILDSKYNKVLADFGLSNVMDHGLFKTSCG 248

QY 181 AAPVIGSKUYAGEVDVWMSGVILYALCGTLPPDDENIPNLFKIKGITYLP 240

DB 249 AAPVIGSKUYAGEVDVWMSGVILYALCGTLPPDDENIPNLFKIKGITYLP 308

QY 241 LARLILPRMLVVEPMKRTITREIREHWFQIRLPRYLAVPPDTTOAKMIDEDTL 300

DB 309 AARLILPRMLVVEPMKRTITREIREHWFQIRLPRYLAVPPDTTOAKMIDEDTL 368

QY 301 MGFNKNHVCESLCSRLQNEATVAYLLDNRFPAATSGYLGADYQESMDRNLQ 359

DB 369 GMGYDKMLVSIQKRLQNEATVAYLLDNRLRTTSGYLGAEQCEAMDSSFSNI 428

QY 360 -SSSSGTRNVYPGSSDPHSSGLRPYYPVERKVALGOSRAHPRREIVETL 418

DB 429 PSSARGNQQLFMES---PVGRLRPHLPKREKVALGOSRAHPRREIVETL 485

QY 419 KKNGHVYVCKMCEPPEVNDTLIDNSFLDSTIMNDANGRLPTVIKEFQLYTKD 478

DB 486 KKGIGHYVCKMCEPPEVNDTLIDNSFLDSTIMNDANGRLPTVIKEFQLYTKD 539

QY 479 DKYLLDMQRTVTPOLLFLDFCAFLYTKRVL 509

DB 540 EKYLLDMQRTVTPOLLFLDFCAFLYTKRVL 570

RESULT 11

AAB03422

ID AAB03422 standard; protein, 515 AA.

XX AAB03422;

AC AAB03422;

XX 03-JAN-2001 (first entry)

XX DE Soybean putative carbon catabolite repression protein SNF1 #4.

XX KM Soybean; carbon catabolite repression; sucrose non-fermenting protein 1;

XX KM SNF1; plant growth.

XX OS Glycine max.

XX PN W0200036115-A2.

XX PD 22-JUN-2000.

XX PF 15-DEC-1999; 99MO-US029824.

XX PR 16-DEC-1998; 98US-0112563P.

XX PA (DUPO) DU FONT DE NEMOURS & CO E. I.

XX PI Allen SM, Heppard EP, Sakai H, Weng Z, Helentjaris TG, Macool DJ;

XX PI Mao G;

XX DR WPI; 2000-431593/37.

XX DR N-PSDB; AA52774.

XX PT New nucleic acids encoding sucrose non-fermenting 1 (SNF1) proteins

XX PT involved in carbon catabolite repression in plants and seeds, useful for

XX PT controlling carbon and nitrogen partitioning pathways during plant growth

XX PS Claim 10; Page 48-50; 59pp; English.

XX CC The present sequence is a putative sucrose non-fermenting protein SNF1

XX CC protein sequence from the soybean. Its coding sequence was isolated by

XX CC searching a seed cDNA library for sequences similar to those known to

XX CC encode SNF1 in Arabidopsis thaliana, Cucumis sativus, Glycine max and

XX CC Oryza sativa. The protein is involved in carbon catabolite repression,

XX CC and so the gene and protein can be used in plants to control the nitrogen

XX CC and carbon partitioning pathways during plant growth and development.

XX CC They can also be used to alter the accumulation of carbohydrates, lipids

XX CC and proteins during plant growth

XX SQ Sequence 515 AA:

Query Match 72.0%; Score 1939; DB 3; Length 515;

Best Local Similarity 72.1%; Pred. No. 5.2e-175;

Matches 373; Conservative 58; Mismatches 76; Indels 10; Gaps 4;

QY 1 MDGSS-KGSHS--EALRNVLGRTLGITGFGKVKIAEHKLTGHRVAIKILNCKRMN 57

DB 1 MDSSTGGGGSVDMFLRNKYLKGTIGISFGKVKIAEHVRTGKVAIKILNRKIKME 60

QY 58 MEKAKKEPKILKLFIPHIIRLYEVITYPTDIYVMEYCKYGLFDYIEKRLQDEA 117

DB 61 MEKVRREIKILRFPMPIIRLYEVITDTPADYVMEYCKYGLFDYIEKRLQDEA 120

QY 118 RRIFFQGIISGEYCHRMNVVHRDLKPENLILDSKYNKVLADFGLSNVMDHGLFKTSCG 177

DB 121 RHFFQGIISGEYCHRMNVVHRDLKPENLILDSKYNKVLADFGLSNVMDHGLFKTSCG 180

QY 119 RRIFFQGIISGEYCHRMNVVHRDLKPENLILDSKYNKVLADFGLSNVMDHGLFKTSCG 177

DB 121 RHFFQGIISGEYCHRMNVVHRDLKPENLILDSKYNKVLADFGLSNVMDHGLFKTSCG 180

QY 178 PNYAAPVIGSKUYAGEVDVWMSGVILYALCGTLPPDDENIPNLFKIKGITYLP 237

DB 181 PNYAAPVIGSKUYAGEVDVWMSGVILYALCGTLPPDDENIPNLFKIKGITYLP 240

QY 238 LALARDLILPRMLVVEPMKRTITREIREHWFQIRLPRYLAVPPDTTOAKMIDEDTL 297

DB 241 LSPGARDLILPRMLVVEPMKRTITREIREHWFQIRLPRYLAVPPDTTOAKMIDEDTL 300

QY 298 DVYMGFNKNHVCESLCSRLQNEATVAYLLDNRFPAATSGYLGADYQESMDRNLQ 357

DB 301 EYVMGFDRLQVLSINRIQNEGTIVYLLDNRFPAATSGYLGADYQESMDRNLQ 360

QY 358 SESSSGSTRNVYPGSSDPHSSGLRPYYPVERKVALGOSRAHPRREIVETL 417

DB 361 GEVASPVVGHSHSTGYMDYQGVGMKQPFVERKVALGOSRAHPRREIVETL 420

PT and development.

PS Claim 10; Page 37-39; 59pp; English.

CC The present sequence is a putative sucrose non-fermenting protein SNFP
CC protein sequence from corn. Its coding sequence was isolated by searching
CC a corn stem cDNA library for sequences similar to those encoding SNFP in
CC Arabidopsis thaliana, Cucumis sativus, Glycine max and Oryza sativa. The
CC protein is involved in carbon catabolite repression, and so the gene and
CC protein can be used in plants to control the nitrogen and carbon
CC partitioning pathways during plant growth and development. They can also
CC be used to alter the accumulation of carbohydrates, lipids and proteins
CC during plant growth

SQ Sequence 579 AA;

Query Match	71.7%;	Score 1931;	DB 3;	Length 579;
Best Local Similarity	73.1%;	Pred. NO. 3.6e-174;		
Matches 372;	Conservative	5;	Mismatches 77;	Indels 6;
				Gaps 3.

```

OY 1 MDSSKSGSHSALNRYNLTGRTIGTGPCKVJLAHEKLTGHRVAKIINCPOQRNMEME 60
OY 1 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 77 MEGAQR---DANPLSGYRIKTLTGIGSPCKVJLAHEIILTGHKVAIKILARRKKIRSMDBEE 133
OY 61 KAKREBKILKFIHPHIIIRLYEVIYPTDIYYVMEXCYKGELFDYIVKGRLOEDFARRI 120
Db 134 KKKREIKILIRLMMHPIIIRLYEYIDTPADI CVMMEVYKSGELFDYIVEKGRLTBEEARRH 193
OY 121 FQOIIISGVEYCHRNWVYHBDLKPENILILSKYVNLADGSLSNVMDHGHFKTSGCSPPY 180
Db 194 FQOIIISGVEYCHRNWVYHBDLKPENILILSKCNVKIADGSLNIMDGHFKTSGCSPPY 253
OY 181 AAEVYISGRLVYAGPEVDVWVSCGVIYLLCGTLPPDDENI PNLFKKI KGGIYTLPSHLSA 240
Db 254 AAEVYISGRLVYAGPEVDVWVSCGVIYLLCGTLPPDDENI PNLFKKI KGGIYTLPSHLSB 313
OY 241 LARDIILPMLVYEPMKRITIRIREHEWQOIRLPRYLAIPPTPTQOAAKMDIEDTLRDVY 300
Db 314 SKRDIILPMLVYDPMKRITIRIREHEWVKIRLPRYLAIPPTPTQOAVKVDDETLNDVY 373
OY 301 NMGFNKNHVCESILCSRLONEATVAAVYLLIDNFRFATSGVYAGDYQESMDRNLNQLASSBS 360
Db 374 KMGFDKNQILIESLQNRLONEATVAAVYLLIDNLRITTSYGILSBSFQSMDSLSQVI -AET 432
OY 361 SSSSGIRNVYPGSSDHPSSGLRPYIPYERKMAIGLGRAPREIMBIVYKALQELNIRWYK 420
Db 492 PPSATELRQHGSESPGSLRQHFAERKMAIGLGRAPREIISVYKALQELNIRWYK 492
OY 421 NGHYVWVKCRWCGEPFVENDTLIDNASNSFLGDSTIMDNDNAGRLPYITIKFEPOLYKTRDK 480
Db 493 IGHYVWVKCMWSPGCE--SMHNSDSEFASASAIETFDVMEKSTPYVKEFIQLYKTRDEK 550
OY 481 YLLDMQRYVGPOLLFLDPCAFETIKURLV 509
Db 551 YLLDLQRVSGSHLLFLDLCSAFETIQURLV 579

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RESULT 14

ABR40709
ID ABR40709 standard; protein; 579 AA.

AC ABR40709;

DT 16-MAY-2003 (first entry)

DE Zea mays oil trait related protein sequence SEQ ID NO:238

KM Plant; oil trait; oil phenotype; altered lipid profile; MAP kinase;
KM receptor-like protein kinase; mitogen activated protein kinase; oil;
KM LIP15-like transcription factor caleosin; ATP citrate lyase; SNF1;
KM CRC-like transcription factor; antisense inhibition; co-suppression;
KM transgenic plant.

OS Zea mays.

PN WO2003002751-A2

PD 09-JAN-2003.

PF 27-JUN-2002; 2002WO-US020152.

PR 29-JUN-2001; 2001US-0301913P.

PA (DUPO) DU PONT DE NEMOURS & CO E. I.

2
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PI Jones TJ, Kinney AJ, Klein TM, Li C, Oliveira IC, Sakai H, Shen B;

XX
X

DR N-PSDB; ACC00744.

PT Novel nucleotide fragment encoding polypeptides having receptor-like
PT protein kinase activity, caleosin-like activity, useful for altering oil
PT phenotypes in plants such as sunflower, coconut, soybean, wheat and rice

PS Claim 12; Page 275-277; 542pp; English

CC The present invention describes an isolated nucleotide fragment (1)
CC comprising a nucleic acid sequence (NS) chosen from a NS encoding a
CC polypeptide (P) having receptor-like protein kinase activity, mitogen
CC activated protein (MAP)-kinase activity, lipid5-like transcription factor
CC activity, caldesin-like activity, ATP citrate lyase activity, SNF1-like
CC activity and CRE-like transcription factor activity. Also described: (1)
CC complement (II) of (I); (2) a chimeric construct (III) comprising (I) or
CC (II), operably linked to a regulatory sequence; (3) a plant (IV)
CC comprising (III) in its genome; (4) seeds (V) obtained from (IV); and (5)
CC oil obtained from (V). (1) or its part can be used in antiense
CC inhibition or co-suppression in a transformed plant. (III) is useful for
CC altering the oil phenotype in a plant such as corn, soybean, wheat, rice,
CC canola, Brassica, sorghum, sunflower or coconut. (III) is also useful for
CC creating transgenic plants having altered lipid profiles. (I) can also be
CC used as a hybridisation probe. ACC00626 to ACC00668 and ABR0501 to
CC ABR40879 represent sequences used in the exemplification of the present
CC invention

Sequence 579 AA;

Query Match	71.7%	Score 1931	DB 6	Length 579
Best Local Similarity	73.1%	Pred. No. 3.6e-174		
Matches 312; Conservative	54;	Mismatches 77;	Indels 6;	Gaps 3;

```

QY      _IDGSSKSGSHSALBNYMLGRITGLGTGCKVXIAHKLTHGHVAIKIINCRQNRNMEME 60
Db      77 MEGAAR---DANPLSGYRIKGLTIGSGCKVXIAHILHTGHVAKIKILNRKKIRSDMBE 133
QY      61 KAKREFKILKLFTHPIHRIIRLYEVITYPTDIYVMEYCKYGEI.PDYIVVEKRLQOEDBAR1 120
Db      134 KYKREIKILIRLFMHPIHRIIRLYEVIDTPADI.CVMMEYVSGEL.FDYIVVEKRLHEEARF 193
QY      121 FOQIIISGYEYCHRNWVAHRDLKPEMLLD.SKKNVYLA.DPGLSNWMDHGF.LTSCSPY 180
Db      194 FOQIIISGYEYCHRNWVAHRDLKPEMLLD.SKKNVAKIADPGLSNIMRDGHFL.TSCSPY 253
QY      181 AAPEVYISGKLYAGPEVDVWSCGVIIYALLCGTL.PPDDENI.PNL.FKKIKGCIYTL.PSHLSA 240
Db      254 AAPEVYISGKLYAGPEVDVWSCGVIIYALLCGTL.PPDDENI.PNL.FKKIKGCIYTL.PSHLSP 313
QY      241 LARDILPMLVYEPKRIITIRIREHOMFOIL.PRYLAW.PPDDTQOAMIEDTLD.RDV 300
Db      314 SARLDILPMLVYDEPKRIITIRIREHWPFKIRL.PRYLAW.PPDDTQOAVKQVDEBETLNDVY 373
QY      301 NMGFKNHVCESLQSRLONEATVAYLLLDNFR.FRATSGYLADVQESMDRNLNQLASSSES 360
Db      374 KMGFKNDLISLQRLQNEATVAYLLLDNLR.LRTSGLGESEFQESMDS.SLOVY.-AET 432

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QY 361 SSSGTRNYPGSSDPHSSGLRPYPYVERKMAIGLOSRAHPREIMWEVLKALQELNVRWK 420
 Db 433 PLSATELRQHFSEBSPGSLRQHFALERKMAIGLOSRAHPREITSEVKAQELNVRWK 492
 QY 421 NGHNVKRCWCPGPEVNDTLDA NSFLGDSITMDNDANGRLPTVIKFEFQLYTKDK 480
 Db 493 IGHVNMKCRWSPGCLF--SMHNSDSFSAESALIEVDVMEKSTPTVAFKFIQLYXTRDEK 550
 QY 481 YLLMQRVTGPQLFLDFCAAFITKLRVL 509
 Db 551 YLLDQRVSGSHLFLDLCSAFLTQLRVL 579

RESULT 15

AA40842
 ID AA40842 standard, protein, 511 AA.

AA40842;
 AC

DT 27-AUG-2003 (revised)
 DT 02-MAR-1994 (first entry)

XX SHPP.
 DE

XX Yeast; SNF1, homologous protein; SHP; Nicotinia tabacum; invertase.
 KW

OS Saccharomyces cerevisiae.
 OS

PN JP05199884-A.
 PN

PD 10-AUG-1993.
 PD

PF 13-DEC-1991; 91JP-00330417.
 PF

PR 13-DEC-1991; 91JP-00330417.
 PR

PA (SUMO) SUMITOMO CHEM CO LTD.
 PA

DR WPI; 1993-284682/36.
 DR

XX P-PSDB; AA40842.
 XX

PT Yeast SNF1 homologous protein phosphatase gene of SOLANACEAE plants -
 PT useful for controlling expression of invertase for the increase of crop
 PT yield.
 PT

PS Claim 1; Page 6; 7pp; Japanese.
 PS

XX This sequence is encoded by the yeast SNF1 homologous protein gene
 CC (SHP). The yeast SHP gene may be obtained from Nicotinia tabacum and
 CC may be used to control expression of invertase for the increase of crop
 CC yield. (Updated on 27-AUG-2003 to correct OS field.)
 CC

XX Sequence 511 AA;
 XX

Query Match 71.4%; Score 1923; DB 2; Length 511;
 Best Local Similarity 72.1%; Pred. No. 1.7e-173; Indels 12; Gaps 7;

Matches 372; Conservative 60; Mismatches 72; Indels 12; Gaps 7;

QY 1 MDGSS--KSGSHSEALRNYNLGRITGTFGKVIKAEHKLGTGRVAIKIINCQWRNMEM 58
 Db 1 MDGSTVGGSSVESFRLRYKLGKTLGIGSPGKVIKAEHTLTGHKVAIVKILNRKKIKMEM 60
 QY 59 BEKAKREFKILFLIHPHILRYEVIYPTDIYVMEYCKYGELEFDYIVKGRLOEDEAR 118
 Db 61 EEKVRREIKILRLFMHPHILRYEVEYPTSDIYVMEYKSGELFDYIVKGRLOEDEAR 120
 QY 119 RIFQOISGVYCHRNMYVHRDLKPENLIDSKYVVKLADFGLSVMDHGHFLKTSQSP 178
 Db 121 KFOOISGVYCHRNMYVHRDLKPENLIDSKYVVKLADFGLSVMDHGHFLKTSQSP 180
 QY 179 NYAAPEVIGSLYAGPEVDVWSCGVLVALLCGTLPPDENIPNLFKKIKGIIYTLPSHL 238
 |||||

Db 181 NYAAPEVIGSLYAGPEVDVWSCGVLVALLCGTLPPDENIPNLFKKIKGIIYTLPSHL 240
 QY 239 SALARDLIPRMLVYEPMKRITIREBHOWFOIRLPYLAAPPEDTQOAMIDEDTRD 298
 Db 241 SAGARDLIPRMLVYEPMKRITIREBHOWFOIRLPYLAAPPEDTQOAKKIDEDILQ 300
 QY 299 VNMGFNKNHVCSLCSRLQNEATVAYLLDNFRATSGYLGADYQESMDRNLNQLASS 358
 Db 301 VVKRGFDRNLSVALCNRVQEGVAYYLLNDFRASSGYMGAFQETMEGYHQINSS 360
 QY 359 ESSSGTRNYPGSSDPHSSGLRPYPYVERKMAIGLOSRAHPREIMWEVLKALQELNVR 418
 Db 361 EVLLP-CWQHLPQIMDFQYVGAR-QFVERKMAIGLOSRAHPREIMWEVLKALQELNVR 418
 QY 419 KNGHNVKRCWCPGPEVNDTLDA NS--FLG-DSTIMDNDANGRLPTVIKFEFQ 473
 Db 419 KNGHNVKRCWCPGPEVNDTLDA NS--FLG-DSTIMDNDANGRLPTVIKFEFQ 473
 QY 474 YKTKDKYLLDMQRVTGPQLFLDFCAAFITKLRVL 509
 Db 476 YKTRBEKYLDDLQRVQGPQLFLDFCAAFITKLRVL 511

Search completed: July 7, 2004, 17:55:08
 Job time : 61 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 7, 2004, 17:52:24 ; Search time 45 Seconds
(without alignments)
3568.861 Million cell updates/sec

Title: US-09-857-522B-4
Perfect score: 2693
Sequence: 1 MDSSKSGSGSEALRNVLG.....GPQLFLDFCAFLTKRLVL 509

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues
Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

SPTREMBL_25:*

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phage:*
- 10: sp_plant:*
- 11: sp_rodent:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*
- 15: sp_virus:*
- 16: sp_bacteriophage:*
- 17: sp_archaea:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2422	89.9	509	10 Q9ZRU3	Q9ZRU3 oryza sativ
2	2422	89.9	509	10 Q852Q1	Q852Q1 oryza sativ
3	2411.5	89.5	508	10 Q9ZNT4	Q9ZNT4 oryza sativ
4	2411.5	89.5	508	10 Q852Q0	Q852Q0 oryza sativ
5	2356.5	87.5	510	10 Q40740	Q40740 oryza sativ
6	2100	78.0	513	10 Q81992	Q81992 hordeum vul
7	2080	77.2	513	10 Q40029	Q40029 hordeum vul
8	2072	76.9	513	10 Q40030	Q40030 hordeum vul
9	1977	73.4	505	10 Q9ZRU1	Q9ZRU1 oryza sativ
10	1977	73.4	505	10 Q852Q2	Q852Q2 oryza sativ
11	1969.5	72.9	535	10 Q8RMD2	Q8RMD2 arabidopsis
12	1963	72.9	504	10 P93113	P93113 cucumis sat
13	1960.5	72.8	514	10 Q9M726	Q9M726 lycopersico
14	1945	72.2	484	10 Q43475	Q43475 hordeum vul
15	1923	71.4	511	10 Q40544	Q40544 nicotiana t
16	1909	70.9	503	10 Q9ZTF6	Q9ZTF6 oryza sativ

17	1903.5	70.7	512	10 P92958	P92958 arabidopsis
18	1903.5	70.7	512	10 Q04122	Q04122 solanum tub
19	1899.5	70.5	512	10 P92968	P92968 arabidopsis
20	1881.5	69.9	514	10 Q9XK25	Q9XK25 glycine max
21	1727	64.1	504	10 Q41485	Q41485 solanum tub
22	1545.5	57.4	494	10 Q9F123	Q9F123 arabidopsis
23	1195.5	44.4	258	10 Q9ZRU2	Q9ZRU2 oryza sativ
24	1146	42.6	552	6 Q7YRX9	Q7YRX9 sus scrofa
25	1137	42.2	472	8 Q98RU9	Q98RU9 guillardia
26	1117.5	41.5	560	13 Q8UVW8	Q8UVW8 xenopus lae
27	1116.5	41.5	291	10 Q9ZRA0	Q9ZRA0 arabidopsis
28	1109	41.2	582	5 Q18645	Q18645 drosophila
29	1106.5	41.1	530	11 Q88RK8	Q88RK8 mus muscula
30	1101.5	40.9	574	4 Q86VS1	Q86VS1 homo sapien
31	1096	40.7	348	10 Q41491	Q41491 solanum tub
32	1087	40.4	626	5 Q952Q4	Q952Q4 caenorhabdi
33	1080	40.1	562	5 Q86FL6	Q86FL6 caenorhabdi
34	1080	40.1	624	5 Q22068	Q22068 caenorhabdi
35	1048	38.9	718	5 Q9XYP6	Q9XYP6 dictyosteli
36	992	36.8	602	3 P87209	P87209 kluyveromyc
37	979	36.4	777	3 Q872H0	Q872H0 neurospora
38	940.5	34.9	880	3 Q9Y880	Q9Y880 cochlidiolu
39	932	34.6	765	3 Q9Y7V4	Q9Y7V4 sclerotinia
40	927	34.4	671	3 Q96W17	Q96W17 trichoderma
41	899.5	33.4	706	3 Q8J2N0	Q8J2N0 fusarium ox
42	828	30.7	175	10 Q8S9G0	Q8S9G0 triticum ae
43	768.5	28.5	833	5 Q8SXS5	Q8SXS5 dictyosteli
44	749	27.8	783	4 Q86YU2	Q86YU2 homo sapien
45	738	27.4	725	13 Q804T2	Q804T2 xenopus lae

ALIGNMENTS

RESULT 1

ID Q9ZRU3 PRELIMINARY; PRT; 509 AA.

AC Q9ZRU3; 01-MAY-1999 (TREMBlrel. 10, Created)

DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)

DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)

DE OSK4.

GN OSK4.

OS Oryza sativa (Rice).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

OC Euphorbiaceae; Oryzaeae; Oryza.

NCBI_Taxid=4530;

[1]

RP SEQUENCE FROM N.A.

RK MEDLINE=9908251; PubMed=9870704;

RA Takano M., Kajiya-Kanagae H., Funatsuki H., Kikuchi S.;

RT "Rice has two distinct classes of protein kinase genes related to SNF1

RT of Saccharomyces cerevisiae, which are differentially regulated in early

RT seed development."

RL Mol. Gen. Genet. 260:388-394 (1998)

CC -1. SIMILARITY: BELONGS TO THE SPK/TKR FAMILY OF PROTEIN KINASES.

DR EMBL; D82035; BAA36299.1; -

DR HSP; D63450; IAO6.

DR Gramene; Q9ZRU3; -

DR GO; GO:0005524; F:ATP binding; IEA.

DR GO; GO:0004714; F:Protein serine/threonine kinase activity; IEA.

DR GO; GO:0016740; F:Protein-tyrosine kinase activity; IEA.

DR GO; GO:0006468; F:Protein amino acid phosphorylation; IEA.

DR InterPro; IPR001772; Kinase Cterm.

DR InterPro; IPR002290; Prot. kinase.

DR InterPro; IPR008271; Ser_Thr_kinase.

DR InterPro; IPR001245; Tyr_kinase.

DR InterPro; IPR000449; UBA_domain.

DR Pfam; PF02149; KAI; 1.

DR Pfam; PF00069; pkinase; 1.

DR Pfam; PF00627; UBA; 1.
DR PRINTS; PR00109; TYRKINASE.
DR PRODOM; PD000001; Prot_kinase; 1.
DR SMART; SM00220; S_TKc; 1.
DR PROSITE; PS00107; PROTEIN KINASE_ATP; 1.
DR PROSITE; PS50011; PROTEIN KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
DR PROSITE; PS50030; UBA; 1.
DR ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
KM KINASE
SQ SEQUENCE 509 AA; 58471 MW; 6E8256D715A1B48 CRC64;

Query Match 89.9%; Score 2422; DB 10; Length 509;
Best Local Similarity 88.6%; Pred. No. 9.4e-199;
Matches 451; Conservative 35; Mismatches 23; Indels 0; Gaps 0;

QY 1 MDGSSKSGHSEALRNVLGRTLGITGFGYKIAEHKLTGHRVAIKILNRQMRNMEE 60
DB 1 MEGNARGGSHSEALKNNVLGRTLGISFGYKIAEHKLTGHRVAIKILNRQMRNMEE 60
QY 61 KAKREFKILKLFHPHILRLYEVIYPTDIYVMEYCKGELFDYIEKGRLODEARRI 120
DB 61 KAKREFKILKLFHPHILRLYEVIYPTDIYVMEYCKGELFDYIEKGRLODEARRI 120
QY 121 FOQIISGVEYCHRMVVRHDLKPENLILDSKYNVKLADFGLSNVMHDGHFLKTS CGSPNY 180
DB 121 FOQIISGVEYCHRMVVRHDLKPENLILDSKYNVKLADFGLSNVMHDGHFLKTS CGSPNY 180
QY 181 AAPVVISGKIYAGPEVDVWSCGVILYALLCGTLPEDDENINLPRKIKGGIYTLPSHLSA 240
DB 181 AAPVVISGKIYAGPEVDVWSCGVILYALLCGTLPEDDENINLPRKIKGGIYTLPSHLSA 240
QY 241 LARDLIRMLVVEPMKRTITREIREHOMFOIRLPRYLAAPPPTDQAQKMIDEDTLDDV 300
DB 241 LARDLIRMLVVEPMKRTITREIREHOMFOIRLPRYLAAPPPTDQAQKMIDEDTLDDV 300
QY 301 NMGNKNHVCESLCSRLQNEATVAYLLDNRFRATSGYLGADYQESMDRNINQLASSES 360
DB 301 NLGVEKHVCESLNRRLQNEATVAYLLDNRFRATSGYLGADYQESLERNLIRFASSES 360
QY 361 SSSGTRNVVPGSSDPHSSGLRPYIPVERKMAIGLSAHPREINVEVTKALQELNVRWK 420
DB 361 ASSNTRHYLPSSSPDHPASGLRPHYPVERKMAIGLSAHPREINVEVTKALQELNVRWK 420
QY 421 NGHNVNCRMCOPPEVNDTLSDASNFIDSTIMDNDANGRLPTVYKFEFOLYKTKDK 480
DB 421 NGHNVNCRMCOPPEVNDTLSDASNFIDSTIMDNDANGRLPTVYKFEFOLYKTKDK 480
QY 481 YLLDMQRTGPGQLFLDFCAAFITKLRVL 509
DB 481 YLLDMQRTGPGQLFLDFCAAFITKLRVL 509

RESULT 2
Q85201 PRELIMINARY; PRT; 509 AA.
AC Q85201;
DT 01-JUN-2003 (Tremblrel. 24, Created)
DT 01-JUN-2003 (Tremblrel. 24, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE SNRKB protein kinase.
GN OSK24.
OS Oryza sativa (japonica cultivar-group). Embryophyta; Tracheophyta;
OC Eukaryota; Viridiplantae; Streptophyta; Liliopsida; Poales; Poaceae;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Euphorbiaceae; Oryzae; Oryza.
CC NCBI_TaxID=39947;
NCBI_TaxID=39947;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Norin 8;
RA Kanegae H., Takano M.;
RT "Rice SNRKBs."
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB101656; BAC56589.1; -.

DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004674; F:Protein serine/threonine kinase activity; IEA.
DR GO; GO:0004713; F:Protein-tyrosine kinase activity; IEA.
DR GO; GO:0006468; P:Protein amino acid phosphorylation; IEA.
DR InterPro; IPR001772; Kinase_Cterm.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR002290; Ser_thr_kinase.
DR InterPro; IPR008271; Ser_thr_kin_AS.
DR InterPro; IPR001245; Tyr_kinase.
DR InterPro; IPR000449; UBA_domain.
DR Pfam; PF02149; KAI; 1.
DR Pfam; PF00069; pkinase; 1.
DR Pfam; PF00627; UBA; 1.
DR PRINTS; PR00109; TYRKINASE.
DR PRODOM; PD000001; Prot_kinase; 1.
DR SMART; SM00220; S_TKc; 1.
DR PROSITE; PS00107; PROTEIN KINASE_ATP; 1.
DR PROSITE; PS50011; PROTEIN KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
DR PROSITE; PS50030; UBA; 1.
KM KINASE
SQ SEQUENCE 509 AA; 58471 MW; 6E8256D715A1B48 CRC64;

Query Match 89.9%; Score 2422; DB 10; Length 509;
Best Local Similarity 88.6%; Pred. No. 9.4e-199;
Matches 451; Conservative 35; Mismatches 23; Indels 0; Gaps 0;

QY 1 MDGSSKSGHSEALRNVLGRTLGITGFGYKIAEHKLTGHRVAIKILNRQMRNMEE 60
DB 1 MEGNARGGSHSEALKNNVLGRTLGISFGYKIAEHKLTGHRVAIKILNRQMRNMEE 60
QY 61 KAKREFKILKLFHPHILRLYEVIYPTDIYVMEYCKGELFDYIEKGRLODEARRI 120
DB 61 KAKREFKILKLFHPHILRLYEVIYPTDIYVMEYCKGELFDYIEKGRLODEARRI 120
QY 121 FOQIISGVEYCHRMVVRHDLKPENLILDSKYNVKLADFGLSNVMHDGHFLKTS CGSPNY 180
DB 121 FOQIISGVEYCHRMVVRHDLKPENLILDSKYNVKLADFGLSNVMHDGHFLKTS CGSPNY 180
QY 181 AAPVVISGKIYAGPEVDVWSCGVILYALLCGTLPEDDENINLPRKIKGGIYTLPSHLSA 240
DB 181 AAPVVISGKIYAGPEVDVWSCGVILYALLCGTLPEDDENINLPRKIKGGIYTLPSHLSA 240
QY 241 LARDLIRMLVVEPMKRTITREIREHOMFOIRLPRYLAAPPPTDQAQKMIDEDTLDDV 300
DB 241 LARDLIRMLVVEPMKRTITREIREHOMFOIRLPRYLAAPPPTDQAQKMIDEDTLDDV 300
QY 301 NMGNKNHVCESLCSRLQNEATVAYLLDNRFRATSGYLGADYQESMDRNINQLASSES 360
DB 301 NLGVEKHVCESLNRRLQNEATVAYLLDNRFRATSGYLGADYQESLERNLIRFASSES 360
QY 361 SSSGTRNVVPGSSDPHSSGLRPYIPVERKMAIGLSAHPREINVEVTKALQELNVRWK 420
DB 361 ASSNTRHYLPSSSPDHPASGLRPHYPVERKMAIGLSAHPREINVEVTKALQELNVRWK 420
QY 421 NGHNVNCRMCOPPEVNDTLSDASNFIDSTIMDNDANGRLPTVYKFEFOLYKTKDK 480
DB 421 NGHNVNCRMCOPPEVNDTLSDASNFIDSTIMDNDANGRLPTVYKFEFOLYKTKDK 480
QY 481 YLLDMQRTGPGQLFLDFCAAFITKLRVL 509
DB 481 YLLDMQRTGPGQLFLDFCAAFITKLRVL 509

RESULT 3
Q9ZNT4 PRELIMINARY; PRT; 508 AA.
AC Q9ZNT4;
DT 01-MAY-1999 (Tremblrel. 10, Created)
DT 01-MAY-1999 (Tremblrel. 10, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE OSK3.

GN OSK3 OR OSK5.
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Eubharitoidae; Oryzaceae; Oryza.
OX NCBI_TaxID=4530;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99086251; PubMed=9870704;
RA Takano M., Kajiya-Kanegae H., Funatsuki H., Kikuchi S.;
RT "Rice has two distinct classes of protein kinase genes related to SNF1
RT of Saccharomyces cerevisiae, which are differently regulated in early
RT seed development.";
RL Mol. Gen. Genet. 260:388-394 (1998).
CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
DR EMBL; D82038; BA36297.1; -.
DR EMBL; D82036; BA36295.1; -.
DR HSSP; Q63450; 1A06.
DR Gramene; Q9ZNT4; -.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR001772; Kinase Cterm.
DR InterPro; IPR000719; Prot. Kinase.
DR InterPro; IPR002290; Ser_thr_kinase.
DR InterPro; IPR008271; Ser_thr_pkin_AS.
DR InterPro; IPR001245; Tyr_pkinase.
DR InterPro; IPR000449; UBA_domain.
DR Pfam; PF02149; KAI; 1.
DR Pfam; PF00627; UBA; 1.
DR Pfam; PF00627; UBA; 1.
DR PRINTS; PR00109; TYRKINASE.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00220; S_TKC; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
DR PROSITE; PS0030; UBA; 1.
DR KAT-binding; Kinase; Serine/threonine-protein kinase; Transferase.
KW SEQUENCE 508 AA; 58250 MW; E935262080B39A59 CRC64;
SQ
Query Match 89.5%; Score 2411.5; DB 10; Length 508;
Best Local Similarity 89.0%; Pred. No. 7.4e-198;
Matches 453; Conservative 29; Mismatches 26; Indels 1; Gaps 1;
QY 1 MDGSSKSGHSEALRNVLGRTLGIGTGKVKLAHEHKTGHRVAIKINCRQMRMEME 60
DB 1 MDGNAKGGHSEALKNYLGRITLGISGKVKLAHEHKTGHRVAIKINCRQMRMEME 60
QY 61 KAKKEFKILKLFHPIHRIIYEVITYPTDIYVMEYCKYGBLFDYIVKGRLOEDEAR 120
DB 61 KAKKEIKILRFLFIHPIHRIIYEVITYPTDIYVMEYCKYGBLFDYIVKGRLOEDEAR 120
QY 121 FOQIISGEYCHRMNVVHRDLKPENLILDSKYNKVLADFGLSNVMDHGHFLKTS 180
DB 121 FOQIISGEYCHRMNVVHRDLKPENLILDSKYNKVLADFGLSNVMDHGHFLKTS 180
QY 181 AAPEVISGKLYAGPEVDVWSCGVLVYALLCGTLPEFDENIPNLFFKIKGGIYTLPSH 240
DB 181 AAPEVISGKLYAGPEVDVWSCGVLVYALLCGTLPEFDENIPNLFFKIKGGIYTLPSH 240
QY 241 LARDLIPMLVVEPMKRTITIREIHQWFOIRLPYLAVPPDDTQAQAMIDEDTLQDV 300
DB 241 LARDLIPMLVVEPMKRTITIREIHQWFOIRLPYLAVPPDDTQAQAMIDEDTLQDV 300
QY 301 NMGKNKHVCSLSRLQNEATVAYLLDNRPRRTSGYLADVOESMDRLNOLASSES 360
DB 301 NMGKNKHVCSLSRLQNEATVAYLLDNRPRRTSGYLADVOESMDRLNOLASSES 360
QY 361 SSSGRTNVPGSSDPHSGRLPRYPVERKMWALGLQSRAPREIMVEVLAQELNVKWK 420
DB 361 SSSGRTNVPGSSDPHSGRLPRYPVERKMWALGLQSRAPREIMVEVLAQELNVKWK 420

DB 361 ASNTRHYLPGSSDPHSGRLPRYPVERKMWALGLQSRAPREIMVEVLAQELNVKWK 420
QY 421 NGHNWVCRWCPGPEVNDTLDA NSFLGSDTIMDNDANRLEPTVLFKEFQYKTD 480
DB 421 NGQYMKCRMSVQ-TQATMDLVNNSFVDSIIMDNGDVNGRLPAVKFELQYKTRDEK 479
QY 481 YLDMQRTVGPQLFLDFCAFLTKRLV 509
DB 480 YLDMQRTVGPQLFLDFCAFLTKRLV 509
RESULT 4
085200
ID 085200 PRELIMINARY; PRT: 508 AA.
AC 085200; 01-JUN-2003 (TRENDEL 24, Created)
DT 01-JUN-2003 (TRENDEL 24, Last sequence update)
DT 01-OCT-2003 (TRENDEL 25, Last annotation update)
DE Ssrk1b protein kinase.
GN OSK3.
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Eubharitoidae; Oryzaceae; Oryza.
OX NCBI_TaxID=39947;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Norin 8;
RA Kanegae H., Takano M.;
RT "Rice Ssrk1s.";
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB101657; BAC56590.1; -.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR001772; Kinase Cterm.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR002290; Ser_thr_kinase.
DR InterPro; IPR008271; Ser_thr_pkin_AS.
DR InterPro; IPR001245; Tyr_pkinase.
DR InterPro; IPR000449; UBA_domain.
DR Pfam; PF02149; KAI; 1.
DR Pfam; PF00069; Dkinase; 1.
DR Pfam; PF00627; UBA; 1.
DR PRINTS; PR00109; TYRKINASE.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00219; TyTKC; 1.
DR SMART; SM00220; S_TKC; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
DR PROSITE; PS50030; UBA; 1.
DR KAI_kinase.
KW SEQUENCE 508 AA; 58250 MW; E935262080B39A59 CRC64;
SQ
Query Match 89.5%; Score 2411.5; DB 10; Length 508;
Best Local Similarity 89.0%; Pred. No. 7.4e-198;
Matches 453; Conservative 29; Mismatches 26; Indels 1; Gaps 1;
QY 1 MDGSSKSGHSEALRNVLGRTLGIGTGKVKLAHEHKTGHRVAIKINCRQMRMEME 60
DB 1 MDGNAKGGHSEALKNYLGRITLGISGKVKLAHEHKTGHRVAIKINCRQMRMEME 60
QY 61 KAKKEFKILKLFHPIHRIIYEVITYPTDIYVMEYCKYGBLFDYIVKGRLOEDEAR 120
DB 61 KAKKEIKILRFLFIHPIHRIIYEVITYPTDIYVMEYCKYGBLFDYIVKGRLOEDEAR 120
QY 121 FOQIISGEYCHRMNVVHRDLKPENLILDSKYNKVLADFGLSNVMDHGHFLKTS 180
DB 121 FOQIISGEYCHRMNVVHRDLKPENLILDSKYNKVLADFGLSNVMDHGHFLKTS 180
QY 181 AAPEVISGKLYAGPEVDVWSCGVLVYALLCGTLPEFDENIPNLFFKIKGGIYTLPSH 240
DB 181 AAPEVISGKLYAGPEVDVWSCGVLVYALLCGTLPEFDENIPNLFFKIKGGIYTLPSH 240

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Db 181 AAEVVISGLYAGEVDVWVSCGVIYLLALCGTLFPDDENIPNLFKKIKGIGYTLPSHLSA 240
Qy 241 LARLDLPRMLVVEPMKRTITREIREHQMFOIRLPRYLAVPPDTQAQAKMIDEDTLQDV 300
Db 241 LARLDLPRMLVVDPMKRTITREIREHQMFOIRLPRYLAVPPDTQAQAKMIDEDTLQDV 300
Qy 301 NMGNKKNHVCESLCSRLQNEATVAYYLLDNRFRATSGYLGADYQESMDRLNOLASSE 360
Db 301 NLGKGKHVCESLKNRLQNEATVAYYLLDNRFRATSGYLGADYQESLERNFRPASSE 360
Qy 361 SSSGTRNVPGSSDPHSSGLRPYPYVERKMGALGQSRAPREIMVEVLKALQELNVRMK 420
Db 361 ASSNTRHYLPSSDPHSSGLRPHYPVERKMGALGQSRAPREIMIEVLKALQELNVRMK 420
Qy 421 NGHYNVKRCWCPGPEVNDTLDAANSFLGDSITMDNDANGRLPYVYKFEQYLYTKDDK 480
Db 421 NGQYNNKCRWMSVGTQATDMLDVNNSFVDDSIIMDNGDVNGRLPAVYKFEIQLYKRD 479
Qy 481 YLLDMQRYTGPQLFLDFCAFLTKRLV 509
Db 480 YLLDMQRYTGPQLFLDFCAFLTKRLV 509

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RESULT 5

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ID 040740 PRELIMINARY; PRT; 510 AA.
AC 040740;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE SNF1-related protein kinase.
GN SNF1.
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaceae; Oryza.
OX NCB1_TaxID=4530;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=tns-8; TISSUE=Endosperm;
RT "SNF1-related protein kinase of rice.";
RL Submitted (ABR-1996) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
DR EMBL; U55768; AB05457.1; -.
DR PIR; T04145; T04145.
DR HSSP; Q63450; 1A06.
DR Gramene; Q40740; -.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR InterPro; IPR001772; Kinase_Cterm.
DR InterPro; IPR000719; Prot_Kinase.
DR InterPro; IPR002290; Ser_thr_kinase.
DR InterPro; IPR008271; Ser_thr_kin_AS.
DR InterPro; IPR000449; UBA_domain.
DR Pfam; PF02149; KAI; 1.
DR Pfam; PF00067; PKinase; 1.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00220; S_TKc; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00117; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
DR PROSITE; PS50030; UBA; 1.
KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 510 AA; 58258 MW; 510489ACDD0C2CB CRC64;

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Query Match 87.5%; Score 2356.5; DB 10; Length 510;
 Best Local Similarity 87.1%; Pred. No. 3.9e-193;
 Matches 444; Conservative 32; Mismatches 33; Indels 1; Gaps 1;

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Qy 1 MDSSKSGSHSEALRNYNLGRITGIGFGKVIKAEHKLTSRVAIKIINCROMNMEME 60
Db 1 MDGNAGCGSHSEALKYNNLGRITGIGSGFGKVIKAEHKLTSRVAIKIINRQRMNMEME 60
Qy 61 KAREEIKLFLIHPHILRYEVIYPTDLYVMEYCKGELFDYVEKRLQEDF ARR 119
Db 61 KAREEIKLRLFIHPHILRYEVIYPTDLYVMEYCKGELFDYVEKRLQEDFVALR 120
Qy 120 IFQOIIISGVYCHRNWVHEDLKPEMLLDKKNVVLADGSLNMWHDGFLTSCGSPN 179
Db 121 IFQOIIISAVYCHRNWVHEDLKPEMLLDKKNVVLADGSLNMWHDGFLTSCGSPN 180
Qy 180 YAAPEVISGLYAGEVDVWVSCGVIYLLALCGTLFPDDENIPNLFKKIKGIGYTLPSHLS 239
Db 181 YAAPEVISGLYAGEVDVWVSCGVIYLLALCGTLFPDDENIPNLFKKIKGIGYTLPSHLS 240
Qy 240 ALARLDLPRMLVVEPMKRTITREIREHQMFOIRLPRYLAVPPDTQAQAKMIDEDTLQDV 239
Db 241 ALARLDLPRMLVVDPMKRTITREIREHQMFOIRLPRYLAVPPDTQAQAKMIDEDTLQDV 300
Qy 300 VNMGNKKNHVCESLCSRLQNEATVAYYLLDNRFRATSGYLGADYQESMDRLNOLASSE 359
Db 301 VNLGYGDHVCESLKNRLQNEATVAYYLLDNRFRATSGYLGADYQESLERNFRPASSE 360
Qy 360 SSSGTRNVPGSSDPHSSGLRPYPYVERKMGALGQSRAPREIMVEVLKALQELNVRMK 419
Db 361 SASNTRHYLPSSDPHSSGLRPHYPVERKMGALGQSRAPREIMIEVLKALQELNVRMK 420
Qy 420 KNHYNVKRCWCPGPEVNDTLDAANSFLGDSITMDNDANGRLPYVYKFEQYLYTKDD 479
Db 421 KNQYNNKCRWMSVGTQATDMLDVNNSFVDDSIIMDNGDVNGRLPAVYKFEIQLYKSRDE 480
Qy 480 KYLLDMQRYTGPQLFLDFCAFLTKRLV 509
Db 481 KYLLDMQRYTGPQLFLDFCAFLTKRLV 510

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RESULT 6

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ID 081992 PRELIMINARY; PRT; 513 AA.
AC 081992;
DT 01-NOV-1998 (TREMBlrel. 08, Created)
DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE SNRK1-type protein kinase (Fragment).
GN KIN12A.
OS Hordeum vulgare (Barley).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;
OC Triticeae; Hordeum.
OX NCB1_TaxID=4513;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Sundance; TISSUE=seed minus seed coat;
RT "Molecular cloning of Bsnr1, a novel putative SNF4-related protein
RT identified in a two-hybrid screen with barley seed SNRK1 protein
RT kinase.";
RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
DR EMBL; AJ007990; CA007813.1; -.
DR HSSP; P00518; 1PHK.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0004688; F:protein amino acid phosphorylation; IEA.
DR InterPro; IPR001772; Kinase_Cterm.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR002290; Ser_thr_kinase.
DR InterPro; IPR008271; Ser_thr_kin_AS.
DR InterPro; IPR001245; Tyr_kinase.

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DR InterPro; IPR000449; UBA_domain.
 DR Pfam; PF02149; KAI; 1.
 DR Pfam; PF00069; pkinase; 1.
 DR Pfam; PF00627; UBA; 1.
 DR PRINTS; PR00109; TYRKINASE.
 DR ProDom; PD000001; Prot_kinase; 1.
 DR SMART; SM00220; S_TKC; 1.
 DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
 DR PROSITE; PS50030; UBA; 1.
 DR ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
 KW NON_TER
 FT TER
 SQ SEQUENCE 513 AA; 58801 MW; 37DFEDBA6295AD CRC64;

Query Match 78.0%; Score 2100; DB 10; Length 513;
 Best Local Similarity 75.8%; Pred. No. 3.7e-171;
 Matches 389; Conservative 61; Mismatches 59; Indels 4; Gaps 2;

1 MDGSSKSGHSEALNNVNLGRTLGITFGKVKIAEHKLTGHRVAIKIINCROMNMEME 60
 1 MDGNNRGGSHSEVLKNVNLGRTLGITFGDVVAEHKLTGQRAVAKILNRKMETMEME 60
 61 KAKREFKILKLT--FIHPHIIIRLYEVITYPTDIYVMEYCKYGLFDYIVKGRLOEDEA 117
 61 KANREIKIMRLFIIDFIHPHIIIRVYEVIEPNDIFVMEYCNNGELLDYIIENGRLQDEA 120
 118 RRFQOIIISGVYCHRRNVVHRDLKPENLILDSKYNVKLADFGLSNVHGDHFLKTSGCS 177
 121 RRFQOIIISGVYCHRRNVVHRDLKPENLILDSKYNVKLADFGLSNVHGDHFLKTSGCS 180
 178 PNYAAPVYISGKLYAGPEVDWVSCGVIIYALLCGTLPPDENIPVLFFKIKGITYLPSH 237
 181 LNYAAPVYISGKLYAGPEVDWVSCGVIIYALLCGSVPPDDNIPSLFRKIKGITYLPSY 240
 238 LSAIARDLIIPMLVVEPMKRTITIREIRHOFQIRLPYLAAPPDITQOAKMIDEDTLR 297
 241 LSDSARDLIPKLTINIDPMKRTITIREIRHVPFKNHLPCLYLAAPPYKQOAMIDEDTLR 300
 298 DVVNMGNKNNVCESLCSRLQNEATVAYLLIDNRFRTSGYLADYQESMDRNLNQLAS 357
 301 EVVNLGYDKHVCESLNNRLQNEATVAYLLIDNRFRTSGYLADYQESMDRNLNQLAS 360
 358 SESSSSGTRNVYVPGSSDPHSSGLRPYVPERKMAIGLSRAHPRIMEVYLKALQELNVR 417
 361 SESASPSTRNVLPGLINDSGGGLRPYVQKMAIGLSGAHPRIMEVYLKALQELNVC 420
 418 WKKGHNVNVCRCMCPGPEVND-TLDASNSFLGSDTINDNDANGRLPTVIKFEFOLYKT 476
 421 WKKGHNVNVCRCMCPGPEVND-TLDASNSFLGSDTINDNDANGRLPTVIKFEFOLYKT 480
 477 KDDRYLLDMQRYTGPQLLFLDFCAAPLTKLRVL 509
 481 KDNKYLIDIQRYTGPQLLFLDFCAAPLTKLRVL 513

RESULT 7

040029 PRELIMINARY; PRT; 513 AA.
 AC 040029;
 DT 01-NOV-1996 (TREMBLrel. 01. Created)
 DT 01-NOV-1996 (TREMBLrel. 01. Last sequence update)
 DT 01-OCT-2003 (TREMBLrel. 25. Last annotation update)
 DE Protein kinase.
 GN BKIN12.
 OS Hordeum vulgare (Barley).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poaceae;
 OC Triticeae; Hordeum.
 OC NCBI_TaxID=4513;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Sunbar;

RX MEDLINE=93258420; PubMed=1302632;
 RA Halford N.G., Vicente-Carbalosa J., Sabelli P.A., Shewry P.R.,
 RA Hannappel U., Kreis M.;
 RT "Molecular analyses of a barley multigene family homologous to the
 RT yeast protein kinase gene SNF1.";
 RL Plant J. 2:791-797(1992).
 CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 DR EMBL; X65606; CAA46556.1; -
 DR PIR; S60303; S60303.
 DR HSP; P00518; 1PRK.
 DR GO; GO:0005524; F:ATP binding; IEA.
 DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
 DR GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
 DR GO; GO:0016740; F:transferase activity; IEA.
 DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
 DR InterPro; IPR001772; Kinase_Cterm.
 DR InterPro; IPR000719; Prot_kinase.
 DR InterPro; IPR002290; Ser_thr_pkinase.
 DR InterPro; IPR008271; Ser_thr_pkin_AS.
 DR InterPro; IPR001245; Tyr_kinase.
 DR InterPro; IPR000449; UBA_domain.
 DR Pfam; PF02149; KAI; 1.
 DR Pfam; PF00069; pkinase; 1.
 DR PRINTS; PR00109; TYRKINASE.
 DR ProDom; PD000001; Prot_kinase; 1.
 DR SMART; SM00220; S_TKC; 1.
 DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
 DR PROSITE; PS50030; UBA; 1.
 DR ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
 SQ SEQUENCE 513 AA; 58715 MW; 3DPF82030365630 CRC64;

Query Match 77.2%; Score 2080; DB 10; Length 513;
 Best Local Similarity 75.0%; Pred. No. 1.9e-169;
 Matches 385; Conservative 62; Mismatches 62; Indels 4; Gaps 2;

1 MDGSSKSGHSEALNNVNLGRTLGITFGKVKIAEHKLTGHRVAIKIINCROMNMEME 60
 1 MDGNNRGGSHSEVLKNVNLGRTLGITFGDVVAEHKLTGQRAVAKILNRKMETMEME 60
 61 KAKREFKILKLT--FIHPHIIIRLYEVITYPTDIYVMEYCKYGLFDYIVKGRLOEDEA 117
 61 KANREIKIMRLFIIDFIHPHIIIRVYEVIEPNDIFVMEYCNNGELLDYIIENGRLQDEA 120
 118 RRFQOIIISGVYCHRRNVVHRDLKPENLILDSKYNVKLADFGLSNVHGDHFLKTSGCS 177
 121 RRFQOIIISGVYCHRRNVVHRDLKPENLILDSKYNVKLADFGLSNVHGDHFLKTSGCS 180
 178 PNYAAPVYISGKLYAGPEVDWVSCGVIIYALLCGTLPPDENIPVLFFKIKGITYLPSH 237
 181 LNYAAPVYISGKLYAGPEVDWVSCGVIIYALLCGSVPPDDNIPSLFRKIKGITYLPSY 240
 238 LSAIARDLIIPMLVVEPMKRTITIREIRHOFQIRLPYLAAPPDITQOAKMIDEDTLR 297
 241 LSDSARDLIPKLTINIDPMKRTITIREIRHVPFKNHLPCLYLAAPPYKQOAMIDEDTLR 300
 298 DVVNMGNKNNVCESLCSRLQNEATVAYLLIDNRFRTSGYLADYQESMDRNLNQLAS 357
 301 DVVNLGYDKHVCESLNNRLQNEATVAYLLIDNRFRTSGYLADYQESMDRNLNQLAS 360
 358 SESSSSGTRNVYVPGSSDPHSSGLRPYVPERKMAIGLSRAHPRIMEVYLKALQELNVR 417
 361 SESASPSTRNVLPGLINDSGGGLRPYVQKMAIGLSGAHPRIMEVYLKALQELNVC 420
 418 WKKGHNVNVCRCMCPGPEVND-TLDASNSFLGSDTINDNDANGRLPTVIKFEFOLYKT 476
 421 WKKGHNVNVCRCMCPGPEVND-TLDASNSFLGSDTINDNDANGRLPTVIKFEFOLYKT 480
 477 KDDRYLLDMQRYTGPQLLFLDFCAAPLTKLRVL 509
 481 KDNKYLIDIQRYTGPQLLFLDFCAAPLTKLRVL 513

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RESULT 8
Q40030 ID Q40030 PRELIMINARY; PRT; 513 AA.
AC Q40030;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Protein kinase (Fragment).
GN BKN12.
OS Hordeum vulgare (Barley).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;
OC Triticeae; Hordeum.
CX NCBI_TaxID=4513;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Sundance;
RX MEDLINE=93258420; PubMed=1302632;
RA Halford N.G., Vicente-Carbajosa J., Sabelli P.A., Shewry P.R.,
RA Hamapel U., Kreis M.,
RT "Molecular analyses of a barley multigene family homologous to the
RT yeast protein kinase gene SNF1."
RL Plant J. 2:791-797(1992).
CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
DR EMBL; X65604; CA46554.1; -.
DR PIR; S60304; S60304.
DR HSSP; P00518; 1PKH.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR001772; Kinase_Cterm.
DR InterPro; IPR000719; Prot_Kinase.
DR InterPro; IPR002290; Ser_thr_kinase.
DR InterPro; IPR008271; Ser_thr_pkin_AS.
DR InterPro; IPR001245; Tyr_pkinase.
DR InterPro; IPR000449; UBA_domain.
DR Pfam; PF02149; KAI; 1.
DR Pfam; PF00069; pkinase; 1.
DR PRINTS; PR00109; TYRKINASE.
DR PRODOM; PD000001; Prot_kinase; 1.
DR SMART; SM00220; S_TKC; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
DR PROSITE; PS50030; UBA; 1.
KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
FT NON_TER 513 513
SQ SEQUENCE 513 AA; 58855 MW; BDE5AB9DDC50984 CRC64;

Query Match 76.9%; Score 2072; DB 10; Length 513;
Best Local Similarity 74.7%; Pred. NO. 9,3e-169;
Matches 383; Conservative 64; Mismatches 62; Indels 4; Gaps 2;

QY 1 MDGSSKSGSHSEALNNVLTGRTGIGTGKVKIAEHKLTGRVAIKINCKQMRNMEME 60
DB 1 MDGNNRGCGSHSEVLKNVNIKTIAGTGFQDVYVAERNYTGORVAIKINRRKMETMEME 60
QY 61 KAKREFKIKL---FIHHIIRLVEVIYTPNDIYVVMVEYCYGELFDYIVKGRLODEA 117
DB 61 KANREIKYMRFLFIDIPHIIRVVEVITFPKDIYVVMVEYCNNGELDYIINGRLODEA 120
QY 118 RRIFOILISGYEYCHRNNVVHRDLKPEMLLDLSKTNVLDLADFGLSNVVMDHGFLEKTS 177
DB 121 RRIFOILAGVYCHRNIVVHRDLKPEMLLDLSKTNVLDLADFGLSNVVMDHGFLEKTS 180
QY 178 PNYAAPVYISGKLVAGPEVDVWSCVYIYALICGLTPDDENIPNLFKIKGIGYITLPSH 237
DB 181 LNYAPVYISGKLVAGPEVDVWSCVYIYALICGSPDDDNIPSLFKIKGIGYITLPSY 240
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QY 238 LSALARDLIPMLVVEBMRITTRIREHOMFOIRLPRVLAVPDDTTOAKMIDEDTLR 297
DB 241 LBSGARLDIPKLNIDPMKRITTFHEIRVHWPFKNHLPCYLAVPPYEQQAKMIDEDTLR 300
QY 298 DVVNMGNKKNVCGESLCSRLQNEATVAYILLDNRFATSGYIGADYQESMDRLNLAS 357
DB 301 EVVNLGYDKCHVCESLNRRLONEETVAYYLLDRFSTSGYIGADHQHMDRSSFNEFTL 360
QY 358 SESSSGTRNVYVSSDPHSSGLRPYYPVERKVALGQSRAPHREIWEVYLKALQELNVR 417
DB 361 SESASPSIRNVLPEINISQGGGLRPYPVQRKVALIGQSGAHPREDITVVKALKELNVC 420
QY 418 WKKNGHVNCRCMCPGPEYND-TLDASNFLGSDSTIMDDANDGRLPVYKEFQLYKT 476
DB 421 WKKNGLYNMCRMCPCGFPQVSDMLDSDNHNFPVDSITMDGNMDGRLPVAVKEFIQLYKT 480
QY 477 KDKRYLLDMORVTGPOLLFLDFCAFLTKLRVL 509
DB 481 KDKRYLLDIQRTGPPQLFLFECGAFYTNLRVL 513
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RESULT 9
Q9ZRJ1 ID Q9ZRJ1 PRELIMINARY; PRT; 505 AA.
AC Q9ZRJ1;
DT 01-MAY-1999 (TREMBlrel. 10, Created)
DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE OSXL.
GN Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaeae; Oryza.
CX NCBI_TaxID=4530;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=99086251; PubMed=9870704;
RA Takano M., Kajiya-Kanegae H., Funatauki H., Kikuchi S.;
RT "Rice has two distinct classes of protein kinase genes related to SNF1
RT of Saccharomyces cerevisiae, which are differentially regulated in early
RT seed development."
RL Mol. Gen. Genet. 260:388-394(1998).
CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
DR EMBL; D82039; BAA36298.1; -.
DR HSSP; Q63450; 1A06.
DR Gramene; Q9ZRJ1; -.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR001772; Kinase_Cterm.
DR InterPro; IPR000719; Prot_Kinase.
DR InterPro; IPR002290; Ser_thr_kinase.
DR InterPro; IPR008271; Ser_thr_pkin_AS.
DR InterPro; IPR001245; Tyr_pkinase.
DR InterPro; IPR000449; UBA_domain.
DR Pfam; PF02149; KAI; 1.
DR Pfam; PF00069; pkinase; 1.
DR PRINTS; PR00109; TYRKINASE.
DR PRODOM; PD000001; Prot_kinase; 1.
DR SMART; SM00220; S_TKC; 1.
DR SMART; SM00165; UBA; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
DR PROSITE; PS50030; UBA; 1.
KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 505 AA; 57614 MW; 5631D07F591FD951 CRC64;
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RA Cheuk R., Chung M.K., Hayashizaki Y., Ishida J., Kamiya A., Kawai J.,
 Kim C., Lin J., Liu X., Narusaka M., Pham P.K., Sakano H.,
 RA Sakurai T., Satou M., Seki M., Shim P., Yamada K., Shinozaki K.,
 RA Ecker J., Theologis A., Davis R.W.,
 RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 DR EMBL: AY093170; AAM13169.1; -.
 DR HSSP: P24941; 1BUH.
 DR GO: GO:0005524; F:ATP binding; IEA.
 DR GO: GO:0004674; F:Protein serine/threonine kinase activity; IEA.
 DR GO: GO:0004713; F:Protein-tyrosine kinase activity; IEA.
 DR GO: GO:0016740; F:transferase activity; IEA.
 DR GO: GO:0006468; P:protein amino acid phosphorylation; IEA.
 DR InterPro: IPR001772; Kinase Cterm.
 DR InterPro: IPR002290; Ser_thr_kinase.
 DR InterPro: IPR008271; Ser_thr_pkin_AS.
 DR InterPro: IPR001245; Tyr_kinase.
 DR InterPro: IPR000449; UBA_domain.
 DR Pfam: PF02149; KAI; 1.
 DR Pfam: PF00069; pkinase; 1.
 DR Pfam: PF00627; UBA; 1.
 DR PRINTS: PR00109; TYRKINASE.
 DR ProDom: PD000001; Prot_kinase; 1.
 DR SMART: SM00220; S_TKc; 1.
 DR SMART: SM00165; UBA; 1.
 DR PROSITE: PS00107; PROTEIN KINASE ATP; 1.
 DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
 DR PROSITE: PS50030; UBA; 1.
 KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
 SQ SEQUENCE 535 AA; 6181 MW; 1963.5; DB 10; Length 535;
 Query Match 73.1%; Score 1969.5; DB 10; Length 535;
 Best Local Similarity 72.8%; Pred. No. 66-160;
 Matches 377; Conservative 52; Mismatches 74; Indels 15; Gaps 4;

1 MDGSSKG--SGHSEALRYNNGRTGIGTPGKVIKAEHKLTHGRVAIKIINCROMRMNM 58
 24 MDGSGTSGRSVESTLPYKIGRTIGISFGKVKIAEHALGKHVAIKILRRKIKNMEM 83
 59 EEKAKREFIKLPTHPHILRYEVIYPTDIYVMEYCKYGELEFDYIVKGRLOEDBAR 118
 84 EEKAREIKIIRLFVHPHILRYEVIETPTDIYVMEYVNGSELFDYIVKGRLOEDBAR 143
 119 RIFQITSGVEYCHRMVVRHDLKPENLILDSKVNKLADGSLNVMHGHFLTKSCGSP 178
 144 NFPOQIISGVEYCHRMVVRHDLKPENLILDSKVNKLADGSLNVMHGHFLTKSCGSP 203
 179 NYAAPEVISGKLYAGPEVDVWSCGVIYALICGTLPPDENIPNLFKKIKGITYLPSHL 238
 204 NYAAPEVISGKLYAGPEVDVWSCGVIYALICGTLPPDENIPNLFKKIKGITYLPSHL 263
 239 SALARDLIPRLVVEPMKRTITRIRREHWFQIRLPRYLAVPPDPTQOAKMIDEDTLRD 298
 264 SPGARLDLIPRLVVDPMKRTVITPEIRQHPWFQALHPRYLAVPPDPTQOAKKIDEBEILQE 323
 299 VVNMGFNNHVCESLCSRLQNEATVAYVLLDNRFRATSGYLGADYQESMDRNLNQLASS 358
 324 VINNGFDNHLIESLRNTQNDGVTYLLLDNRRASSGYLGAFQETME-GTPRMHPA 382
 359 ESSSGTNYVGGSDPHSSGLRPYVYERKMAIGLQSRAPREIMVVLKALQELNRW 418
 383 ESSVASPVSHRLPGLMEYQGVGLRSQYVYERKMAIGLQSRAPREIMVVLKALQELNRW 442
 419 KKNGHYVNCWCPGFPVNDTLDA-----SNSFLGDSITMDNDANGSLPTVYKEEF 471
 443 KKHGHYVNCWCPGFPVNDTLDA-----SNSFLGDSITMDNDANGSLPTVYKEEF 497
 472 QLYTKDKKYLIDMQRVYVGPQLLPLDPCAALPLTKLRVL 509
 498 QLYTKRDKKYLIDMQRVYVGPQLLPLDPCAALPLTKLRVL 535

RESULT 12
 P93113 ID P93113 PRELIMINARY; PRT; 504 AA.
 AC P93113
 DT 01-MAY-1997 (TrEMBLrel. 03, Created)
 DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 OS SNF1-related protein kinase.
 DE Cucumis sativus (Cucumber).
 CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 CC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 CC Eucosids I; Cucurbitales; Cucurbitaceae; Cucumis.
 NC NCB1_TaxID=3659;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Cotyledon;
 RA Gumpel N.J.;
 RL Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 DR EMBL: Y10036; CA71142.1; -.
 DR PIR: T10449; T10449.
 DR HSSP: O63450; 1A06.
 DR GO: GO:0005524; F:ATP binding; IEA.
 DR GO: GO:0004674; F:Protein serine/threonine kinase activity; IEA.
 DR GO: GO:0004713; F:Protein-tyrosine kinase activity; IEA.
 DR GO: GO:0016740; F:transferase activity; IEA.
 DR GO: GO:0006468; P:protein amino acid phosphorylation; IEA.
 DR InterPro: IPR001772; Kinase Cterm.
 DR InterPro: IPR000719; Prot_kinase.
 DR InterPro: IPR002290; Ser_thr_kinase.
 DR InterPro: IPR008271; Ser_thr_pkin_AS.
 DR InterPro: IPR001245; Tyr_kinase.
 DR InterPro: IPR000449; UBA_domain.
 DR Pfam: PF02149; KAI; 1.
 DR Pfam: PF00069; pkinase; 1.
 DR Pfam: PF00627; UBA; 1.
 DR PRINTS: PR00109; TYRKINASE.
 DR ProDom: PD000001; Prot_kinase; 1.
 DR SMART: SM00220; S_TKc; 1.
 DR SMART: SM00165; UBA; 1.
 DR PROSITE: PS00107; PROTEIN KINASE ATP; 1.
 DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
 DR PROSITE: PS50030; UBA; 1.
 KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
 SQ SEQUENCE 504 AA; 57839 MW; 4CB485ACD5C384 CRC64;
 Query Match 72.9%; Score 1963; DB 10; Length 504;
 Best Local Similarity 74.8%; Pred. No. 26-159;
 Matches 374; Conservative 53; Mismatches 65; Indels 8; Gaps 4;

16 NYNIGRTIGTGEKVKIAEHLKTHGRVAIKIINCROMRMMEKAKREFIKLPTHP 75
 7 NYKLGKTLGSGFQKVKIAEHALGKHVAIKILRRKIKVLDWEKAREIKILRLVHP 66
 76 HIRLYEVIYPTDIYVMEYCKYGELEFDYIVKGRLOEDBARIFPOQIISGVEYCHRM 135
 107 HIRLYEVIETPTDIYVMEYVNGSELFDYIVKGRLOEDBARNFQOQIISGVEYCHRM 126
 136 VVRHDLKPENLILDSKVNKLADGSLNVMHGHFLTKSCGSPNYAAPEVISGKLYAGPE 195
 127 VVRHDLKPENLILDSKVNKLADGSLNVMHGHFLTKSCGSPNYAAPEVISGKLYAGPE 186
 196 VDVWSCGVIYALICGTLPPDENIPNLFKKIKGITYLPSHLASALARDLIPRLVVEPM 255
 127 VVRHDLKPENLILDSKVNKLADGSLNVMHGHFLTKSCGSPNYAAPEVISGKLYAGPE 186
 187 VDVWSCGVIYALICGTLPPDENIPNLFKKIKGITYLPSHLSSGARELIPSLVVDPM 246
 256 KRITIRREHWFQIRLPRYLAVPPDPTQOAKMIDEDTLRDVNMGFNNHVCESLCS 315
 247 KRITIRREHWFQIRLPRYLAVPPDPTQOAKKIDEBEILQEYVNMGFNNHVCESLCS 306
 316 RLQNEATVAYVLLDNRFRATSGYLGADYQESMDRNLNQLASSSSSGTNRNVYVGGSDP 375


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Db 307 RIQNEATAYAYLLDNRFRVSSGYIGAEFOETMEGFNRHMPDPTNAVGRHLPGVNDY 366
Qy 376 HSSGLRPYVYERKALGOSRAHPREIMTEVVKALQELNVRKKNHYNKCRMGCP 435
Db 367 QGMGIRAQFVYERKALGOSRAHPREIMTEVVKALQELNVRKKNHYNKCRMGCP 426
Qy 436 -----EVVDITDASNSFLGD-STIMDNDANGRLPTVKKPEPOLYKTDODKYLDMQVY 489
Db 427 GHHGMINNPVH-SNHYFGDSTIENDGV-VKSPNVIKFEVOLYKTRKRYLLDLQKQ 484
Qy 490 GPOLFLDFCAFLTKLRVL 509
Db 485 GPOLFLDFCAFLTKLRVL 504

RESULT 13
Q9M726 PRELIMINARY; PRT; 514 AA.
ID Q9M726
AC Q9M726;
DT 01-OCT-2000 (TReMBLrel. 15, Created)
DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE SNF1.
GN SNF1.
OS Lycopersicon esculentum (Tomato).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC Lamiales; Solanales; Solanaceae; Solanum.
OX NCBI_TaxID=4081;
RN [1]
RP SEQUENCE FROM N.A.
RA Bradford K.J., Dahal P., Downie B., Nonogaki H., Alvarado V.;
RT "Yeast SNF1 kinase homolog from tomato."
RL Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.
CC -1 SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
EMBL: AF143743; AAF6639.1; -
DR HSSP: Q63450; 1A06
DR GO: GO:0005524; F:ATP binding; IEA.
DR GO: GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO: GO:0004713; F:protein-tyrosine kinase activity; IEA.
DR GO: GO:0006740; F:transferase activity; IEA.
DR GO: GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro: IPR001772; Kinase_Cterm.
DR InterPro: IPR000719; Prot_Kinase.
DR InterPro: IPR002290; Ser_thr_kinase.
DR InterPro: IPR008271; Ser_thr_pkin_AS.
DR InterPro: IPR001245; Tyr_kinase.
DR InterPro: IPR000449; UBA_domain.
DR Pfam: PF02149; KAI; 1.
DR Pfam: PF00069; pkinase; 1.
DR Pfam: PF00627; UBA; 1.
DR PRINTS: PR00109; TYRKINASE.
DR ProDom: PD000001; Prot_kinase; 1.
DR SMART: SM00220; S_TKc; 1.
DR SMART: SM00165; UBA; 1.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
DR PROSITE: PS50030; UBA; 1.
DR ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
KW SEQUENCE 514 AA; 58825 MW; 587765211B17FCAC CRC64;

Query Match 72.8%; Score 1960.5; DB 10; Length 514;
Best Local Similarity 72.9%; Pred. No. 3.3e-159;
Matches 376; Conservative 63; Mismatches 68; Indels 9; Gaps 6;
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Db 61 EEKVRREKIKLFLPHPIIRLYEVIETPSDIYVMEYVSGELFDYIVKGRLOEDBAR 120
Qy 119 RIFQOITISGVYCHRRNVVYRDLKPEVULLDSKNNVCLADPGLSNWHDGFLTSCGSP 178
Db 121 NFPOOITISGVYCHRRNVVYRDLKPEVULLDSKNNVCLADPGLSNWHDGFLTSCGSP 180
Qy 179 NYAPVYISGLVYGPEDVWVSCGVIYALICGLPFDENIPLYFKIKIGIYTLPSHL 238
Db 181 NYAPVYISGLVYGPEDVWVSCGVIYALICGLPFDENIPLYFKIKIGIYTLPSHL 240
Qy 239 SALARDLIPRLVYEPKIRITIREIRHOWFQIRLPYLAAPPDPTQOAKMIDEDTLRD 298
Db 241 SAGARDLIPRLVYDPKMRMTIPEIRLHPWQALPRYLAVPPDPTQOAKKIDEITLQ 300
Qy 299 VVMNGFKNHVCESLCSRLQNEATVAYLLDNRFRATSGTGLADYQESMDRINQLASS 358
Db 301 VVMNGFKNHVCESLCSRLQNEATVAYLLDNRFRATSGTGLADYQESMDRINQLASS 360
Qy 359 ESSSGTRNRYVPGSSDPSGLRPYVYERKALGOSRAHPREIMTEVVKALQELNVRW 418
Db 361 ETAAAPVQGRFPDGMVQOAGAR-QPIERKALGOSRAHPREIMTEVVKALQELNVRW 419
Qy 419 KNGHYNVYKRCWCPPEVNDITDAS-----NSFLG-DSTIMDNDANGRLPTVKKPEQL 473
Db 420 KKGQYNNKCRWVPSLPGHHEGVMGVMHGNGQFGDDSSIENDGAT-KLTNNVYKFEVOL 478
Qy 474 YKTDKDKYLLDMQVYTGQQLFLDFCAFLTKLRVL 509
Db 479 YKTRKRYLLDLQRLQGPOLFLDFCAFLTKLRVL 514

RESULT 14
Q43475 PRELIMINARY; PRT; 484 AA.
ID Q43475
AC Q43475;
DT 01-NOV-1996 (TReMBLrel. 01, Created)
DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE SNF1-related protein kinase (Fragment).
GN BKIN2.
OS Hordeum vulgare (Barley).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; liliopsids; Poales; Poaceae; Pooidae;
OC Triticeae; Hordeum.
OX NCBI_TaxID=4513;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=cv. Sundance; TISSUE=Endosperm;
RC MEDLIN=95284374; PubMed=7766906;
RA Hannappel U., Vicente-carbajosa J., Barker J.H., Shewry P.R.,
RA Halford N.G.;
RT "Differential expression of two barley SNF1-related protein kinase
RT genes."
RL Plant Mol. Biol. 27:1235-1240(1995).
CC -1 SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
EMBL: X82548; CA57898.1; -
DR PIR: S59941; S59941.
DR HSSP: Q63450; 1A06.
DR GO: GO:0005524; F:ATP binding; IEA.
DR GO: GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO: GO:0004713; F:protein-tyrosine kinase activity; IEA.
DR GO: GO:0006740; F:transferase activity; IEA.
DR GO: GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro: IPR001772; Kinase_Cterm.
DR InterPro: IPR000719; Prot_Kinase.
DR InterPro: IPR002290; Ser_thr_kinase.
DR InterPro: IPR008271; Ser_thr_pkin_AS.
DR InterPro: IPR001245; Tyr_kinase.
DR InterPro: IPR000449; UBA_domain.
DR Pfam: PF02149; KAI; 1.
DR Pfam: PF00069; pkinase; 1.
DR Pfam: PF00627; UBA; 1.
DR PRINTS: PR00109; TYRKINASE.
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DR ProdDom: PD000001; Prot Kinase; 1.
DR SMART: SM00220; S TKC; 1.
DR SMART: SM00165; UBA; 1.
DR PROSITE; PS00107; PROTEIN KINASE_ATP; 1.
DR PROSITE; PS50011; PROTEIN KINASE_DOM; 1.
DR PROSITE; PS0108; PROTEIN_KINASE_ST; 1.
DR ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
KW NON_TER 1 484
FT NON_TER 1 484
SQ SEQUENCE 484 AA; 55322 MW; E83748B410C2EC33 CRC64;
Query March 72.2%; Score 1945; DB 10; Length 484;
Best Local Similarity 76.0%; Pred. No. 6.5e-158;
Matches 374; Conservative 47; Mismatches 61; Indels 10; Gaps 4;
QY 20 GRTVIGTFFGVKIAEHKLTGHRVAIKIINCQRNNMEKAKREFKILFLPHPIIR 79
DB 1 GRTVIGTFFGVKIAEHKLTGHRVAIKIINCQRNNMEKAKREFKILFLPHPIIR 60
QY 80 LYEVIYPTDIYVMEYCKYGEIPDYIYVEKRLQDEARRIFQOIIISGVYCHRNMYVHR 139
DB 61 LYEVIYPTDIYVMEYCKYGEIPDYIYVEKRLQDEARRIFQOIIISGVYCHRNMYVHR 120
QY 140 DLKPEMLLDKRYNKLADFGISNMVMDHFLKTSQCSPNYAAPEVISGKLAYGEVDVW 199
DB 121 DLKPEMLLDKRYNKLADFGISNMVMDHFLKTSQCSPNYAAPEVISGKLAYGEVDVW 180
QY 200 SCGVILVALLCGTLPPDDENIPNLFKIKGGIYTLPSHLAALDLIPRLVVEPMKRT 259
DB 181 SCGVILVALLCGTLPPDDENIPNLFKIKGGIYTLPSHLAALDLIPRLVVEPMKRT 240
QY 260 IREIREHQMFOIRLPRYLAVPPPTTQQAAMIDEDTLRDVNMGNKXHVCSLRON 319
DB 241 IREIREHQMFOIRLPRYLAVPPPTTQQAAMIDEDTLRDVNMGNKXHVCSLRON 300
QY 320 EATVAYYLLDNRPRATSGYLADYQESMDRNLQLA-SSSSSSSGTNTY-VPSSDPHS 377
DB 301 EATVAYYLLDNRPRATSGYLADYQESMDRNLQLA-SSSSSSSGTNTY-VPSSDPHS 354
QY 378 SGLRPYVVERKMAIGLOSRAHPREIMVEVTKALQELNVRKNGHNVKRCWCPGPEV 437
DB 355 SGLRPYVVERKMAIGLOSRAHPREIMVEVTKALQELNVRKNGHNVKRCWCPGPEV 413
QY 438 NDTLDANSFLGDSGTIMDNDANGRLPVIKFEFQLYTKDXYLLDMQRTYGPQLFLD 497
DB 414 NDTLDANSFLGDSGTIMDNDANGRLPVIKFEFQLYTKDXYLLDMQRTYGPQLFLD 472
QY 498 FCAAFLETLQRYL 509
DB 473 FCAAFLETLQRYL 484
RESULT 15
Q40544 PRELIMINARY; PRT; 511 AA.
AC Q40544;
DT 01-NOV-1996 (Tremblrel. 01, Created)
DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE Protein Kinase.
OS Nicotiana tabacum (Common tobacco).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC Lamiales; Solanales; Solanaceae; Nicotiana.
OX NCBI_TaxID=4097;
RN (1)
RP SEQUENCE FROM N.A.
RA Machida Y.;
RL Submitted (JUN-1994) to the EMBL/Genbank/DBJ databases.
RX MEDLINE=94217693; PubMed=8164654;

RA Muranaka T., Banno H., Machida Y.;
RT "Characterization of tobacco protein kinase NPK5, a homolog of
RT Saccharomyces cerevisiae SNF1 that constitutively activates expression
RT of the glucose-repressible SUC2 gene for a secreted invertase of S.
RT cerevisiae."
RL Mol. Cell. Biol. 14:2958-2965(1994).
CC EMBL; D26602; BAA05649.1; -.
DR PIR; A56009; A56009.
DR HSP; Q63450; 1A06.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR001772; Kinase Cterm.
DR InterPro; IPR000719; Prot Kinase.
DR InterPro; IPR002290; Ser_Thr_kinase.
DR InterPro; IPR008271; Ser_Thr_kinase.
DR InterPro; IPR001245; Tyr_kinase.
DR InterPro; IPR000449; UBA_domain.
DR Pfam; PF02149; KAI; 1.
DR Pfam; PF00069; Kinase; 1.
DR Pfam; PF00627; UBA; 1.
DR PRINTS; PR00109; TYRKINASE.
DR ProdDom; PD000001; Prot Kinase; 1.
DR SMART; SM00220; S TKC; 1.
DR PROSITE; PS00107; PROTEIN KINASE_ATP; 1.
DR PROSITE; PS50011; PROTEIN KINASE_DOM; 1.
DR PROSITE; PS0108; PROTEIN_KINASE_ST; 1.
DR ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
KW SEQUENCE 511 AA; 58339 MW; 1263939CD753519 CRC64;
Query March 71.4%; Score 1923; DB 10; Length 511;
Best Local Similarity 72.1%; Pred. No. 5.4e-156;
Matches 372; Conservative 60; Mismatches 72; Indels 12; Gaps 7;
QY 1 MDGSS-KSGSHSALNNYNGRTIGTGFVKYIAEHKLTGHRVAIKIINCQRNNMEM 58
DB 1 MDGSS-KSGSHSALNNYNGRTIGTGFVKYIAEHKLTGHRVAIKIINCQRNNMEM 60
QY 59 EEKAKREFKILFLPHPIIRLVEVIYPTDIYVMEYCKYGEIPDYIYVEKRLQDEAR 118
DB 61 EEKAKREFKILFLPHPIIRLVEVIYPTDIYVMEYCKYGEIPDYIYVEKRLQDEAR 120
QY 119 RIFQOIIISGVYCHRNMYVHRDLKPEMLLDKRYNKLADFGISNMVMDHFLKTSQSP 178
DB 121 RIFQOIIISGVYCHRNMYVHRDLKPEMLLDKRYNKLADFGISNMVMDHFLKTSQSP 180
QY 179 NYAAPEVISGKLAYGEVDVWSCGVLVYALLCGTLPPDDENIPNLFKIKGGIYTLPSHL 238
DB 181 NYAAPEVISGKLAYGEVDVWSCGVLVYALLCGTLPPDDENIPNLFKIKGGIYTLPSHL 240
QY 239 SALARDLIIPRLVVEPMKRTITIREIREHQMFOIRLPRYLAVPPPTTQQAAMIDEDTLRD 298
DB 241 SAGARDLIIPRLVVEPMKRTITIREIREHQMFOIRLPRYLAVPPPTTQQAAMIDEDTLRD 300
QY 299 VVMNGFKNVYCSLGRNLNEATVAYYLLDNRFRATSGYLADYQESMDRNLQLA-SS 358
DB 301 VVMNGFKNVYCSLGRNLNEATVAYYLLDNRFRATSGYLADYQESMDRNLQLA-SS 360
QY 359 ESSSSGGRNYPGSSDHSGLRPYVVERKMAIGLOSRAHPREIMVEVTKALQELNVRW 418
DB 361 EVLLP-CMQLHFGIMDQYQGAR-QFVEKRMALGLOSRAHPREIMVEVTKALQELNVRW 418
QY 419 KNGHNVKRCWCPGPEVNDTLDANS-FLG-DSTIMDNDANGRLPYTKFEFQL 473
DB 419 KNGHNVKRCWCPGPEVNDTLDANS-FLG-DSTIMDNDANGRLPYTKFEFQL 473
QY 474 YKTDDKTYLLDMQRTYGPQLFLDFCAAFLETLQRYL 509
DB 476 YKTDDKTYLLDMQRTYGPQLFLDFCAAFLETLQRYL 511

Mon Jul 12 09:11:04 2004

us-09-857-522b-4.rpt

Page 11

Search completed: July 7, 2004, 17:56:36
Job time : 47 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 7, 2004, 17:52:54 ; Search time 20 Seconds

(without alignments)
2448.074 Million cell updates/sec

Title: US-09-857-522B-4

Sequence: 1 MDSSKSGSHSEALRNYNLG.....GPELLFDPCAFITKLRVL 509

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 2000000000Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summariesDatabase : PIR 78: *
1: pir1: *
2: pir2: *
3: pir3: *
4: pir4: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2356.5	87.5	510	2 T04145	serine/threonine p
2	2080	77.2	513	1 S60303	serine/threonine-s
3	2068	76.8	513	1 S60304	serine/threonine-s
4	2062.5	76.6	502	1 A41361	serine/threonine-s
5	1969.5	73.1	512	1 JCI146	serine/threonine-s
6	1963	72.9	504	2 T10449	probable serine/ch
7	1923	71.4	511	1 A56009	serine/threonine-s
8	1903.5	70.7	512	2 T52633	serine/threonine-s
9	1900	70.6	473	1 S59941	serine/threonine-s
10	1853.5	68.8	512	2 T07788	probable serine/ch
11	1727	64.1	504	2 T07415	probable serine/ch
12	1148	42.6	552	1 S51025	[hydroxymethylglut
13	1144	42.5	552	1 A53621	[hydroxymethylglut
14	1137	42.2	472	2 B50100	SNF-related kinase
15	1096	40.7	348	2 T07660	probable serine/ch
16	1080	37.6	562	2 T29858	hypothetical prote
17	1013.5	37.6	633	1 A26030	serine/threonine-s
18	992	36.8	602	2 S75213	FOO2 protein - yea
19	981.5	36.4	576	2 T41587	probable carbon ca
20	894.5	33.2	622	1 S44859	serine/threonine-s
21	730.5	27.1	713	2 UC7500	qlk protein - chic
22	725.5	26.9	798	2 S27966	probable serine/ch
23	724	26.9	887	2 T20941	hypothetical prote
24	718	26.7	1192	2 T18611	probable serine/ch
25	718	26.7	1246	2 G89287	protein H39823.1 l
26	717.5	26.6	745	2 G01025	serine/threonine p
27	710.5	26.4	481	2 T149072	protein kinase - m
28	709.5	26.3	1398	2 T13741	hypothetical prote
29	701.5	26.0	440	2 T14736	probable serine/ch

30	700	26.0	440	2 T14735	probable serine/ch
31	696.5	25.9	774	2 T48609	probable serine/ch
32	692.5	25.7	445	2 T09903	serine/threonine-s
33	691.5	25.7	441	2 C84667	probable protein k
34	682.5	25.3	480	2 A86427	probable serine/ch
35	676.5	25.1	915	2 S74283	probable protein k
36	675.5	25.1	532	2 T38326	serine threonine p
37	667.5	24.8	453	2 G86141	protein T25K16.13
38	667	24.8	651	2 S52244	p59Bg1 protein - A
39	664	24.7	174	2 G01743	AMP-activated prot
40	659.5	24.5	1142	2 S59359	G1N4 protein - yea
41	644.5	23.9	1518	2 S37928	probable purine p
42	644	23.9	445	2 T50802	serine/threonine p
43	627	23.3	401	2 B90120	SNF1-related prote
44	626	23.2	1147	2 S64930	serine/threonine-s
45	618.5	23.0	421	2 E96522	hypothetical prote

ALIGNMENTS

RESULT 1		T04145		serine/threonine protein kinase homolog - rice	
C:Species: Oryza sativa (rice)		C:Date: 23-Apr-1999		#sequence_revision 23-Apr-1999 #text_change 21-Jan-2000	
C:Accession: T04145		R:Tsal, T.H.; Le, H.T.		submitted to the EMBL Data Library, April 1996	
A:Description: SNF1-related protein kinase of rice.		A:Reference number: Z15239		A:Accession: T04145	
A:Status: preliminary; translated from GB/EMBL/DBJ		A:Molecule type: mRNA		A:Residues: 1-510 <TSA>	
A:Cross-references: EMBL:U55768; NID:G1477683; PIDN:AAB05457.1; PID:G1477684		A:Experimental source: strain tns-8, endospore		A:Gene: RSK1	
C:Superfamily: AMP-activated protein kinase; protein kinase homology		F:15-270/Domain: protein kinase homology <KIN>		Query Match	
Best Local Similarity		87.5%; Score 2356.5; DB 2; Length 510;		Pred. No. 1.5e-93;	
Matches 444; Conservative 32; Mismatches 33; Indels 1; Gaps 1;		1 MDSSKSGSHSEALRNYNLGRITGIGTFGKVI AEHLTGHRVAIKIINCRQNMMEER 60		1 MDGNKXGSHSEALKNYNLGRITGIGSFQVKIAEHLTGHRVAIKILNRQNMMEER 60	
61 KAKREFKILKFIHPHILRLVEVLYPTDIYVMEYCKGELFPIYIEKRLQDE-ARR 119		61 KAKREIKILRLFIHPHILRLVEVLYPTDIYVMEYCKGELFPIYIEKRLQDEARR 120		120 IFQGIISGVYCHRNMMVHRDLKRENLLDSKVNVKLADGSLNVMDGHLTKTSCSPN 179	
121 IFSQIISAVYCHRNMMVHRDLKRENLLDSKVNVKLADGSLNVMDGHLTKTSCSPN 180		180 YAAPEVLSGLVYAGPEVDVMSGVLVYALLCGTLPPDDENI PNLFKIKGIIYTLPSHLS 239		181 YAAPEVLSGLVYAGPEVDVMSGVLVYALLCGTLPPDDENI PNLFKIKGIIYTLPSHLS 240	
240 ALARDLIPMLVVEPMKRIITREIREQWFOIRPLRLANPPPTTQAAKIDEDTLRDV 299		241 ALARDLIPMLVVDPMKRIITREIREQWFOIRPLRLANPPPTTQAAKIDEDTLQDV 300		300 VNMGFNKHVCEISLCSRLQNEATVAYVLLLDNFRATSGVIGADYOSQNRNLQLASSE 359	
301 VNLGYGDHVCESLRNFPQNEATVAYVLLLDNFRATSGVIGADYOSLRNRPASSE 360		360 SSSSGTRNRYVPGSSDPHSGLRPPYPERKVALGLQSRAPPREIMEVVLKALQELNRWK 419		361 SASGNTRHVLPGSSDPHSGLRPPYPERKVALGLQSRAPPREIMEVVLKALQELNRWK 420	

Db 481 KDNKYLIDQRTVGQQLLFLEFCGAFNLNVL 513

RESULT 4

A11361

serine/threonine-specific protein kinase (EC 2.7.1.-) RKINI - rye

C:Species: Secale cereale (rye)

C:Date: 12-Jun-1992 #sequence_revision 12-Jun-1992 #text_change 11-Jun-1999

C:Accession: A11361

R:Alderson, A.; Sabelli, P.A.; Dickinson, J.R.; Cole, D.; Richardson, M.; Kreis, M.; She

Proc. Natl. Acad. Sci. U.S.A. 88, 8602-8605, 1991

A:Title: Complementatation of snf1, a mutation affecting global regulation of carbon meta

A:Reference number: A11361; MUID:92020901; PMID:1924320

A:Accession: A11361

A:Molecule type: mRNA

A:Residues: 1-502 <ALD>

A:Cross-references: GB:M74113; NID:g169835; PIDN:AAA33921.1; PID:g169836

C:Function:

A:Description: catalyzes the formation of peptidyl-L-serine-phosphate or peptidyl-L-threonit

C:Superfamily: AMP-activated protein kinase; protein kinase homology

C:Keywords: ATP; autophosphorylation; magnesium; phosphoprotein; phosphotransferase; ser

F:12-269/Domain: protein kinase homology <KIN>

F:20-28/Region: protein kinase ATP-binding motif

F:43,62,140,142/Active site: Lys, Glu, Asp, Lys #status predicted

F:145,149/Binding site: magnesium (Asn, Asp) #status predicted

Query Match 76.6%; Score 2062.5; DB 1; Length 502;

Best Local Similarity 77.9%; Pred. No. 4.5e-81;

Matches 401; Conservative 37; Mismatches 58; Indels 19; Gaps 6;

Qy 1 MDSSKSGSHSEALRNVLGRTIGTGKTKIAEHKLTGHRVAKIINCRMRMEME 60

Db 1 MDG---GSEHEALKNVYLKILGVTAKVILAEHKTRKVAIKVNRKMPREHE 57

Qy 61 KAKEFKILKLP---IHPIIRLVEVITPTDIYVMEYCKYGELEFDYIVKGRLODEA 117

Db 58 KAKEIKILRLFPIDLIHPIIRVVEVITPTDIFVMEYCKYGELEFDYIVKGRLODEA 117

Qy 118 RRIQOIIISGVEYCHRNNVVHRDLKPENLILDSKYNVLADFGLSNVMDGHFLKTS 177

Db 118 RRIQOIIISAVEYCHRNKVRHDLKPENLILDSKYNVLADFGLSNVMDGHFLKTS 177

Qy 178 PNYAPEVITSGKLVAPEVDVWSCGVIYALLCGTLPPDDNIPMLFKIKIGIYTLPSH 237

Db 178 LNYAPEVITSGKLVAPEVDVWSCGVIYALLCGVLPDDNIPMLFKIKIGIYTLPIY 237

Qy 238 LSLARLDLIPMLVPEPKRITIREIREHOFQIRLPRYLAVPPDDTQOAKMIDEDTLR 297

Db 238 LSLARLDLIPMLVPEPKRITIREIREHOFQIRLPRYLAVPPDDTQOAKMIDEDTLR 297

Qy 298 DVVNGFNKNVYCSGLRQNEATVAYLLLDNRFRTSGYLGADESDRNLNQLAS 357

Db 298 DVVNGFNKNVYCSGLRQNEATVAYLLLDNRFRTSGYLGADESDRNLNQLAS 357

Qy 358 SESSSGTRNVVPSGSDHSSGLRPYVERKMLGL-OSRAHPREIWEVLKALQELNV 416

Db 358 SESSSGTRNVVPSGSDHSSGLRPYVERKMLGL-OSRAHPREIWEVLKALQELNV 416

Qy 417 RAKNGH-VYKWCWCPGPEVND-TLDASNPLGDSITIMNDANGRLPVIYFEFOLY 474

Db 417 RAKNGH-VYKWCWCPGPEVND-TLDASNPLGDSITIMNDANGRLPVIYFEFOLY 474

Qy 408 CMKNGGCVNMKCMKCPGPRVSDMLDANHSFVDDCAIKONGDANSRLPAVITFEIOLY 467

Db 408 CMKNGGCVNMKCMKCPGPRVSDMLDANHSFVDDCAIKONGDANSRLPAVITFEIOLY 467

Qy 475 KTKDDKYLIDMQRTVGQQLLFLEFCGAFNLNVL 509

Db 475 KTKDDKYLIDMQRTVGQQLLFLEFCGAFNLNVL 509

Qy 468 KTKDDKYLIDMQRTVGQQLLFLEFCGAFNLNVL 502

Db 468 KTKDDKYLIDMQRTVGQQLLFLEFCGAFNLNVL 502

Qy 475 KTKDDKYLIDMQRTVGQQLLFLEFCGAFNLNVL 509

Db 475 KTKDDKYLIDMQRTVGQQLLFLEFCGAFNLNVL 509

Qy 468 KTKDDKYLIDMQRTVGQQLLFLEFCGAFNLNVL 502

Db 468 KTKDDKYLIDMQRTVGQQLLFLEFCGAFNLNVL 502

Qy 475 KTKDDKYLIDMQRTVGQQLLFLEFCGAFNLNVL 509

Db 475 KTKDDKYLIDMQRTVGQQLLFLEFCGAFNLNVL 509

Qy 468 KTKDDKYLIDMQRTVGQQLLFLEFCGAFNLNVL 502

Db 468 KTKDDKYLIDMQRTVGQQLLFLEFCGAFNLNVL 502

Qy 475 KTKDDKYLIDMQRTVGQQLLFLEFCGAFNLNVL 509

Db 475 KTKDDKYLIDMQRTVGQQLLFLEFCGAFNLNVL 509

Qy 468 KTKDDKYLIDMQRTVGQQLLFLEFCGAFNLNVL 502

Db 468 KTKDDKYLIDMQRTVGQQLLFLEFCGAFNLNVL 502

Qy 475 KTKDDKYLIDMQRTVGQQLLFLEFCGAFNLNVL 509

Db 475 KTKDDKYLIDMQRTVGQQLLFLEFCGAFNLNVL 509

Qy 468 KTKDDKYLIDMQRTVGQQLLFLEFCGAFNLNVL 502

Db 468 KTKDDKYLIDMQRTVGQQLLFLEFCGAFNLNVL 502

Qy 475 KTKDDKYLIDMQRTVGQQLLFLEFCGAFNLNVL 509

Db 475 KTKDDKYLIDMQRTVGQQLLFLEFCGAFNLNVL 509

Qy 468 KTKDDKYLIDMQRTVGQQLLFLEFCGAFNLNVL 502

Db 468 KTKDDKYLIDMQRTVGQQLLFLEFCGAFNLNVL 502

Qy 475 KTKDDKYLIDMQRTVGQQLLFLEFCGAFNLNVL 509

Db 475 KTKDDKYLIDMQRTVGQQLLFLEFCGAFNLNVL 509

Db 420 KKHGHYMKCMWV-----NSASQGLMSNSMHNNDNYGDESSIIENEAAYVSPVAVFEI 474
Qy 472 QLYTKDDKYLIDMQRVTGPGOLLFLDFCAFLTKLRLV 509
Db 475 QLYTKRDDKYLIDLRVQVGPQFLFLDCAFLAQLRLV 512

RESULT 6

T10449
probable serine/threonine-specific protein kinase (EC 2.7.1.-) - cucumber
N:Alternate names: SNF1-related protein kinase
C:Species: Cucumis sativus (cucumber)
C:Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 20-Jun-2000
C:Accession: T10449
R:Gumpel, N.J.
submitted to the EMBL Data Library, December 1996
A:Reference number: Z17020
A:Accession: T10449
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-504 <GDM>
A:Cross-references: EMBL:Y10036
A:Experimental source: cv. Masterpiece; cotyledon
C:Function:
A:Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threonin
C:Superfamily: AMP-activated protein kinase; protein kinase homology
C:Keywords: ATP; phosphotransferase; serine/threonine-specific protein kinase
F:6-260/Domain: protein kinase homology <KIN>

Query Match 72.9%; Score 1963; DB 2; Length 504;

Best Local Similarity 74.8%; Pred. No. 7.5e-77;
Matches 374; Conservative 53; Mismatches 65; Indels 8; Gaps 4;

Qy 16 NYNLGRTLGIGTFGKVKIAEHLTGRVAIKI INCRQNMNMEBEKAREFKIKLFTHP 75
Db 7 NYKLGTGIGSGFGKVKIAEHALTGHKVAIKILNRKIKNDMEKVRREIKILFTFMRP 66
Qy 76 HIILYEYVTPPTDIYVMEYCKYGELEFDYIVEKRLQEDEARLPQOIIISGVYCHRMN 135
Db 67 HIIRLYEIVETPSDIYVMEYKSGELFDYIVEKRLQEDEARLPQOIIISGVYCHRMN 126
Qy 136 VVHDLKPEENLLDSKYNVKLADFGLSNVMDGHFLKTS CGSPNYAAPEVISGKLYAGPE 195
Db 127 VVHDLKPEENLLDSKYNVKLADFGLSNVMDGHFLKTS CGSPNYAAPEVISGKLYAGPE 186
Qy 196 VDWSGCVILYALLCGTLPPDDENIPNLFKKIKGSIYTLPSHLSALARDLIPMLVYEDM 255
Db 187 VDWSGCVILYALLCGTLPPDDENIPNLFKKIKGSIYTLPSHLSGABELIPMLVYEDM 246
Qy 256 KRITIREIREHOWPQIRLPYLAVPPTDTPQAAKIDEDTLRDVYVMGFGNQHVCESLCS 315
Db 247 KRITIREIREHOWPQIRLPYLAVPPTDTPQAAKIDEDTLRDVYVMGFGNQHVCESLCS 306
Qy 316 RLONEATVAYVILLDNFRATSGYLADYQESMDENLQLAS SESSASSETGNYVPGSSDP 375
Db 307 RLONEATVAYVILLDNFRATSGYLADYQESMDENLQLAS SESSASSETGNYVPGSSDP 366
Qy 376 HSSGLRPYVYERKAKALGOSRAHREIMTEVYLKALRELINAMKKIGYNNKCMWLPIIP 435
Db 367 QGMGLRAPFPYERKAKALGOSRAHREIMTEVYLKALRELINAMKKIGYNNKCMWLPIIP 426
Qy 436 -----EVVDITLDASNSFLGD-STIMDNDANGRLPTVYKFEFOLYKTKDDKYLIDMQRVT 489
Db 427 GHHEGMINNPVA-SNHYFGDKSTIITENDGV-VKSPNVIKFEVQLYKTRKYLIDLRQVQ 484
Qy 490 GPOLLFLDFCAFLTKLRLV 509
Db 485 GPQFLFLDLCALFLAQLRLV 504

RESULT 7
A56009

serine/threonine-specific protein kinase (EC 2.7.1.-) NPK5 - common tobacco
C:Species: Nicotiana tabacum (common tobacco)
C:Date: 28-Apr-1995 #sequence_revision 28-Apr-1995 #text_change 16-Jun-2000
C:Accession: A56009
R:Murataka, T.; Banno, H.; Machida, Y.
Mol. Cell. Biol. 14, 2958-2965, 1994
A:Title: Characterization of tobacco protein kinase NPK5, a homolog of Saccharomyces cere
tase of Saccharomyces cerevisiae.
A:Reference number: A56009; MUID:94217693; PMID:8164654
A:Accession: A56009
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-511 <MUR>
A:Cross-references: GB:D26602; NID:g496384; PIDN:BA05649.1; PID:g496385
C:Function:
A:Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threonin
C:Superfamily: AMP-activated protein kinase; protein kinase homology
C:Keywords: ATP; magnesium; phosphotransferase; serine/threonine-specific protein kinase
F:17-271/Domain: protein kinase homology <KIN>
F:25-33/Region: protein kinase ATP-binding motif
F:148-67,142,144/Active site: Lys, Glu, Asp, Lys #status predicted
F:147,151/Binding site: magnesium (Asn, Asp) #status predicted

Query Match 71.4%; Score 1923; DB 1; Length 511;
Best Local Similarity 72.1%; Pred. No. 3.8e-75;
Matches 372; Conservative 60; Mismatches 72; Indels 12; Gaps 7;

Qy 1 MDGSS-KSGSHSALNNVNLGRTLGIGTFGKVKIAEHLTGRVAIKI INCRQNMNMEBEKAREFKIKLFTHP 58
Db 1 MDGTVGSGSSVSEFSLNNYKLGIGTFGKVKIAEHALTGHKVAIKILNRKIKNDMEKVRREIKILFTFMRP 60
Qy 59 BEKAREFKIKLFTHPHIIRLYEVITPTDIYVMEYCKYGELEFDYIVEKRLQEDEARLPQOIIISGVYCHRMN 118
Db 61 BEKAREFKIKLFTFMRPHIIRLYEVETPSDIYVMEYKSGELFDYIVEKRLQEDEARLPQOIIISGVYCHRMN 120
Qy 119 RIPOQIIISGVYCHRMNVVHDLKPEENLLDSKYNVKLADFGLSNVMDGHFLKTS CGSP 178
Db 121 KFFQOIIISGVYCHRMNVVHDLKPEENLLDSKYNVKLADFGLSNVMDGHFLKTS CGSP 180
Qy 179 NYAAPEVISGKLYAGPEVDWSGCVILYALLCGTLPPDDENIPNLFKKIKGSIYTLPSHLS 238
Db 181 NYAAPEVISGKLYAGPEVDWSGCVILYALLCGTLPPDDENIPNLFKKIKGSIYTLPSHLS 240
Qy 239 SALARDLIPMLVYERKAKALGOSRAHREIMTEVYLKALRELINAMKKIGYNNKCMWLPIIP 298
Db 241 SAGARDLIPMLVYERKAKALGOSRAHREIMTEVYLKALRELINAMKKIGYNNKCMWLPIIP 300
Qy 299 VVNMGFKNHVCBSLCSRLONEATVAYVILLDNFRATSGYLADYQESMDENLQLAS 358
Db 301 VVNMGFKNHVCBSLCSRLONEATVAYVILLDNFRATSGYLADYQESMDENLQLAS 360
Qy 359 ESSSSGTRNYPVPGSSDHSGLRPYVYERKAKALGOSRAHREIMTEVYLKALRELINAMKKIGYNNKCMWLPIIP 418
Db 361 EVLLIP-CWQHLPGMDIQOYGAR-QFVERKMAIGLOSRAHREIMTEVYLKALRELINAMKKIGYNNKCMWLPIIP 418
Qy 419 KKNHYNVAVKRCWCPPEVNDITLDASNS---FLG-DSTIMDNDANGRLPTVYKFEFOL 473
Db 419 KKGIVYNNKCMWLPIIPVYERKAKALGOSRAHREIMTEVYLKALRELINAMKKIGYNNKCMWLPIIP 475
Qy 474 YKTKDDKYLIDMQRVTGPGOLLFLDFCAFLTKLRLV 509
Db 476 YKTRERKYLIDLRVQVGPQFLFLDCAFLAQLRLV 511

RESULT 8

T52633
serine/threonine-specific protein kinase (EC 2.7.1.-) AKIN11 [validated] - Arabidopsis th
N:Alternate names: SNF1 protein kinase homolog AKIN11
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 24-Oct-2000 #sequence_revision 24-Oct-2000 #text_change 03-Nov-2000
C:Accession: T52633
R:Bhalerao, R.P.; Salchert, K.; Bako, L.; Okresz, L.; Szabados, L.; Murataka, T.; Machida
Proc. Natl. Acad. Sci. U.S.A. 96, 5322-7, 1999

A:Title: Regulatory interaction of PRL1 WD protein with Arabidopsis SNF1-like protein K1
A:Reference number: Z5116; MUID:99238528; PMID:10220464
A:Accession: T52633
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-512 <BHA>
A:Cross-references: EMBL:X99279; PIDN:CAAG671.1
A:Experimental source: cultivar Columbia
C:Gene: AKIN11
C:Function:
A:Description: EC 2.7.1.-; serine/threonine-specific protein kinase AKIN11 [validated, M
C:Superfamily: AMP-activated protein kinase; protein kinase homology
C:Keywords: ATP; phosphotransferase; serine/threonine-specific protein kinase

Query Match 70.7%; Score 1903.5; DB 2; Length 512;
Best Local Similarity 70.7%; Pred. No. 2.5e-74;
Matches 362; Conservative 58; Mismatches 89; Indels 3; Gaps 1;

QY 1 MDGSSK---SGSHSALNNYLGRTLGITGKVKYKIAHKLTHRVAIKINCRGRME 57
DB 1 MDHSSNRFGNNVGSILPNYKLGKTLGSGFGKVAIAHVVTGKVAIKILNRRKIKME 60
QY 58 MEERAKREFKILKLFHPHIIIRLYEVITYPTDIYVMEYCKYGLFDYIVKGRLOEBA 117
DB 61 MEKVRRIKILRLFMHPIIRQYEVITTSIDYVMEYKSGELFDYIVKGRLOEBA 120
QY 118 RRIFOQIISGVEYCHRNNAVHRDLKPNLLDSKYNKVLADFGLSNVMDGHFLKTS 177
DB 121 RNFFQOIIISGVEYCHRNNAVHRDLKPNLLDSRCNIKIALDFGLSNVARDGHFLKTS 180
QY 178 PNYAPAEVTSKLYAGPEVDVWSCGVTLLYALCGTLPPDDNIPVLFKIKGITYLPSH 237
DB 181 PNYAPAEVTSKLYAGPEVDVWSCGVTLLYALCGTLPPDDNIPVLFKIKGITYLPSH 240
QY 238 LSAARLDLPMLVPEPKRITIREIRHOFQIRLPYLAVPDPDTQAKMIDEDTLR 297
DB 241 LSSERDLIPMLVDPYKRTITPEIRKHFQTHLPYLAVPDPDTQAKMIDEDTLR 300
QY 298 DVVNMGNKHNVCESLCSRLQNEATVAAYLLLDNRFRTSGYLADYQESMDRLNQAS 357
DB 301 EVVNMGNFBNQVLESLRRRTQNDATVTYLLLDNRFVPSGYLESEFQETDSCSNPRT 360
QY 358 SESSSSGGRNVVPSDDPHSSGLRPYVPERKMLGLQSRAPREIMVEYKALQELNVR 417
DB 361 PEAGASPVGHMIPAHVDHYGLGARSQVVDKRMALGLQSHAPREIMVEYKALQELNVC 420
QY 418 WKKGHYVVKRCWCPGPEVNDTLDAVNSFLGDSITIMDDANGRLPTVIKFEFQLYTK 477
DB 421 WKKTGHYMKCRWVPGLDGQNTVMNNQLHFRDESSITIEDCATSPVIYIFELQLYKAR 480

QY 478 DDKYLLDMQRTVGFQQLFLDFCAFLTKLRYL 509
DB 481 EEKYLIDIQVNGFQFLFLDFCAFLTELRYL 512

RESULT 9
S59941
serine/threonine-specific protein kinase (EC 2.7.1.-) BKIN2 - barley (fragment)
C:Species: Hordeum vulgare (barley)
C>Date: 15-Feb-1996 #sequence_revision 01-Mar-1996 #text_change 26-Feb-1999
C:Accession: S59941
R:Hanappel, U.; Vicente-Carabajosa, J.; Barker, J.H.A.; Shewry, P.R.; Halford, N.G.
Plant Mol. Biol. 27, 1235-1240, 1995
A:Title: Differential expression of two barley SNF1-related protein kinase genes.
A:Reference number: S59941; MUID:95284374; PMID:7766906
A:Accession: S59941
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-473 <HAN>
A:Cross-references: EMBL:X82548
C:Genetics:

A:Gene: BKIN2
C:Function:
A:Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threonin
C:Superfamily: AMP-activated protein kinase; protein kinase homology
C:Keywords: ATP; magnesium; phosphotransferase; serine/threonine-specific protein kinase
F:124/Domain: protein kinase homology (fragment) <KIN>
F:121,40,115,117/Active site: Lys, Glu, Asp, Lys #status predicted
F:120,124/Binding site: magnesium (Asn, Asp) #status predicted

Query Match 70.6%; Score 1900; DB 1; Length 473;
Best Local Similarity 75.9%; Pred. No. 3.3e-74;
Matches 365; Conservative 45; Mismatches 61; Indels 10; Gaps 4;

QY 26 GTFGKVAIEHKLTHRVAIKINCRGRNMEKAKREFKILKLFHPHIIIRLYEYIY 85
DB 1 GSGFKVAIEHIIITGHKVAIKILNRRKIKSMEMEKYREIKILRLFMHPIIRLYEYID 60
QY 86 TPTDIYVMEYCKYGLFDYIVKGRLOEBAARRIFOQIISGVEYCHRNNAVHRDLKREN 145
DB 61 TPADIYVMEYKSGELFDYIVKGRLOEBAARRFOQIISGVEYCHRNNAVHRDLKREN 120
QY 146 LLDKSNVKNVLADFGLSNVMDGHFLKTSGSPYAAPAEVTSKLYAGPEVDVWSCGVT 205
DB 121 LLDKSNVKNVLADFGLSNVMDGHFLKTSGSPYAAPAEVTSKLYAGPEVDVWSCGVT 180
QY 206 YALCGTLPPDDNIPVLFKIKGITYLPSHLSALARDLPRLVPEPKRITIREIRE 265
DB 181 YALCGTLPPDDNIPVLFKIKGITYLPSHLSALARDLPRLVPEPKRITIREIRE 240
QY 266 HOFQIRLPYLAVPDPDTQAKMIDEDTLRDVNMGNKHNVCESLCSRLQNEATVAAY 325
DB 241 HSWFKARLPYLAVPDPDTQAKMIDEDTLRDVNMGNKHNVCESLCSRLQNEATVAAY 300
QY 326 YLLDNRFRTSGYLADYQESMDRLNQAL-SESSSSGGRNV-VGSSDPHSSGLRPY 383
DB 301 YLLDNKILRTTSGYLGAEYQESMDSSFSQISPEPSSASAEARQYSGSG-----FGLRQH 354
QY 384 YPVERKMLGLQSRAPREIMVEYKALQELNVRKMGHYVVKRCWCPGPEVNDTLDA 443
DB 355 PAERKMLGLQSRAPREIMVEYKALQELNVRKMGHYVVKRCWCPGPEVNDTLDA 412
QY 444 SNSEFGDSITIMDDANGRLPTVIKFEFQLYTKDDYKYLDMQRTVGFQQLFLDFCAFL 503
DB 413 NNGFGVESAIIEADGLDGKTHYVFEIQLYKTRGDYLLDQVSGFQQLFLDFCAFL 472

QY 504 T 504
DB 473 T 473

RESULT 10
T07788
probable serine/threonine-specific protein kinase (EC 2.7.1.-) SNF1 - potato
N:Alternate names: StubSNF1 protein
C:Species: Solanum tuberosum (potato)
C>Date: 14-May-1999 #sequence_revision 14-May-1999 #text_change 21-Jan-2000
C:Accession: T07788
R:Lakatos, L.; Banfalvi, Z.
submitted to the EMBL Data Library, January 1997
A:Reference number: Z16133
A:Accession: T07788
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-512 <LAK>
A:Cross-references: EMBL:U083797; NID:G1935915; PIDN:AAB52224.1; PID:G1935916
C:Genetics:
A:Gene: SNF1
C:Function:
A:Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threonine
C:Superfamily: AMP-activated protein kinase; protein kinase homology
C:Keywords: ATP; phosphotransferase; serine/threonine-specific protein kinase
F:17-271/Domain: protein kinase homology <KIN>

Query Match 68.8%; Score 1853.5; DB 2; Length 512;
Best Local Similarity 69.9%; Pred. No. 3.3e-72;
Matches 360; Conservative 62; Mismatches 84; Indels 9; Gaps 6;

QY 1 MDGSS-KQSGHSEA-LRRYNIIGRTIGTGFGRKVAIEHKLTHGRVAIKIINCROMNMEM 58
DB 1 MDGTAAGTSSVDSFLRNRYKLGKTLGIGSFGKVAIEHTLLIGHVAIVKILNRKRIKIMDM 60

QY 59 EEKAKREKIKLTIHPHITRLYEVIYPTDIYVMECKYGELEDTYVEKGRLOEDBEAR 118
DB 61 EEKVSREKIKLIRLMHGHISRLYEVEITPDSIYVMEVSKGELPDYVEKGRLOEDBEAR 120

QY 119 RIFPOIISGVEYCHRNWVHRDLKPENLIDSKYVNLADFGLSNMWHDGHLKTSQSGSP 178
DB 121 NFPOIISGVEYCHRNWVHRDLKPENLIDSKYVNLADFGLSNMWHDGHLKTSQSGSP 180

QY 179 NYAAPEVISGKLYAGPEVDWVSCGVILYALLCGTLPDPDENIENLFFKIKGCIYTLPSHL 238
DB 181 NYAAPEVISGKLYAGPEVDWVSCGVILYALLCGTLPDPDENIENLFFKIKGCIYTLPSHL 240

QY 239 SALARDLIPMLVVEPMKRTITIREHQQFOIRLPRYLAVPPDPTQOAKMIDEDTLRD 298
DB 241 SAGARDLIPMLVVEPMKRTITIREHQQFOIRLPRYLAVPPDPTQOAKMIDEDTLRD 300

QY 299 VVNMGFNKNHVCESLCSRLONEATVAYYLLDNRFRATSGYLGADVOESMDRNLNQLASS 358
DB 301 VVNMGFNKNHVCESLCSRLONEATVAYYLLDNRFRATSGYLGADVOESMDRNLNQLASS 360

QY 359 ESSSSGTRNYPGSSDPHSSGLRPYPERKVALGOSRAHPREIMVEVLKALQELNVRW 418
DB 361 EPLIPCMQRF-PGIMDYQOAGAR-QPIERKVALGOSRAHPREIMVEVLKALQELNVRW 418

QY 419 KKNCHYVWKCPWCGPEFVNNTLDAS---NSFLGDSITIMNDANGRLPVIVKEEPOLY 474
DB 419 KKIQQYNNKCVWSVPVHMGVSMHGMQFEDDSITILENDGTDLINVVKPEVOLY 478

QY 475 KTQDKYLLDMQRYTGPOLLFDFCAALFTKLRVL 509
DB 479 QTRBKYLIDLDQD-QGSGFLFLDLCALTLQLRVL 512

RESULT 11
T07415
probable serine/threonine-specific protein kinase (EC 2.7.1.1.-) PKIN1 - potato
N:Alternate names: SNPL-related protein kinase
C:Species: Solanum tuberosum (potato)
C:Date: 14-May-1999 #sequence_revision 14-May-1999 #text_change 20-Jun-2000
C:Accession: T07415
R:Halford, N.G.
submitted to the EMBL Data Library, March 1996
A:Reference number: Z16022
A:Accession: T07415
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-504 <HAL>
A:Cross-references: EMBL:X95997; NID:q1216279; PIDN:CAA65244.1
C:Genetics:
A:Gene: PKIN1
A:Introns: 62/1; 123/3; 184/3; 228/3; 290/3; 320/3; 348/3; 389/3; 466/3
C:Function:
A:Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threonine
C:Superfamily: AMP-activated protein kinase; protein kinase homology
C:Keywords: ATP; phosphotransferase; serine/threonine-specific protein kinase
F:15-269/Domain: protein kinase homology <KIN>

Query Match 64.1%; Score 1727; DB 2; Length 504;
Best Local Similarity 65.4%; Pred. No. 7.6e-67;
Matches 334; Conservative 69; Mismatches 88; Indels 20; Gaps 6;

QY 4 SSKSGHSEA-LRRYNIIGRTIGTGFGRKVAIEHKLTHGRVAIKIINCROMNMEM 61
DB 2 SSRGGIAESPYLRRYVKTIGHSGFGKVAIEHKLTHGRVAIKIILRRRIKTPDMEK 61

QY 62 AKREFKIKLFIHPHITRLYEVIYPTDIYVMECKYGELEDTYVEKGRLOEDBEARIF 121
DB 62 LRREIKICRFLFHPHIVIRLVEIETPDIYVMEVSKGELPDYVEKGRLOEDBEARKIF 121

QY 122 QOIISGVEYCHRNWVHRDLKPENLIDSKYVNLADFGLSNMWHDGHLKTSQSGSPNYA 181
DB 122 QOIISGVEYCHRNWVHRDLKPENLIDSKYVNLADFGLSNMWHDGHLKTSQSGSPNYA 181

QY 182 APEVISGKLYAGPEVDWVSCGVILYALLCGTLPDPDENIENLFFKIKGCIYTLPSHL 241
DB 182 APEVISGKLYAGPEVDWVSCGVILYALLCGTLPDPDENIENLFFKIKGCIYTLPSHL 241

QY 242 ARDIPMLVVEPMKRTITIREHQQFOIRLPRYLAVPPDPTQOAKMIDEDTLRDVN 301
DB 242 ARDIPMLVVEPMKRTITIREHQQFOIRLPRYLAVPPDPTQOAKMIDEDTLRDVN 301

QY 302 MGRKKNHVCESLCSRLONEATVAYYLLDNRFRATSGYLGADVOESMDRNLNQLASS 361
DB 302 MGRKKNHVCESLCSRLONEATVAYYLLDNRFRATSGYLGADVOESMDRNLNQLASS 361

QY 362 SSGTRNYPGSSDPHSSGLRPYPERKVALGOSRAHPREIMVEVLKALQELNVRKKN 421
DB 362 QLSTGNGVSEBS-----LRPFKEKMMVLGLQSPNPKHIMQVLGTLLELNVKPKI 415

QY 422 GHYVWKCPWCGPEFVNNTLDASNSFLGDSITIMNDANGRL---PVIVKEEPOLY 475
DB 416 GHYVWKCPWCGPEFVNNTLDASNSFLGDSITIMNDANGRL---PVIVKEEPOLY 475

QY 476 TKQDKYLLDMQRYTGPOLLFDFCAALFTKLRVL 506
DB 470 TEDEKYLIDLDQRIISGFLFLDLCALTLQLRVL 500

RESULT 12
S51025
[hydroxymethylglutaryl]-CoA reductase (NADPH2) kinase (EC 2.7.1.109) - human
N:Alternate names: AMPK
N:Contents: [acetyl-CoA carboxylase] kinase (EC 2.7.1.128); [hydroxymethylglutaryl]-CoA reductase
C:Species: Homo sapiens (man)
C:Date: 01-Aug-1995 #sequence_revision 01-Sep-1995 #text_change 03-Jun-2002
C:Accession: S51025; I38503
R:Berl, R.K.; Marley, A.E.; See, C.G.; Sopwith, W.F.; Aguan, K.; Carling, D.; Scott, J.; FEBS Lett. 356, 117-121, 1994
A:Title: Molecular cloning, expression and chromosomal localisation of human AMP-activated
A:Reference number: S51025; MUID:95080410; PMID:7988703
A:Accession: S51025
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-552 <BBR>
R:Aguan, K.; Scott, J.; See, C.G.; Sarkar, N.H.
Gene 149, 345-350, 1994
A:Title: Characterization and chromosomal localization of the human homologue of a rat A
A:Reference number: I38503; MUID:95047501; PMID:7959015
A:Accession: I38503
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-179, 'T', 181-270, 'G', 272-402, 'RO', 405-552 <RES>
A:Cross-references: EMBL:U06454; NID:g758366; PIDN:AAA64745.1; PID:g758367
C:Genetics:
A:Gene: GDB:PRKAA2; PRKAA; AMPK; hAMPK
A:Cross-references: GDB:451905; OMIM:600497
A:Map position: 1p31-1p31
C:Function:
A:Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threonine
A>Note: in vivo substrates include hydroxymethylglutaryl-CoA reductase (NADPH) and acetyl
C:Superfamily: AMP-activated protein kinase; protein kinase homology
C:Keywords: ATP; magnesium; phosphotransferase; serine/threonine-specific protein kinase
F:14-268/Domain: protein kinase homology <KIN>
F:22-30/Region: protein kinase ATP-binding motif
F:45,64,139,141/Active site: Lys, Asp, Lys #status predicted
F:144,148/Binding site: magnesium (Asn, Asp) #status predicted

Query Match 42.6%; Score 1148; DB 1; Length 552;

Best Local Similarity 46.1%; Pred. No. 3e-42;
Matches 239; Conservative 85; Mismatches 109; Indels 86; Gaps 12;

Qy 2 DSSKSGSHSALNNYIGRTLGITGFGKVAIAEHKLTGHRVAIKIINCROMNMEMBEK 61
8 DGRVK-IGH-----YVLGDTLGVGTGFGKVAIGEHQLTGHRVAIKIINRQKIRSLDVGK 60

Dy 62 AKREFKILKLFHPHIIIRLVEVITPTDLYVMECKYGGELFDYIVKGRLOEDBARIF 121
61 IKREIQNLKLFHPHIIIRLVEVITPTDLYVMECKYGGELFDYIVKGRLOEDBARIF 120

Qy 122 QOIIISGVYCHRNWVVRDLKPENLIDSKNVYLAQFGLSNVMDHFLKTSGSPNYA 181
121 QOIIISAVDYCHRNWVVRDLKPENLIDAHNAKIDFGLSNMDSGFLKTSGSPNYA 180

Dy 182 APEVISGLYAGPEVDWVSCGVILYALLCGTLPPDENIPMLFKKIGGYITLPSHLSAL 241
181 APEVISGLYAGPEVDWVSCGVILYALLCGTLPPDEHVPFLFKKIGGYEYIPEYLNRS 240

Qy 242 ARDLIPMLVVEPMKRTITREIRHQPQIRLPRYLAAPPDPTQAKMIDEDTLRDYV- 300
241 VATTLMHMLQVDPPLKRAITIKDIRHEWPKODLPSTLF--PEDPSYDANVIDDEAVKEVCE 298

Dy 301 NMGFNKNHVCESLCS-RLQNEATVAYYLLDNRFRTSGYLGADYQESMDENLQ----- 354
299 KFECTESBVMNSLVSQDPODLAAVAHYHLIDNR-----RIMNQASBFF 341

Qy 355 LASSESSS---GTRNVYPGSSDPHSSGLRPYY-----PVB-----RK 389
342 LASSPPGSGFMDDSAMHIIIPGLKHPERMPPLIADSPKARCPDLADNTTKPKSLAVKAK 401

Dy 390 WALGLQSPAHPREIWEVYLKALQELNVKKNKNGHYNVKCRKCPGPEVNDTLDSNSFLG 449
402 WHLGIRSQSKPYDIAMAEVYRAMKQDLDFEMKVVNAHYHLVR-----RKNPVYTG 448

Qy 450 DSTIMDNDANDNGRLPTVIKPEFQLYKTKDDKYLDMGRV 488
449 N-----YKMSLQLYLVNRSYLLDFKSI 472

Db 449 N-----YKMSLQLYLVNRSYLLDFKSI 472

RESULT 13
A53621
[hydroxymethylglutaryl-CoA reductase (NADPH2)] kinase (EC 2.7.1.109) - rat
N:Contains: [acetyl-CoA carboxylase] kinase (EC 2.7.1.128); [hydroxymethylglutaryl-CoA
C:Species: Rattus norvegicus (Norway rat)
C>Date: 07-Jul-1995 #sequence_revision 07-Jul-1995 #text_change 03-Jun-2002
C:Accession: A53621; S53729
R:Carling, D.; Aguan, K.; Woods, A.; Verhoeven, A.J.M.; Bert, R.K.; Brennan, C.H.; Sidel
J.; Biol. Chem. 269, 11442-11448, 1994
A>Title: Mammalian AMP-activated protein kinase is homologous to yeast and plant protein
A:Reference number: A53621; MUID:94209324; PMID:7908907
A:Accession: A53621
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-552 <CAR>
A:Cross-references: GB:Z29486; NID:9488375; PIDN:CAA82620.1; PID:9488376
R:Guo, G.; Widmer, J.; Stapleton, D.; Teh, T.; Cox, T.; Kemp, B.E.; Witters, L.A.
Biochim. Biophys. Acta 1266, 73-82, 1995
A>Title: Catalytic subunits of the porcine and rat 5'-AMP-activated protein kinase are
A:Reference number: S53729; MUID:95234757; PMID:7718624
A:Accession: S53729
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-354, 'S', 356-461, 'D', 463-552 <GMO>
A:Cross-references: GB:U12149; NID:9862472; PIDN:AAA85033.1; PID:9862473
C:Function:
A:Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threonin
C:Superfamily: AMP-activated protein kinase; protein kinase homology
C:Keywords: ATP; magnesium; phosphotransferase; serine/threonine-specific protein kinase
F:14-268/Domain: protein kinase homology <KIN>
F:12-30/Region: protein kinase ATP-binding motif
F:45,64,139,141/Active site: Lys, Glu, Asp, Lys #statue predicted
F:144,148/Binding site: magnesium (Asn, Asp) #statue predicted

Query Match 42.5%; Score 1144; DB 1; Length 552;
Best Local Similarity 45.9%; Pred. No. 4.4e-42;
Matches 238; Conservative 86; Mismatches 109; Indels 86; Gaps 12;

Qy 2 DSSKSGSHSALNNYIGRTLGITGFGKVAIAEHKLTGHRVAIKIINCROMNMEMBEK 61
8 DGRVK-IGH-----YVLGDTLGVGTGFGKVAIGEHQLTGHRVAIKIINRQKIRSLDVGK 60

Dy 62 AKREFKILKLFHPHIIIRLVEVITPTDLYVMECKYGGELFDYIVKGRLOEDBARIF 121
61 IKREIQNLKLFHPHIIIRLVEVITPTDLYVMECKYGGELFDYIVKGRLOEDBARIF 120

Qy 122 QOIIISGVYCHRNWVVRDLKPENLIDSKNVYLAQFGLSNVMDHFLKTSGSPNYA 181
121 QOIIISAVDYCHRNWVVRDLKPENLIDAHNAKIDFGLSNMDSGFLKTSGSPNYA 180

Dy 182 APEVISGLYAGPEVDWVSCGVILYALLCGTLPPDENIPMLFKKIGGYITLPSHLSAL 241
181 APEVISGLYAGPEVDWVSCGVILYALLCGTLPPDEHVPFLFKKIGGYEYIPEYLNRS 240

Qy 242 ARDLIPMLVVEPMKRTITREIRHQPQIRLPRYLAAPPDPTQAKMIDEDTLRDYV- 300
241 VATTLMHMLQVDPPLKRAITIKDIRHEWPKODLPSTLF--PEDPSYDANVIDDEAVKEVCE 298

Dy 301 NMGFNKNHVCESLCS-RLQNEATVAYYLLDNRFRTSGYLGADYQESMDENLQ----- 354
299 KFECTESBVMNSLVSQDPODLAAVAHYHLIDNR-----RIMNQASBFF 341

Qy 355 LASSESSS---GTRNVYPGSSDPHSSGLRPYY-----PVB-----RK 389
342 LASSPPGSGFMDDSAMHIIIPGLKHPERMPPLIADSPKARCPDLADNTTKPKSLAVKAK 401

Dy 390 WALGLQSPAHPREIWEVYLKALQELNVKKNKNGHYNVKCRKCPGPEVNDTLDSNSFLG 449
402 WHLGIRSQSKPYDIAMAEVYRAMKQDLDFEMKVVNAHYHLVR-----RKNPVYTG 448

Qy 450 DSTIMDNDANDNGRLPTVIKPEFQLYKTKDDKYLDMGRV 488
449 N-----YKMSLQLYLVNRSYLLDFKSI 472

Db 449 N-----YKMSLQLYLVNRSYLLDFKSI 472

RESULT 14
B90100
SNF-related kinase [imported] - Guillardia theta nucleomorph
C:Species: nucleomorph Guillardia theta
A>Note: a nucleomorph is the vestigial nucleus of a eukaryotic endosymbiont
C>Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 15-Jun-2001
C:Accession: B90100
R:Douglas, S.; Zauner, S.; Fraunholz, M.; Beaton, M.; Penny, S.; Deng, L.T.; Wu, X.; Reith
Nature 410, 1091-1096, 2001
A>Title: The highly reduced genome of an enslaved algal nucleus.
A:Reference number: A99082; MUID:11323671; PMID:11323671
A:Accession: B90100
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-472 <DOU>
A:Cross-references: GB:AF165818; NID:913794554; PIDN:AAK39929.1; GSPDB:GN00150
C:Genetics:
A:Gene: kin(enf1)
A:Map position: 1
A:Genome: nucleomorph
C:Superfamily: AMP-activated protein kinase; protein kinase homology
C:Keywords: nucleomorph

Query Match 42.2%; Score 1137; DB 2; Length 472;
Best Local Similarity 46.6%; Pred. No. 7.7e-42;
Matches 233; Conservative 89; Mismatches 112; Indels 66; Gaps 12;

Qy 17 YNLGRTLGITGFGKVAIAEHKLTGHRVAIKIINCROMNMEMBEKAKREFKILKLFHPH 76
12 YVLGDTLGVGTGFGKVAIGEHQLTGHRVAIKIINRQKIRSLDVGK 60

Db 12 YVLGDTLGVGTGFGKVAIGEHQLTGHRVAIKIINRQKIRSLDVGK 60

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OM protein - protein search, using sw model

Run on: July 7, 2004, 17:51:24 ; Search time 17 seconds
(without alignments)

1559.042 Million cell updates/sec

Title: US-09-857-522B-4
Perfect score: 2693
Sequence: 1 MDGSSKSGSHSEALRNVLG.....GPQLLPLDFCAFLTKLRVL 509

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2062.5	76.6	502	1 RK11_SECE	Q02723 secale cere
2	1969.5	73.1	535	1 K110_ARATH	Q38997 arabidopsi
3	1148	42.6	552	1 AAK2_HUMAN	P54646 homo sapien
4	1144	42.5	552	1 AAK2_RAT	Q09137 rattus norv
5	1119	41.6	548	1 AAK1_RAT	P54645 rattus norv
6	1115	41.4	550	1 AAK1_HUMAN	Q11311 homo sapien
7	1016.5	37.7	620	1 SNF1_CANAL	P52497 candida alb
8	1013.5	37.6	633	1 SNF1_YEAST	P06782 saccharomyc
9	1010.5	37.5	619	1 SNF1_CANTR	O94168 candida tro
10	1002.5	37.2	611	1 SNF1_CANGA	Q00372 candida gla
11	981.5	36.4	576	1 SNF1_SCHRO	O74536 schizosacch
12	894.5	33.2	622	1 YNA3_CAEEL	P45894 caenorhabdi
13	737.5	27.4	752	1 SNR4_HUMAN	O96134 homo sapien
14	737.5	27.4	786	1 SNR4_HUMAN	P57059 homo sapien
15	731.5	27.2	776	1 SNUL_RAT	O97105 rattus norv
16	731	27.1	779	1 SNUL_MOUSE	O60670 mus musculu
17	724.5	26.9	776	1 MKR3_HUMAN	P27448 homo sapien
18	709.5	26.3	794	1 K111_HUMAN	Q87448 homo sapien
19	708	26.3	736	1 ST29_HUMAN	O81wq3 homo sapien
20	696.5	25.9	774	1 MKR2_MOUSE	O05512 mus musculu
21	676.5	25.1	1037	1 KCC4_YEAST	P25389 saccharomyc
22	659.5	24.5	1142	1 G1N4_YEAST	Q12263 saccharomyc
23	659	24.5	661	1 ARK5_HUMAN	O60285 homo sapien
24	644.5	23.9	1518	1 KKK1_YEAST	P34244 saccharomyc
25	626	23.2	1147	1 K1N2_YEAST	P1186 saccharomyc
26	605	22.5	1064	1 K1N1_YEAST	P1185 saccharomyc
27	602.5	22.4	891	1 K1N1_SCHRO	P22987 schizosacch
28	570.5	21.2	775	1 CDR2_SCHRO	P87050 schizosacch
29	560.5	20.8	714	1 HUNK_MOUSE	O88866 mus musculu
30	548.5	20.4	714	1 HUNK_HUMAN	P57058 homo sapien
31	533.5	19.8	353	1 ASK2_ARATH	P43292 arabidopsi
32	532	19.8	800	1 K1N4_YEAST	O01919 saccharomyc
33	530	19.7	363	1 ASK1_ARATH	P43291 arabidopsi

34	527.5	19.6	593	1 CDR1_SCHRO	P07334 schizosacch
35	513.5	19.1	295	1 KMLC_DICDI	P25323 dictyosteli
36	505	18.8	364	1 ST2A_MOUSE	O61241 mus musculu
37	503	18.7	332	1 AAI2_WHEAT	Q02066 triticum ae
38	489.5	18.2	580	1 SRK1_SCHRO	O94547 schizosacch
39	488	18.1	367	1 ST2A_HUMAN	O9bxa7 homo sapien
40	482.5	17.9	424	1 KPSH_HUMAN	P11801 homo sapien
41	481	17.9	460	1 CDS1_SCHRO	O09170 schizosacch
42	475	17.6	358	1 ST2B_HUMAN	O96pf2 homo sapien
43	473.5	17.6	370	1 DAK2_MOUSE	Q8vdf3 mus musculu
44	473.5	17.6	432	1 STXB_XENLA	Q91604 xenopus lae
45	472	17.5	454	1 DAK3_HUMAN	O43293 homo sapien

ALIGNMENTS

```
RESULT 1
RK11_SECE
ID RK11_SECE STANDARD; PRT; 502 AA.
AC Q02723;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Carbon catabolite derepressing protein kinase (EC 2.7.1.-).
GN RK1N1.
OS Secale cereale (Rye).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;
OC Triticeae; Secale.
OX NCBI_TaxID=4550;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Endosperm;
RX MEDLINE=92020901; PubMed=1924320;
RA Alderson A., Sabelli P.A., Dickinson J.R., Cole D., Richardson M.,
RA Kreis M., Shewry P.R., Halford N.G.;
RT "Complementation of snf1, a mutation affecting global regulation of
RT carbon metabolism in yeast, by a plant protein kinase cDNA."
RL Proc. Natl. Acad. Sci. U.S.A. 88:8602-8605(1991).
CC CC
CC -1- FUNCTION: ESSENTIAL FOR RELEASE FROM GLUCOSE REPRESSION.
CC -1- SIMILARITY: Belongs to the Ser/Thr family of protein kinases. SNF1
CC subfamily.
CC
CC -1- SIMILARITY: Contains 1 UBA domain.
CC
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CC or send an email to license@ebi.ac.uk).
CC -----
CC EMBL: M74113; AAA33921.1; -.
CC PIR: A41361; A41361.
CC DR HSSP; P00518; 1PHK.
CC DR InterPro; IPR001772; Kinase_Cterm.
CC DR InterPro; IPR000719; Prot_Kinase.
CC DR InterPro; IPR008271; Ser_Thr_kinase.
CC DR InterPro; IPR002290; Ser_Thr_kinase.
CC DR InterPro; IPR001245; Tyr_Kinase.
CC DR InterPro; IPR000449; UBA_domain.
CC DR Pfam; PF02149; KAI; 1.
CC DR Pfam; PF00069; Kinase; 1.
CC DR Pfam; PF00627; UBA; 1.
CC DR PRINTS; PRO0109; TYRKINASE.
CC DR ProDom; PD000001; Prot_kinase; 1.
CC DR SMART; SMO0220; S_TKC; 1.
CC DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
CC DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
CC DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
CC DR PROSITE; PS50030; UBA; 1.
CC DR Transferase; Serine/threonine-protein kinase; Phosphorylation;
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KM ATP-binding; Carbohydrate metabolism.
 FT DOMAIN 14 269 PROTEIN KINASE.
 FT DOMAIN 290 330 UBA.
 FT NP BIND 20 28 ATP (BY SIMILARITY).
 FT BINDING 43 43 ATP (BY SIMILARITY).
 FT ACT SITE 140 140 BY SIMILARITY.
 FT MOD_RES 173 173 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
 SO SEQUENCE 502 AA; 57711 MM; OC9AF827F8989927 C6C64;
 Query Match 76.6%; Score 2062.5; DB 1; Length 502;
 Best Local Similarity 77.9%; Pred. No. 2.7e-138;
 Matches 401; Conservative 37; Mismatches 58; Indels 19; Gaps 6;
 QY 1 MDGSSKSGSEALRNVLGRTLGIGTGKXKIAEHKLTGHRVAIKINCQOMNMEER 60
 1 MDG---GSEHEALKNYLGKLGVGTAKYIIEHKTRKRAIKVLRQMAPEMEE 57
 DB 61 KAKKEFKILKLF---IHPIIRLYEVITYPTDIYVMEYCKYGLFDYIVKGRLOEDEA 117
 58 KAKREIKILRLFDILIHPIIRLYEVITYPTDIYVMEYCKYGLFDYIVKGRLOEDEA 117
 QY 118 RRTFOQIISAVEYCHRNKVRHDLKPEMLLDSTKNVLADEFGLSNWMHDFLKTSGS 177
 118 RRTFOQIISAVEYCHRNKVRHDLKPEMLLDSTKNVLADEFGLSNWMHDFLKTSGS 177
 DB 178 PNVAPEYISGKLYAGEPEVDVSCGVIYALCGTLPDDENIPTLFFKIKGIGIYTLPSH 237
 178 LNYAPEYISGKLYAGEPEVDVSCGVIYALCGAVPDDDNIRLFFKIKGIGIYTLPIY 237
 QY 238 LSLALADLIPMLVPEPKRTITREIRHWFQIRLPRYLAVPDDTTOAAMIDEDTLR 297
 238 LSDIVRDLISMLIYDPMKRITIGIRKHSWFQNRLLPRYLAVPDDTTOAAMIDEDTLR 297
 DB 298 DVNMGFPMKRVCSGLRQNEATVAYLLDNRFRATSGYLGADYQESMDRNLQGLAS 357
 298 DVNMGFPMKRVCSGLRQNEATVAYLLDNRFRATSGYLGADYQESMDRNLQGLAS 357
 QY 358 SESSSGSTRNVVYSGSDPHSSGSLRPYVPERKMAIGL-QSRAHPREIWEVYLKALQELNV 416
 349 -ESSASPSTRNVVYSGSDPHSSGSLRPYVPERKMAIGLQOSRAHPREIWEVYLKALQELNV 407
 QY 417 RWMKNGH-YNVKRCWCPGPEVND-TLDASNSFLGDSITIMNDANGELPVIYKEFQLY 474
 408 CWKNGGDCYNNKCRKCPGFPVSDMLLDANHSFVDCAIKNGDANSRLPAVKEIQLY 467
 QY 475 KTKQDKYLLDMQRTVGPQLPLDFCAFLTLKRLV 509
 468 KTKQDKYLLDMQRTVGPQLPLDFCAFLTLKRLV 502
 DB
 RESULT 2
 K110_ARATH STANDARD; PRT; 535 AA.
 ID_K110_ARATH Q38997; Q39076; Q8RMW2;
 AC Q38997; Q04728; Q39076; Q8RMW2;
 DT 15-JUL-1999 (Rel. 38, Created)
 DT 15-MAR-2004 (Rel. 43, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE SNF1-related protein kinase KIN10 (EC 2.7.1.-) (AKIN10).
 GN KIN10 OR SKIN10 OR AT3G01090 OR TAP13.22.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC eucosids II; Brassicales; Brassicaceae; Arabidopsids.
 OC NCBI_TaxID=3702;
 OX
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORM 2).
 RX MEDLINE=93013041; PubMed=1339373;
 RA le Guen L., Thomas M., Bianchi M., Halford N.G., Kreis M.;
 RT "Structure and expression of a gene from Arabidopsis thaliana
 RL encoding a protein related to SNF1 protein kinase.";
 RL Gene 120:249-254(1992).
 RP
 --SEQUENCE FROM N.A. (ISOFORM 2).

RC STRAIN=cv. Columbia;
 RL Lessard P., Kreis M., Thomas M.;
 RL Submitted (JEC-1996) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Columbia;
 RX MEDLINE=21016720; PubMed=11130713;
 RA Salanoubat M., Lemke K., Rieger M., Ansoerge W., Unselid M.,
 RA Fartmann B., Valle G., Bloeker H., Perez-Alonso M., Obermaier B.,
 RA Delisany M., Boutry M., Grivell L.A., Mache R., Puigdomenech P.,
 RA De Simone V., Choisme N., Artiguenave F., Robert C., Brottier P.,
 RA Wincker P., Catolico L., Weissenbach J., Saurin W., Querret F.,
 RA Schaefer M., Mueller-Auer S., Gabel C., Fuchs M., Benes V.,
 RA Mumbach E., Dronow H., Erfle H., Jordan N., Banger S.,
 RA Wiedemann R., Kranz H., Vose H., Holland R., Brandt P., Nyakatura G.,
 RA Verzi A., D'Angelo M., Pallavicini A., Toppo S., Simonati B.,
 RA Conrad A., Hornischer K., Kauer G., Loenert T.H., Nordstiek G.,
 RA Reichelt J., Scharte M., Schoen O., Barque M., Terol J., Clement J.,
 RA Navarro P., Collado C., Perez-Perez A., Ottenwelder B., Duchemin D.,
 RA Cooke R., Laudie M., Berger-Llauro C., Purnelle B., Masuy D.,
 RA de Haan M., Maarse A.C., Alcaraz J.-P., Cortet A., Casacuberta E.,
 RA Monfort A., Argirio A., Flores M., Lignori R., Vitale D.,
 RA Mannheim G., Haase D., Schoof H., Ruda S., Zaccaria P., Mewes H.-W.,
 RA Mayer K.F.X., Kaul S., Town C.D., Koo H.L., Tallon L.J., Jenkins J.,
 RA Rooney T., Rizzo M., Walts A., Utterback T., Fujii C.Y., Shea T.P.,
 RA Creasy T.H., Haas B., Maiti R., Wu D., Peterson J., Van Aken S.,
 RA Pat G., Miltescher J., Sellers P., Gill J.E., Feldlyum T.V.,
 RA Pruss D., Lin X., Nieman W.C., Salzberg S.L., White O., Venter J.C.,
 RA Frazer C.M., Kaneko T., Nakamura Y., Sato S., Kato T., Asanizu E.,
 RA Sasamoto S., Kimura T., Iessawa K., Kawashima K., Kishida Y.,
 RA Kiyokawa C., Kohara M., Matsumoto M., Matsuno A., Muraki A.,
 RA Nakayama S., Nakazaki N., Shino S., Takeuchi C., Wada T.,
 RA Watanabe A., Yamada M., Yasuda M., Tabata S.;
 RT "Sequence and analysis of chromosome 3 of the plant Arabidopsis
 thaliana.";
 RL Nature 408:820-822(2000).
 RN [4]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RC STRAIN=cv. Columbia;
 RX MEDLINE=22954850; PubMed=14593172;
 RA Yamada K., Lim J., Dale J.M., Chen H., Shinn P., Palm C.J.,
 RA Southwick A.M., Wu H.C., Kim C.J., Nguyen M., Pham P.K., Cheuk R.F.,
 RA Karlin-Newmann G., Liu S.K., Lam B., Sakano H., Wu T., Yu G.,
 RA Miranda M., Quach H.L., Tripp M., Chang C.H., Lee J.M., Tortum M.J.,
 RA Chan M.M., Tang C.C., Onodera C.S., Deng J.M., Akiyama K., Ansari Y.,
 RA Arakawa T., Banh J., Banno F., Brooks S.Y., Carinci P.,
 RA Chao Q., Choy N., Enju A., Goldsmith A.D., Gujral M., Hansen N.F.,
 RA Hayashizaki Y., Johnson-Hopson C., Hsuan V.W., Iida K., Karnes M.,
 RA Khan S., Koesema E., Ishida J., Jiang P.X., Jones T., Kawai J.,
 RA Kamuya A., Meyers C., Nakajima M., Narusaka M., Seki M., Sakurai T.,
 RA Satou M., Tamse R., Vayberg M., Wallender E.K., Wong C., Yamamura Y.,
 RA Yuan S., Shinozaki K., Davis R.W., Theologis A., Ecker J.R.;
 RT "Empirical analysis of transcriptional activity in the Arabidopsis
 genome.";
 RL Science 302:842-846(2003).
 RN [5]
 RP PARTIAL SEQUENCE FROM N.A. (ISOFORM 2).
 RC STRAIN=cv. Columbia;
 RX MEDLINE=95115691; PubMed=7816049;
 RA le Guen L., Thomas M., Kreis M.;
 RT "Gene density and organization in a small region of the Arabidopsis
 thaliana genome.";
 RL Mol. Gen. Genet. 245:390-396(1994).
 CC -I- FUNCTION: May play an important role in a signal transduction
 cascade regulating gene expression and carbohydrate metabolism in
 higher plants.
 CC -I- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Name=1;
 CC IsoId=Q38997-1; Sequence=Displayed;
 CC Note=No experimental confirmation available;
 CC Name=2;
 CC IsoId=Q38997-2; Sequence=VSP_009001;

```
CC -1- TISSUE SPECIFICITY: Expressed in roots, shoots and leaves.
CC -1- SIMILARITY: Belongs to the Ser/Thr family of protein kinases. SNF1
CC subfamily.
CC -1- SIMILARITY: Contains 1 UBA domain.
CC -----
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DR EMBL; M93023; AAA32736.1; -;
DR EMBL; X79707; CA56146.1; -;
DR EMBL; AC008261; AAF26165.1; -;
DR EMBL; AY093170; AAM13169.1; -;
DR EMBL; BT010386; AAC66829.1; -;
DR EMBL; X94757; CA664384.1; -;
DR PIR; JCI446; JCI446.
DR HSSP; O63450; 1A06.
DR InterPro; IPR001772; Kinase_Cterm.
DR InterPro; IPR000719; Prot_Kinase.
DR InterPro; IPR008271; Ser_Thr_Pkin_AS.
DR InterPro; IPR002290; Ser_Thr_Pkinase.
DR InterPro; IPR001245; Tyr_Pkinase.
DR InterPro; IPR000449; UBA_domain.
DR Pfam; PF02149; KAI; 1.
DR Pfam; PF00069; pkinase; 1.
DR Pfam; PF00627; UBA; 1.
DR PRINTS; PR00109; TYRKINASE.
DR PRODOM; PD000001; Prot_kinase; 1.
DR SMART; SM00220; S_TKc; 1.
DR SMART; SM00165; UBA; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
DR PROSITE; PS50030; UBA; 1.
DR Transferrase; Serine/threonine-protein kinase; ATP-binding;
KW Phosphorylation; Alternative splicing.
FT DOMAIN 42 294 PROTEIN_KINASE.
FT NP_BIND 48 56 ATP (BY SIMILARITY).
FT DOMAIN 315 355 UBA.
FT ACT_SITE 165 165 BY SIMILARITY.
FT BINDING 71 71 ATP (BY SIMILARITY).
FT MOD_RES 198 198 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
FT VARSPIC 1 23 Missing (in isoform 2).
FT VARSPIC 1 23 /FTid=VSP_009001.
SQ SEQUENCE 535 AA; 61181 MW; PFFC383223PD8317 CRC64;

Query Match 73.1%; Score 1969.5; DB 1; Length 535;
Best Local Similarity 72.8%; Pred. No. 1.1e-131;
Matches 377; Conservative 52; Mismatches 74; Indels 15; Gaps 4;

QY 1 MDGSSKG--SGHSAALNRYNGRTLGIGTGFGRVIAEKKLGHVVAIKIINCRQRMNEM 58
DB 24 MDGSGTSGRSVSEIILPYKLGKRTLGSGFGRVIAEALGHVVAIKILRRKIKNEM 83
QY 59 EEKAKREFPIKLPFHPIHRLVEVIYPTDIIYVMEYCKYGEFDYIVKGRIOEDBEAR 118
DB 84 EEKVRREIKILRLFMHPHRIILVEVIEPTDIIYVMEVNSGELFDYIVKGRIOEDBEAR 143
QY 119 RIFQOIIISGVYCHRNWVHRDLKPNILLDSKRNVLADGLSNVMDHGHFLKTCGSP 178
DB 144 NFFQOIIISGVYCHRNWVHRDLKPNILLDSKCNVKAIDGLSNIMRDGHFLKTCGSP 203
QY 179 NYAAPVYISGLVAGPEVDWVSCGIIYALCGTLPPDDENIPLVFKIKIGIYTLPSHL 238
DB 204 NYAAPVYISGLVAGPEVDWVSCGIIYALCGTLPPDDENIPLVFKIKIGIYTLPSHL 263
QY 239 SALARDIIPRLVVEPMKRIIRIREHOFQIRLPRYLAVPPTDTQOAKMIDEDTLRD 298
DB 264 SPGARDLIPRLVVDPMKRVITPEIRGHPWFQALHPRYLAVPPTDTQOAKMIDEDTLQ 323

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QY 299 VYMWGFKNHVCEISGLQNEATVAYYLLDNRFRATSGVAGDOESMDRLNQASS 358  
DB 324 VINWGFPRNHLIESLRNRQNDGTVIYLLDNRFRASGVLGAFQETHE-GTPRNHQA 382  
QY 359 ESSSSGTNRNVPGSSDDHSPRLPYPERKMAIGLOSRAHPRIMEVVKALQELNVRW 418  
DB 383 ESVASPVSHRLPGLMEVQVGLSQYVERKMAIGLOSRAHPRIMEVVKALQDLNVCW 442  
QY 419 KKNGHVVKRCWCPGPEVNDTLDA-----SNSFIQDSTINDNDANGRLPTVIKPEF 471  
DB 443 KKIHHYMKCRWV-----NSSADGMLNSMHDNNVYGDDESSIIENAAVKSPPVVFKEI 497  
QY 472 QLYTKDQKYLDMQRYTGPQLPLDFCAAFITLQRTL 509  
DB 498 QLYTKRDKYLLDLQVQGFQFLDCAAFVLAQLRVL 535
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RESULT 3
AAK2_HUMAN STANDARD; PRT; 552 AA.
AC P54646; Q9H1E8; Q9UD43;
DT 01-OCT-1996 (Rel. 34, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE 5'-AMP-activated protein kinase, catalytic alpha-2 chain (EC 2.7.1.-)
DE (AMPK alpha-2 chain)
GN PRKAA2 OR AMPK2 OR AMPK.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Heart;
RX MEDLINE=95047501; PubMed=7959015;
RA Aguan K., Scott J., See C.G., Sarkar N.H.;
RT "Characterization and chromosomal localization of the human homologue
RT of a rat AMP-activated protein kinase-encoding gene: a major
RT regulator of lipid metabolism in mammals.";
RL Gene 149:345-350(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Skeletal muscle;
RX MEDLINE=95080410; PubMed=7988703;
RA Berl R.K., Marley A.E., See C.G., Sopwith W.F., Aguan K., Carling D.,
RA Scott J., Carey F.;
RT "Molecular cloning, expression and chromosomal localisation of human
RT AMP-activated protein kinase.";
RL FEBS Lett. 356:117-121(1994).
RN [3]
RP SEQUENCE OF 33-552 FROM N.A.
RA Cobley V.;
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Responsible for the regulation of fatty acid synthesis
CC by phosphorylation of acetyl-CoA carboxylase. It also regulates
CC cholesterol synthesis via phosphorylation and inactivation of
CC hormone-sensitive lipase and hydroxymethylglutaryl-CoA reductase.
CC Appears to act as a metabolic stress-sensing protein kinase
CC switching off biosynthetic pathways when cellular ATP levels are
CC depleted and when 5'-AMP rises in response to fuel limitation
CC and/or hypoxia. This is a catalytic subunit.
CC -1- SUBUNIT: Heterotrimer of a catalytic subunit, a beta and a gamma
CC non-catalytic subunits.
CC -1- SIMILARITY: Belongs to the Ser/Thr family of protein kinases. SNF1
CC subfamily.
CC -----
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CC EMBL; U06454; AAA64745.1; -.
DR EMBL; AL035705; CAC17574.1; -.
DR PIR; S51025; S51025.
DR HSSP; Q63450; 1A06.
DR Genew; HGNC:9377; PRKAA2.
MM; 600497; -.
DR GO; GO:0004672; F:protein kinase activity; TAS.
DR GO; GO:000468; P:protein amino acid phosphorylation; TAS.
DR GO; GO:0007165; P:signal transduction; TAS.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR008271; Ser_thr_Pkin_AS.
DR InterPro; IPR001245; Ser_thr_Pkinase.
DR InterPro; IPR001245; Tyr_Pkinase.
DR Pfam; PF00069; Pkinase; 1.
DR PRINTS; PR00109; TYRKINASE.
DR PRODOM; PD000001; Prot_kinase; 1.
DR SMART; SM00220; S_TKC; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
KW Cholesterol biosynthesis; Fatty acid biosynthesis; Transferase;
KW Serine/threonine-protein kinase; ATP-binding; Phosphorylation;
KW Multigene family.
FT DOMAIN 16 268 PROTEIN_KINASE.
FT NP_BIND 22 30 ATP (BY SIMILARITY).
FT BINDING 45 45 ATP (BY SIMILARITY).
FT ACT_SITE 139 139 BY SIMILARITY.
FT MOD_RES 172 172 PHOSPHORYLATION (AUTO-) (POTENTIAL).
FT CONFLICT 180 180 A -> T (IN REF. 1).
FT CONFLICT 271 271 D -> G (IN REF. 1).
FT CONFLICT 403 404 HL -> RO (IN REF. 1).
SQ SEQUENCE 552 AA; 6231 MM; C46AFCID5104975 CFC64;
Query Match 42.6%; Score 1148; DB 1; Length 552;
Best Local Similarity 46.1%; Pred. No. 1.le-73;
Matches 239; Conservative 85; Mismatches 109; Indels 86; Gaps 12;

QY 2 DGGSGSGHSEALRNRYNGRTLGCTPRKVVIAEKLTHGVAKIINCROMMEHEK 61
DB 8 DGRYK-IGH-----YVIGDTLVGTGTFKXVIGHQTLGHVAVAKIINRQKISLDVVGK 60
QY AKREKKIKLFLPHIIRLYEVIYPTPIYVMEYCKGELFDYIVKGRLOEDEARIF 121
DB 62 AKREKKIKLFLPHIIRLYEVIYPTPIYVMEYCKGELFDYIVKGRLOEDEARIF 121
DB 61 IKREIQLNKLFRPHIIRLYEVIYPTPIYVMEYCKGELFDYIVKGRLOEDEARIF 120
QY 122 QOIIISGVYCHRNWVHRDLKPEMLLDKSNVVLADFGLSNVMDGHFLKTCGSPNYA 181
DB 121 QOIIISGVYCHRNWVHRDLKPEMLLDKSNVVLADFGLSNVMDGHFLKTCGSPNYA 180
QY 182 APEYISGLVAGPEVDWSCGVIIYALLCGTLPPDENIENLFFKIKIGITLTLSSLSAL 241
DB 181 APEYISGLVAGPEVDWSCGVIIYALLCGTLPPDENIENLFFKIKIGITLTLSSLSAL 240
QY 242 ARDILPRYLVEPMKRTIRIREIREFQFRLPRTIAPPPDPTQOAKMIEDTLRDV- 300
DB 241 VATLMMLQVDFPKRATIKIRIHEWFKDLPSTLF--PEDPSIDANVIDEAVKEVCE 298
QY 301 NMGNKNHVCESLCS-RLQNEATVAYVLLDNRFRATSGYLADYQESMDRLNQ----- 354
DB 299 KFECESEVSNVSLVSGDPQDLAVVYHLIDNR-----RIMNQASBFY 341
QY 355 LASESSSSS---GTRNYPGSSDPHSSGLRPY-----PVE-----RK 389
DB 342 LASSPPSSGFMFDDSMHIPPGLKPRHEMPPLIDSPRARCPLDLANTTKPSLAVKKAK 401
QY 390 WALGLGSAHPREITVEVLKALQELNVRKKGNGHNVCRMCOPGPEVNDTLDSNSFLG 449
DB 402 WHLGIRSGSKYDIDMAEYVRAMKQJDFMKVYVNAHYHLAVR-----RKNPTVG 448
QY 450 DSTIMDNDANGRLPTVIKFEFQLYKTQDKYLLDMQEV 488

DB 449 N-----YVKMSLQLYLVNRSYLLDFKSI 472

RESULT 4
AAK2_RAT STANDARD; PRT; 552 AA.
AC Q09137;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE 5'-AMP-activated protein kinase, catalytic alpha-2 chain (EC 2.7.1.-)
GN (AMPK alpha-2 chain).
OS PRKAA2 OR AMPK2 OR AMPK.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RC TISSUE=Liver;
RX MEDLINE=94209324; PubMed=7908907;
RA Catling D., Aguan K., Woods A., Verhoeven A.J.M., Beri R.K.,
RT Brennan C.H., Sidebottom C., Davison M.D., Scott J.,
RT "Mammalian AMP-activated protein kinase is homologous to yeast and
RT plant protein kinases involved in the regulation of carbon
RT metabolism";
RL J. Biol. Chem. 269:11442-11448 (1994).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley; TISSUE=Liver;
RX MEDLINE=95234757; PubMed=7718624;
RA Gao G., Widmer J., Stapleton D., Teh T., Cox T., Kemp B.E.,
RA Witters L.A.;
RT "Catalytic subunits of the porcine and rat 5'-AMP-activated protein
RT kinase are members of the SNF1 protein kinase family";
RL Biochem. Biophys. Acta 1266:73-82 (1995).
CC -1- FUNCTION: Responsible for the regulation of fatty acid synthesis
CC by phosphorylation of acetyl-CoA carboxylase. It also regulates
CC cholesterol synthesis via phosphorylation and inactivation of
CC hormone-sensitive lipase and hydroxymethylglutaryl-CoA reductase.
CC Appears to act as a metabolic stress-sensing protein kinase
CC switching off biosynthetic pathways when cellular ATP levels are
CC depleted and when 5'-AMP rises in response to fuel limitation
CC and/or hypoxia. This is a catalytic subunit.
CC -1- SUBUNIT: Heterotrimer of a catalytic subunit, a beta and a gamma
CC non-catalytic subunits.
CC -1- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=Long;
CC IsoId=Q09137-1; Sequence=Displayed;
CC Name=Short;
CC IsoId=Q09137-2; Sequence=VSP_004949, VSP_004950;
CC Note=Lacks the sequence parts essential for kinase activity and
CC is therefore inactive;
CC -1- TISSUE SPECIFICITY: Skeletal muscle, lower levels in liver, heart
CC and kidney.
CC -1- INDUCTION: By AMP.
CC -1- SIMILARITY: Belongs to the Ser/Thr family of protein kinases. SNF1
CC subfamily.
CC -----
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CC -----
DR EMBL; Z29486; CAA82620.1; -.
DR EMBL; U12149; AAA85033.1; -.
DR PIR; A53621; A53621.
DR HSSP; Q63450; 1A06.
DR InterPro; IPR000719; Prot_kinase.


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DR InterPro: IPR008271; Ser thr pkin AS.
DR InterPro: IPR002290; Ser thr pkinase.
DR InterPro: IPR001245; Tyr_kinase.
DR Pfam: PF00069; Kinase; 1.
DR PRINTS: PR00109; TYRKINASE.
DR ProDom: PD000001; Prot_kinase; 1.
DR SMART: SM00220; S_TKC; 1.
DR PROSITE: PS00107; PROTEIN KINASE ATP; 1.
DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
DR Cholesterol biosynthesis; Fatty acid biosynthesis; Transferase;
KW Serine/threonine-protein kinase; ATP-binding; Phosphorylation;
KM Alternative splicing; Multigene family.
FT DOMAIN 16 268 PROTEIN KINASE.
FT NP BIND 22 30 ATP (BY SIMILARITY).
FT BINDING 45 45 ATP (BY SIMILARITY).
FT ACT_SITE 139 139 BY SIMILARITY.
FT MOD_RES 172 172 PHOSPHORYLATION (AUTO-) (POTENTIAL).
FT VARSPLIC 32 388 Missing (in isoform short).
FT VARSPLIC 392 552 Missing (in isoform short).
FT FTID=VSP_004949.
FT CONFLICT 355 355 M -> S (IN REF. 2).
FT CONFLICT 462 462 N -> D (IN REF. 2).
SQ SEQUENCE 552 AA; 62257 MW; 2829E07F674D89B1 CRC64;

Query Match 42.5%; Score 1144; DB 1; Length 552;
Beet Local Similarity 45.9%; Pred. No. 2.1e-73;
Matches 238; Conservative 86; Mismatches 109; Indels 86; Gaps 12;

QY 2 DGSSKSGSHSALRNRYNLGRTIGTGFQKVIKAEHKLGHRAIKIINGROMNMEMEK 61
DB 8 DGRK-IGH-----YVLDGLTGVSTFKKAVIKGEQLTGHKVAKILRKQIRSLDVVK 60
QY 62 AKREFKILKLFHPHILRYEVIYTPDIYVMEYCKYGEFDYIVKGRLOEDERRIF 121
DB 61 IKREIQNKLFRRHPHILKLYGVISPTDFPMWMEYVSGELFDYICKHGRVEVEYEARLIF 120
QY 122 QQIISGVEYCHRMVYVHDLKPENILDSKYNVLADEGLSNWMDGFLKTSQSPNYA 181
DB 121 QQIISADVYCHRHVYVHDLKPENVLLDAQNAKADGLSNMMSDGEFLRTSCSPNYA 180
QY 182 APEYISGLVAGPEVDVMSGVILYALCGTLPDDENIPMLFKIKGIVTLPSHLSAL 241
DB 181 APEYISGLVAGPEVDVMSGVILYALCGTLPDDENIPMLFKIKGIVTLYEYLNRS 240
QY 242 ARDLIPRLVVEPMKRTIRIREHQMQLPRYLAVPDPDTQQAAMIDEDTLRDVY 300
DB 241 IATLMHMLQVDPKRAIKIDIREHEWFKQDPSYLF--PEDPSYDANVIDDEAVKEVCE 298
QY 301 NMGNKKNHVCESLGS-RLQNEATVAYVYLLDNRPATISGYIGADYQESMDRNLNO----- 354
DB 299 KFECTESSEVMNLSVSGDPQDLAAVYHILIDNR-----RIMQASEFY 341
QY 355 LASESSSSS---GTYNVYVPGSSDPHSGSLRPYV-----PVE-----RK 389
DB 342 LASSPPGCSFMDADAMHITPGLKHPERMPPLIADSPAKRPLDALNTTKSLAVKAK 401
QY 390 WALGLQSRAPREIMVEYLKALQELINWKKNGHYNVKCRWCPGPEVNDTLDASNSFLG 449
DB 402 WHLGIRSQSKPYDIIMAEVYRAMKQIDPEMKVYNAVHLVR-----RKNPVTG 448
QY 450 DSTIMDNDANGRLPTVIKFEFQLYKTDKTLDMQVY 488
DB 449 N-----YVKMSLQLYLVNRSYLLDFKSI 472

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DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE 5'-AMP-activated protein kinase, catalytic alpha-1 chain (EC 2.7.1.-)
DE (AMPK_alpha-1 chain).
GN PRKAA1 OR AMPK1.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;

[1]
SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RP STRAIN=Sprague-Dawley; TISSUE=Hypothalamus, and liver;
RC MEDLINE=95050763; PubMed=7961907;
RX Medline=96132781; PubMed=8557660;
RA Stapleton D., Mitchell K.I., Gao G., Widmer J., Michel B.J.,
RA Teh T., House C.M., Fernandez C.S., Cox T., Witters L.A.,
RA Kemp B.E.;
RT "Mammalian AMP-activated protein kinase subfamily.";
RL J. Biol. Chem. 271:611-614(1996).
[2]
PARTIAL SEQUENCE.
RP STRAIN=Sprague-Dawley; TISSUE=Hypothalamus, and liver;
RX MEDLINE=95050763; PubMed=7961907;
RA Stapleton D., Gao G., Mitchell B.J., Widmer J., Mitchell K.,
RA Teh T., House C.M., Witters L.A., Kemp B.E.;
RT "Mammalian 5'-AMP-activated protein kinase non-catalytic subunits are
RT homologs of proteins that interact with yeast Snf1 protein kinase.";
RL J. Biol. Chem. 269:29343-29346(1994).

-1- FUNCTION: Responsible for the regulation of fatty acid synthesis
by phosphorylation of acetyl-CoA carboxylase. It also regulates
cholesterol synthesis via phosphorylation and inactivation of
hormone-sensitive lipase and hydroxymethylglutaryl-CoA reductase.
Appears to act as a metabolic stress-sensing protein kinase
switching off biosynthetic pathways when cellular AMP levels are
depleted and when 5'-AMP rises in response to fuel limitation
and/or hypoxia. This is a catalytic subunit.
-1- SUBUNIT: Heterotrimer of a catalytic subunit, a beta and a gamma
non-catalytic subunits.
-1- TISSUE SPECIFICITY: Low expression in kidney, liver, lung, heart
and brain.
-1- SIMILARITY: Belongs to the Ser/Thr family of protein kinases. SNF1
subfamily.

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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC
DR HSSP; U40819; AAC52355.1; -.
DR GO; GO:0005622; C:intracellular; ISS.
DR GO; GO:00008189; F:apoptosis inhibitor activity; ISS.
DR GO; GO:0004691; F:CAMP-dependent protein kinase activity; ISS.
DR GO; GO:00042557; F:eukaryotic elongation factor-2 kinase activ. .; NAS.
DR GO; GO:0000187; P:activation of MAPK; ISS.
DR GO; GO:0046318; P:negative regulation of glucosylceramide bio. .; ISS.
DR GO; GO:0017148; P:negative regulation of protein biosynthesis; NAS.
DR GO; GO:0045768; P:positive regulation of anti-apoptosis; ISS.
DR GO; GO:0045542; P:positive regulation of cholesterol biosynth. .; ISS.
DR GO; GO:0046321; P:positive regulation of fatty acid oxidation; NAS.
DR GO; GO:0045722; P:positive regulation of gluconeogenesis; NAS.
DR GO; GO:0046326; P:positive regulation of glucose import; NAS.
DR GO; GO:0006468; P:protein amino acid phosphorylation; NAS.
DR GO; GO:0001666; P:response to hypoxia; ISS.
DR InterPro: IPR000719; Prot_kinase.
DR InterPro: IPR008271; Ser thr pkin AS.
DR InterPro: IPR002290; Ser thr pkinase.
DR InterPro: IPR001245; Tyr_kinase.
DR Pfam; PF00069; Kinase; 1.
DR PRINTS; PR00109; TYRKINASE.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00220; S_TKC; 1.

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DR PROSITE; PS00107; PROTEIN KINASE ATP, 1.
 DR PROSITE; PS00108; PROTEIN KINASE ST; 1.
 DR PROSITE; PS0011; PROTEIN KINASE DM; 1.
 KM Cholesterol biosynthesis; fatty acid biosynthesis; Transferase;
 KM Serine/threonine-protein kinase; ATP-binding; Phosphorylation;
 KM Multigene family.
 FT DOMAIN 16 268 PROTEIN KINASE.
 FT NP BIND 22 30 ATP (BY SIMILARITY).
 FT BINDING 45 45 ATP (BY SIMILARITY).
 FT ACT_SITE 139 139 BY SIMILARITY.
 FT MOD_RES 172 172 PHOSPHORYLATION (AUTO-) (POTENTIAL).
 SQ SEQUENCE 548 AA; 62599 MW; 5CCA3281C195F867 CRC64;
 Query Match 41.6%; Score 1119; DB 1; Length 548;
 Best Local Similarity 45.6%; Pred. No. 1,2e-71;
 Matches 233; Conservative 85; Mismatches 117; Indels 76; Gaps 11;
 QY 2 DGSSKSGSHSALRNRYNIGRTLGITGFGKXIAEHKLTHRAVAIKIINCRQRMMEEEK 61
 DB 8 DGRVY-IGH-----YLGDTLGVGTFGKVKVGHKLTHRAVAIKIINCRQRIIDVVGK 60
 QY 62 AKREKIKLFIHIIITLVEIYTPDTIYVMECKGELFDYIVKGRLODEARRIF 121
 DB 61 IRREIQNKLPFRPHIITLYQVISTPDSIFMMEVSGSELPDYICXNGRLDEKESRLF 120
 QY 122 QOISGVEYCHRNWVHRDLKPENLIDSKYNVLADFGLSNWMHGHFKTSCGSPYVA 181
 DB 121 QOISGVDYCHRNWVHRDLKPENLIDSKYNVLADFGLSNWMHGHFKTSCGSPYVA 180
 QY 182 APEVISGLVAGPEVDVWSCVILYALLCGTLPPDENIPLFKKIGIYTLPSHLSAL 241
 DB 181 APEVISGLVAGPEVDVWSSGVILYALLCGTLPPDDHVTPLFKKICGIFYPYQYANPS 240
 QY 242 ARDLIRNLVVEPMKRTIRIREHWFQILPRTLANPPDDTQOAMIDETLR---- 297
 DB 241 VISLTKHMLQVDPMKRATIKQIRIEHWFQILPRTLANPPDDTQOAMIDETLR---- 297
 QY 298 -----DVNWMGFKNHNVCESLCSRLQNEATVAYILLDDR---FRATSGYLADVQES 347
 DB 299 KFECESEEVLSCLYNRN-----QDPLAVAYHLIIDNRRIINNEAKDYIATSPDS 349
 QY 348 M-DENLQO-----LASESSSSGTRNVYPGSSDPHSGSLRPYVERKMAIGLOSR 397
 DB 350 FLDDHLHTRPHERVPLVAETPRARHTLDELNPQSKH-OGVR-----KAKMHLGISQ 403
 QY 398 AHPRIMEVLKAOELVNRKNGHNVKRCWCGCFEVDITLDASNFIQDSTIMOND 457
 DB 404 SRPNDIMEVCRATIKQIDYEMKVNPYLRV----- 435
 QY 458 DANGRLPTVIKFEFQLYTKDKDKYLLDMQRV 488
 DB 436 RKNPVTSTFSKMSQLQYVDRTYLLDRSI 466
 RESULT 6
 AAK1_HUMAN STANDAD: PRT: 550 AA.
 ID 013131: 000286: 09UN04:
 AC 15-JUL-1998 (Rel. 36, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE 5'-AMP-activated protein kinase, catalytic alpha-1 chain (EC 2.7.1.-)
 DE (AMP alpha-1 chain).
 GN PRKAA1 OR AMPK1.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_Taxid=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Mammary gland;
 RA Yano K.;
 FT "Nucleotide sequence of cDNA for human AMP-activated protein kinase

RT alpha-1.";
 RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Blood;
 RX MEDLINE=2049367; PubMed=11042152;
 RA Zhang Q.-H., Ye M., Wu X.-Y., Ren S.-X., Zhao M., Zhao C.-Y., Fu G.,
 RA Shen Y., Fan H.-Y., Lu G., Zhong M., Xu X.-R., Han Z.-G., Zhang J.-W.,
 RA Tao J., Huang Q.-H., Zhou J., Hu G.-X., Gu J., Chen S.-J., Chen Z.;
 RT "Cloning and functional analysis of cDNAs with open reading frames for
 RT 300 previously undefined genes expressed in CD34+ hematopoietic
 RT stem/progenitor cells.";
 RL Genome Res. 10:1546-1560 (2000).
 RN [3]
 RP SEQUENCE OF 27-200 FROM N.A.
 RC TISSUE=Intestine;
 RA Taborda E.N., Hickey D.A.;
 RL Submitted (APR-1995) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP SEQUENCE OF 294-550 FROM N.A.
 RC TISSUE=Liver;
 RX MEDLINE=9613781; PubMed=8557660;
 RA Stapleton D., Mitchell K.I., Gao G., Widmer J., Mitchell B.J.,
 RA Teh T., House C.M., Fernandez C.S., Cox T., Witters L.A.,
 RA Kemp B.E.;
 RT "Mammalian AMP-activated protein kinase subfamily.";
 RL J. Biol. Chem. 271:611-614 (1996).
 CC -1- FUNCTION: Responsible for the regulation of fatty acid synthesis
 CC by phosphorylation of acetyl-CoA carboxylase. It also regulates
 CC cholesterol synthesis via phosphorylation and inactivation of
 CC hormone-sensitive lipase and hydroxymethylglutaryl-CoA reductase.
 CC Appears to act as a metabolic stress-sensing protein kinase
 CC switching off biosynthetic pathways when cellular ATP levels are
 CC depleted and when 5'-AMP rises in response to fuel limitation
 CC and/or hypoxia. This is a catalytic subunit (By similarity).
 CC -1- SUBUNIT: Heterotrimer of a catalytic subunit, a beta and a gamma
 CC non-catalytic subunits.
 CC -1- PPM: Autophosphorylated (By similarity).
 CC -1- SIMILARITY: Belongs to the Ser/Thr family of protein kinases. SNF1
 CC subfamily.
 CC
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 CC
 CC EMBL; AB022017; BAA36547.1; -;
 CC EMBL; AF100763; AAD43027.1; -;
 CC EMBL; U22456; AAA64850.1; -;
 CC EMBL; Y12856; CAA73361.1; -;
 CC PIR; G01743; G01743.
 CC HSSP; Q63450; 1A06.
 CC GeneW; HGNC:9376; PRKAA1.
 CC MIM; 602739; -;
 CC GO; GO:0005622; C:intracellular; IC.
 CC GO; GO:0008189; F:apoptosis inhibitor activity; NAS.
 CC GO; GO:0004691; F:AMP-dependent protein kinase activity; NAS.
 CC GO; GO:0042571; F:cytokinetic elongation factor-2 kinase activ. . .; ISS.
 CC GO; GO:0000187; P:activation of MAPK; NAS.
 CC GO; GO:0046318; P:negative regulation of glucosylceramide bio. . .; NAS.
 CC GO; GO:0017148; P:negative regulation of protein biosynthesis; ISS.
 CC GO; GO:0045768; P:positive regulation of anti-apoptosis; NAS.
 CC GO; GO:0045542; P:positive regulation of cholesterol biosynth. . .; NAS.
 CC GO; GO:0046311; P:positive regulation of fatty acid oxidation; ISS.
 CC GO; GO:0045722; P:positive regulation of gluconeogenesis; ISS.
 CC GO; GO:0046326; P:positive regulation of glucose import; ISS.
 CC GO; GO:0006468; P:protein amino acid phosphorylation; ISS.
 CC GO; GO:0001666; P:response to hypoxia; NAS.
 CC InterPro; IPR000719; Prot_kinase.
 CC InterPro; IPR008271; Ser_thr_kin_AS.

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DR InterPro; IPR002290; Ser thr kinase.
DR InterPro; IPR001245; Tyr_kinase.
DR Pfam; PF00069; pkinae; 1.
DR PRINTS; PR00109; TYRKINASE.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00220; S_TKC; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR Cholesterol biosynthesis; Fatty acid biosynthesis; Transferase;
  Serine/threonine-protein kinase; ATP-binding; Phosphorylation.
FT DOMAIN 18 270
FT NP BIND 24 32
FT BINDING 47 47
FT ACT SITE 141 141
FT MOD RES 174 174
FT CONFLICT 28 28
FT CONFLICT 193 193
FT CONFLICT 199 199
FT CONFLICT 260 260
SQ SEQUENCE 550 AA; 62793 MW; 3316183D744D325 CRC64;

Query Match 41.4%; Score 1115; DB 1; Length 550;
Best Local Similarity 45.4%; Pred. No. 2,3e-71;
Matches 232; Conservative 86; Mismatches 117; Indels 76; Gaps 11;

QY 2 DSSGSGSHSELRNYNGRTIGITGTFGKVKIAEKLIGHRAIKIINCGRKMMEMEEK 61
DB 10 DGRVY-ICH-----YIIADTLGVGTGFKVKGKHELTGKRAVKVILRQKIRSLDVVGK 62
QY 62 AKREPKILKLFTHPIIRLYEVIYPTDIYVMEYCKTGELPDYIVKGRLOEDERRIF 121
DB 63 IRRRELQNLKLRHPHIIKLYQVISTPDIEMMEYVSGELFDYICAKGRLEDEKSRILF 122
QY 122 QOIIISGVYCHRMNVVHDLKRENLLDSKYNVLADFGLSNVMDGHFLKTCGSPNYA 181
DB 123 QOIIISGVYCHRMNVVHDLKRENLLDAHNAKIALDFGLSNMDSGDFLRTSCGSPNYA 182
QY 182 APEVSGLYAGPEVDWSSCYILYALLCGTLPPDENIPIVFKIKIGITLPSHSLAL 241
DB 183 APEVSGLYAGPEVDWSSCYILYALLCGTLPPDDHVPFLFKICDGIPTQYLPNS 242
QY 242 ARDLIPRLVYVEPKRITIRIREIHEQFOLRLPRILVAVPPPTTQAKIMBEDTLR---- 297
DB 243 VISLAKMLQYDPMKRASTIKDREHEWFKQDLPKILF--PEDPSYSSIMIDDEALKVCE 300
QY 298 -----DVNMGNKKNHVCESLCSRLQNEATVAYLLLDNR---FRATSGYLADYQES 347
DB 301 KEEGSEEVLSCLVVRNH-----QDPLAVAYHLLIDNRRIWNEAKDFYLATSPDPS 351
QY 348 M--DRLNQ-----LASSESSSGTRNVYPGSSDHSGLRPYFVERKMALGLOS 397
DB 352 FLDDHHLTRPHERVPLVAETPRARHTLDELPOKSKH-QGVR-----KAKMHLGIRSQ 405
QY 398 AHPREIWEVYKALQELNVKNGHNVKRCWCGPEVNDTLDAASFLGDSTIMND 457
DB 406 SRPNDIMEVCAIKQLDYEMKVNVPTLYRVR----- 437
QY 458 DANGRLPTVIKPEFQOLYTKDKYLLDMQRY 488
DB 438 RKNPVTSTYSKMSQLYQVDSRTYLLDPRSI 468

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OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; mitosporic Saccharomycetales; Candida.
OX NCBI_TaxID=5476;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 3254 / B-311;
RX MEDLINE=98053924; PubMed=9393775;
RA Peter R., Chang Y.C., Kwon-Chung K.J.;
RT "A gene homologous to Saccharomyces cerevisiae SNF1 appears to be
  essential for the viability of Candida albicans."
RL Infect. Immun. 65:4909-4917(1997).
RN [2]
RP SEQUENCE OF 7-620 FROM N.A.
RC STRAIN=ATCC 3254 / B-311;
RA Peter R., Kwon-Chung K.J.;
RL Submitted (MAR-1996) to the EMBL/GenBank/DBJ databases.
CC -I- FUNCTION: Essential for release from glucose repression. It
  interacts and has functional relationship to the regulatory
  protein SNF4. Could phosphorylates CAT8 (by similarity).
CC -I- SUBCELLULAR LOCATION: Associated with the nuclear membrane (by
  similarity).
CC -I- SIMILARITY: Belongs to the Ser/Thr family of protein kinases. SNF1
  subfamily.
-----
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-----
DR EMBL; L78129; AA848643.1; -.
DR EMBL; U39263; AA92456.1; -.
DR HSSP; Q63450; 1A06.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR008271; Ser_Thr_kinase.
DR InterPro; IPR002290; Ser_thr_kinase.
DR Pfam; PF00069; pkinae; 1.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00220; S_TKC; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR Transferase; Serine/threonine-protein kinase; ATP-binding;
  Phosphorylation; Carbohydrate metabolism; Nuclear protein.
KW DOMAIN 16 29
FT NP BIND 53 67
FT BINDING 82 82
FT ACT SITE 175 175
FT MOD RES 208 208
FT CONFLICT 7 8
FT CONFLICT 228 234
FT CONFLICT 242 255
FT CONFLICT 387 387
FT CONFLICT 416 416
FT CONFLICT 494 494
SQ SEQUENCE 620 AA; 70005 MW; 1806C652B5061D2B CRC64;

Query Match 37.7%; Score 1016.5; DB 1; Length 620;
Best Local Similarity 41.5%; Pred. No. 2,4e-64;
Matches 225; Conservative 85; Mismatches 133; Indels 99; Gaps 14;

QY 17 YNLGRTIGITGFGVKIAEHLTGHRAVAKIINCGRKMMEMERKAREFKILKLFTHPH 76
DB 53 YQIKTIGBSGSGFGVKLAQHILGTQKVALKIKRKTAKSDMQRVREISYLRLLRHPH 112
QY 77 IIRLYEVIYPTDIYVMEYCKTGELPDYIVKGRLOEDERRIFQOIIISGVYCHRMNV 136
DB 113 IIRLYEVIYCKSDIIVWEVAG--KELPDYIVQGRKMEDEARRFPQOIIIAVEYCHRHKI 171

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QY 137 VHRDLKPEKENTLLDSKRYNFKLADFGLSNVMDHGHFKTSCGSPNY-AAPEVISGKLYVAGE 195
DB 172 VHRDLKPEKENTLLDQGLAVKIDFGLSNIMTMDGNLTKSCGSPNMPAPEVISGKLYVAGE 231
QY 196 VDWSCGVILYALLCGTLPDPDENI PNLFKIKGQIYTLPSHLSALARDLIPRLVVEPM 255
DB 232 VDWASAGVILYVLMCGRLPFDEDFI PALFKISNGVYTLPNYLSAGAKHLLTRMLVYNPL 291
QY 256 KRITIRERHQQWFOIRLPRYLAVPPPTTQOAKM-IDEDTLRVV-VNMGFNK---HV 309
DB 292 NRITIHETMEDWFKODMPDYLPPDUSKKNOSKIDVEDIVRLSVTGMCDRCKYVNV 351
QY 310 CE-----SLCSRLQNEATVAYYLLDNRFRATSGYLGADYQESMDRMINQLAS 357
DB 352 IEKANKQVAAAGNSSQSGSKSNELLDALNKEHN-----ALVKDLKSKSENIIESFLS 405
QY 358 SSSSSS-----GTNNYVFG-----SSDPHSS-----GLRPYVPE 387
DB 406 QSPPEPSPNNGSTSSAPGVQOSLTYQTLATVPDLSLTPNSTIALPTSLPSIRAYVAE 465
QY 388 RK-----MALGOSRAHPREIWEVVKALQELNVRKKNKH---Y 424
DB 466 TKQNGDPSQOAHPPPTKSKTRMHGIRSRYPIDVGEIYRALKNLGAEMAKFTBEELW 525
QY 425 NVKGRMCPGFPEVNDTLDASNSFLGDSYIMNDNDANGRLPTVIRFEPOLYTKDXYLLD 484
DB 526 TIRFRW-----KYDTSAQF-----ECGSAPILMQMQLDPLQLENNYLV 565
QY 485 MQ 486
DB 566 FK 567

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RESULT 8

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SNF1_YEAST
ID SNF1_YEAST STANDARD; PRT; 633 AA.
AC P06782;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Carbon catalbolite derepressing protein kinase (EC 2.7.1.-).
GN SNF1 OR CMT1 OR CCRI OR PAS14 OR GLC2 OR YDR477W OR D8035.20.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OC NCBI_TaxID=4932;
RX MEDLINE=66289463; PubMed=3526554;
RA Celenza J.L., Carlson M.;
RT "A Yeast gene that is essential for release from glucose repression
RT encodes a protein kinase."
RL Science 233:1175-1180 (1986).
RN [2]
RN SEQUENCE FROM N.A.
RA Dietrich F.S., Mulligan J., Allen E., Araujo R., Aviles E.,
RA Benito A., Carpenter J., Chen E., Cherry J.M., Chung E., Duncan M.,
RA Huntie-Smith S., Hyman R., Kemp C., Lashkari D., Lew H., Lin D.,
RA Mosedale D., Nakahara K., Namath A., Oefner P., Oh C., Petel F.X.,
RA Roberts T., Schramm S., Schroeder M., Shogren T., Shroff N.,
RA Wilentz A., Yelton M., Botstein D., Davis R.W.;
RA Submitted (AUG-1995) to the EMBL/GenBank/DBJ databases.
RN [3]
RN SEQUENCE OF 274-284: 528-539 AND 622-630, AND PHOSPHORYLATION SITE.
RX MEDLINE=991331988; PubMed=7905477;
RA Mitchellhill K.I., Scapleton D., Gao G., House C., Michell B.,
RA Katsis F., Witters L.A., Kemp B.E.;
RT "Mammalian AMP-activated protein kinase shares structural and
RT functional homology with the catalytic domain of yeast Snf1 protein
RT kinase."
RL J. Biol. Chem. 269:2361-2364 (1994).
CC -1- FUNCTION: Essential for release from glucose repression. It
CC interacts and has functional relationship to the regulatory

```

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CC protein SNF1. Interacts also with S1P1, S1P2 and GABR3. Could
CC phosphorylate CAT8.
CC -1- SUBCELLULAR LOCATION: Associated with the nuclear membrane.
CC -1- SIMILARITY: Belongs to the Ser/Thr family of protein kinases. SNF1
CC subfamily.
CC -----
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DR EMBL: M13971; AAA35058.1; -.
DR EMBL: U33050; AAB64904.1; -.
DR PIR: A26030; A26030.
DR HSSP: P24941; IHCL.
DR GerMOnLine: 140969; -.
DR SCD: S0002885; SNF1.
DR GO: GO:0005737; C:cytoplasm; IPI.
DR GO: GO:0005634; C:nucleus; IPI.
DR GO: GO:0000324; C:vacuole (sensu Fungi); IPI.
DR GO: GO:0004679; F:SNF1A/AMP-activated protein kinase activity; IDA.
DR GO: GO:0007155; F:cell adhesion; IMP.
DR GO: GO:0006995; P:cellular response to nitrogen starvation; IDA.
DR GO: GO:0030447; P:filamentous growth; IMP.
DR GO: GO:0006468; P:protein amino acid phosphorylation; IDA.
DR GO: GO:0006109; P:regulation of carbohydrate metabolism; IGI.
DR InterPro: IPR000719; Prot_kinase.
DR InterPro: IPR008271; Ser_thr_kinase.
DR InterPro: IPR002290; Ser_thr_kinase.
DR Pfam: PF00069; Pkinase; 1.
DR ProDom: PD000001; Prot_kinase; 1.
DR SMART: SM00220; S_TKC; 1.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
DR Transferrase: Serine/threonine-protein kinase; ATP-binding;
KW phosphorylation; Carbohydrate metabolism; Nuclear protein.
FT DOMAIN 18 32 POLY-HIS.
FT NP_BIND 55 306 PROTEIN_KINASE.
FT BINDING 61 69 ATP (BY SIMILARITY).
FT ACT_SITE 84 84 ATP (BY SIMILARITY).
FT ACT_SITE 177 177 BY SIMILARITY.
FT MOD_RES 210 210 PHOSPHORYLATION (AUO-).
SQ SEQUENCE 633 AA; 72045 MW; F5C63565C986C4E3 CRC64;
Query Match 37.6%; Score 1013.5; DB 1; Length 633;
Best Local Similarity 40.0%; Pred. No. 4e-64;
Matches 227; Conservative 82; Mismatches 147; Indels 111; Gaps 14;
QY 2 DGSGSGHSEALRNVLGRTIGTGKVKIKAEKLTGHRVAKIKINQOMNMEEEK 61
DB 48 DGAHIG-----NVOIVTLGSGFGKVLAAHTTGQKVLKIKNKVLAQSKDMQGR 99
QY 62 AKREFKIKLFIHPHRIRLTEVITYTPDIYVWMEYCYGSLFPIYIEKGLQDEARIRF 121
DB 100 IERISTYLRILRHPIHITKLDVIKSKDEILTWIEYAG-NELFPIYIYORDMSQGEARRF 158
QY 122 QOITISVEYCHRNNAVHRDLKPEKENTLLDSKRYNFKLADFGLSNVMDHGHFKTSCGSPNYA 181
DB 159 QOITISAVEYCHRNHIVHRDLKPEKENTLLDEHNLVYKIDFGLSNIMTMDGNLTKSCGSPNYA 218
QY 182 APEVISGKLYVAGEVVDVWSCGVILYALLCGTLPDPDENI PNLFKIKGQIYTLPSHLSAL 241
DB 219 APEVISGKLYVAGEVVDVWSCGVILYVLMCGRLPDPDSDIPLFKNLSNGVYTLPKFISPG 278
QY 242 ARDILPMLVVEPMKRTTIREIRHQQWFOIRLPRYLAVPP-----DTQOAK 289
DB 279 AAGILKRMILVNPANRISHIEMODWFKYDLPERYL-LPFDLKRHPREENNDKSDG 337
QY 290 MDEDTLRD-VVN-----MGFNKNVCGESLCSRLQ---NEATVAYYLLDNRFRATSGY 339

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Db 338 SPDDDEIDNINILSTMGYEKDEIYESLESSSEDTPAFNEIRDAYMLIKENKSLIKOMK 397
 Qy 340 LGAIYQSEMDNUNL-----LASS----- 358
 Db 398 ANKSVSDLDLTFLLSQSPPTFOQOSKSHOKSOVDHETAKOHARRMASALTQORTYHQSPFM 457
 Qy 359 --SSSSSGTRNVPVPS-----SDPHSGGLRPYVPERK--WALGLQSRAPRE 402
 Db 458 DQYKEEDSTVILPISLPQIHRANMLAOGSPAAKISPLVTKSKSTRHHPGIRSRSYLD 517
 Qy 403 IMVEVLAKQELANRWKKNKH---YNVACRWCPCGPEVNDTLDAANSFLLGDTTMDNDA 459
 Db 518 VMGEIYIALKNLGAEMAKPSEEDLMTIKLR-----KYDIGKKT-----NT 558
 Qy 460 NGRLLPTVYKFEFOLYKTKDDKYLDMQ 486
 Db 559 NEKIPDLKMWIQLFQIETNNYLVDFK 585

RESULT 9

SNF1_CANTR STANDARD; PRT; 619 AA.
 AC 094168;
 DT 15-JUL-1999 (Rel. 38, Created)
 DT 15-JUL-1999 (Rel. 38, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Carbon catabolite derepressing protein kinase (EC 2.7.1.1-).
 GN SNF1.
 OS Candida tropicalis (Yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; mitosporic Saccharomycetales; Candida.
 OX NCBI_TaxID=5482;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Kanai T., Ogawa K., Ueda M., Tanaka A.;
 RT "Genetic evaluation of the function of SNF1 in Candida tropicalis.";
 RL Submitted (MAR-1999) to the EMBL/Genbank/DBJ databases.
 CC -1- FUNCTION: Essential for release from glucose repression. It
 interacts and has functional relationship to the regulatory
 protein SNF4. Could phosphorylates CAT8 (By similarity).
 CC -1- SUBCELLULAR LOCATION: Associated with the nuclear membrane (By
 similarity).
 CC -1- SIMILARITY: Belongs to the Ser/Thr family of protein kinases. SNF1
 subfamily.
 CC -----
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 or send an email to license@ebi.ac.uk).
 CC -----
 DR EMBL; AB024535; BAA75889.1; -.
 DR HSSP; O63450; 1A06.
 DR InterPro; IPR000719; Prot. kinase.
 DR InterPro; IPR008271; Ser_Thr_Pkin_AS.
 DR InterPro; IPR002290; Ser_Thr_Pkinase.
 DR Pfam; PF00069; Pkinase; 1.
 DR ProDom; PD000001; Prot. kinase; 1.
 DR SMART; SMO0220; S_TKC; 1.
 DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
 DR PROSITE; PS00108; PROTEIN KINASE_ST; 1.
 DR PROSITE; PS50011; PROTEIN KINASE_DOM; 1.
 KM Transferrase; Serine/threonine-protein kinase; ATP-binding;
 KM Phosphorylation; Carbohydrate metabolism; Nuclear protein.
 FT DOMAIN 17 29
 FT NP_BIND 52 303 PROTEIN KINASE
 FT NP_BIND 58 66 ATP (BY SIMILARITY).
 FT BINDING 81 81 ATP (BY SIMILARITY).
 FT ACT_SITE 174 174 BY SIMILARITY.
 FT MOD_RES 207 207 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).

SEQ SEQUENCE 619 AA; 70323 MW; 0FCF1FC3DC8706D7 CRC64;

Query Match 37.5%; Score 1010.5; DB 1; Length 619;

Best Local Similarity 40.0%; Pred. No. 6,4e-64; Matches 219; Conservative 91; Mismatches 128; Indels 109; Gaps 12;

Qy 17 YNLGRTIGIGFGYKIAEHLTGRVAIKIINCQRNMNEBEKAREFKILFLTIHPH 76
 Db 52 YQIITKIGESFGYKLAQHVGTQXALKIINKTKLAKSMQGRVEREISYLLNHPH 111
 Qy 77 IIRLYEVIYPTDIIYVMEYCKGELFDYIYVEKRLQDEARRIPOQIISGEVCHRMV 136
 Db 112 IIRLYDVYKSDKEIIMVIEFAG--KEIPDYIYQKMEDEARRPFOQIIAIVEYCHRHKI 170
 Qy 137 VHRDLKPEENLLDSKNVYKLADEGLSNVMDGHLTKSCSPNPAABEVISGKIYAQREV 196
 Db 171 VHRDLKPEENLLDQLVNKLADFGLSNIMDGNFLKTKSCSPNPAABEVISGKIYAQREV 230
 Qy 197 DVMSGVILYALCGTLPPFDENIPNLFKKIKGSIYTLPSHLASALARDLIPRMLVPEPMK 256
 Db 231 DVMSGVILYMLCGRLPPDDEFIPALFKISNGVYTLPSYLSGAKHLTRMLVYAPLN 290
 Qy 257 RITIREIREHQPQIRLPRLVAVPPPTQOAKM-IDEDTLRDV--VMNGFNKNVYCESL- 313
 Db 291 RITHEIMEDEWFKQMDPDYLLPDDLKSKITSKIDIDEDVIALSVTMGYDRDEISVIE 350
 Qy 314 -----CRLQNEALVAAYLLDNRFRATSGIAGLDYQESMDRNLNQLAS- 357
 Db 351 KANREAAAGATPTNQSKSTNEVDAYLLMKENH-----TLVYDLKSKSENIESPLSL 404
 Qy 358 -----SSSSSGTR-----NYVPGS----- 372
 Db 405 SPPSSSFPNPGSSNAPGVQSLITYQTATVPDLSTLPSTIAILPISLIRAYTME 464
 Qy 373 ---SDPHSS--GLRPYVPERKVALGLQSRAPREIMVEVLAKQELANRWKKNKH---Y 424
 Db 465 TKVNDPQOQIPAPPTKTLKTRHHPGIRSRSYPLDVNGEIRYALKNGAEMAKPTEBELW 524
 Qy 425 NVKCRWCPGPEVNDTLDAANSFLGDTTMDNDANRL-----PYIKPEFOLYKTKDD 479
 Db 525 TIRLRW-----KYDSTQLRWORTNLMKQIQLFQLEPN 559

RESULT 10

SNF1_CANGA STANDARD; PRT; 611 AA.
 ID SNF1_CANGA
 AC 000372;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Carbon catabolite derepressing protein kinase (EC 2.7.1.1-).
 GN SNF1.
 OS Candida glabrata (Yeast) (Torulopsis glabrata).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; mitosporic Saccharomycetales; Candida.
 OX NCBI_TaxID=5478;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=NCCL884;
 RX MEDLINE=97101049; PubMed=8945576;
 RA Pelter R., Kwon-Chung K.U.;
 RT "Disruption of the SNF1 gene abolishes trehalose utilization in the
 pathogenic yeast Candida glabrata.";
 RL Infect. Immun. 64:5269-5273 (1996).
 CC -1- FUNCTION: Essential for release from glucose repression. It
 interacts and has functional relationship to the regulatory
 protein SNF4. Could phosphorylates CAT8 (By similarity).
 CC -1- SUBCELLULAR LOCATION: Associated with the nuclear membrane (By
 similarity).

DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
 DR PROSITE; PS00030; UBA; 1.
 KW Transferase; Serine/threonine-protein kinase; ATP-binding.
 FT DOMAIN 34 285 PROTEIN KINASE.
 FT NP BIND 40 345 UBA.
 FT BINDING 48 48 ATP (BY SIMILARITY).
 FT ACT SITE 63 63 ATP (BY SIMILARITY).
 FT ACT SITE 156 156 BY SIMILARITY.
 SQ SEQUENCE 576 AA; 65996 MW; E5857E8F171E7B50 CRC64;

Query Match 36.4%; Score 981.5; DB 1; Length 576;
 Best Local Similarity 38.0%; Pred. No. 6.5e-62;
 Matches 228; Conservative 78; Mismatches 165; Indels 129; Gaps 12;

QY 1 MDGSSKSGG---HSEALRNVLG---RTIGITFGKVKIAEHLGHRVAIKINCR 51
 DB 9 MENSTNRGARVLPPEAISKRIGYIIRETLEGSGFSGVKLATYTKYQOKALKFISRQ 68
 QY 52 QMRNMEMEKAKREBKIKLFIHPHILRYEVIYPTDIYVMEYCKYGEIPDYVEKGR 111
 DB 69 LIKSDMNRVREISYKLRLPHIILKLYDITPTDIWVIEYAG-GELFDYVEKGR 127
 QY 112 LQEDERRIPQOIIISGVEYCHRMNVHRDLKPENLILDSKYNVKLADFGLSNVMDGHFL 171
 DB 128 MTEDEGRFPQOIIICAIEXCHRHKIYHRDLKPENLILDLNINVKIADFGLSNIMTDGNFL 187
 QY 172 KTSQSSPNYAAPEVYSGLYAGPEVDVWSCGYIYALLCGTLPDDENIPNLFKIKKGI 231
 DB 188 KTSQSSPNYAAPEVINGKLYAGPEVDVWSCGYIYALLCGTLPDDENIPNLFKIKKNCV 247
 QY 232 YTLPSHLALARDLPRMLVYEPKRIIRIREHQQFOIRLPRYLAVERPPTTQQAAMI 291
 DB 248 YVMPFLSPGASLRIRMIIVADPMORITIIQELRRPMPRNVLDPYL---PMEEVQSGYA 304
 QY 292 DEDTLRDVNV-MGFKNHVCESLCSRLQNEATVAYLLLDNRFRATSYGLADYQESMDR 350
 DB 305 DSRIVSKLGEAMGFEDYIVELARDENNEVKEAVNLLHENVQIEKSHLSKKVDSFL 364
 QY 351 NLNQLAESSESSSGIRNVYVPGSSDPHSSGLR-----PYRPE----- 387
 DB 365 SVSPAPSEYSELOKSKROBLIDPTLEGPRWTVPDPTYAKQITISNICVLVPTAEKMK 424
 QY 388 -----RKWALGLQSRHAPREIMVEYLKALQELNVKMK--- 419
 DB 425 LEMRTLADAAGAVTSGSTRKKSRNKNHFGVRCGADPELILAYRLLQRAAGAFYVPK 484
 QY 420 -----KNGHYNVKCRWCPPEVNDTLDAVNSFLGSDTIMDNDANGRLP-----T 465
 DB 485 PVNGKYRSDMYTIKSRW-----EIPHCCKREGKNT 513
 QY 466 VIKPEFQLYKTKDKYLLDMOR-----VTGPO-----LFLDFCAAFLYKL 506
 DB 514 YAYIELQLYEVWPGFMDLVKSNGYKDYISHERPDAHGMDDLKSSPFPLDLCAMLVCKL 573

RESULT 12
 YNA3_CAEEL STANDARD; PRT; 622 AA.
 AC P45894;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Putative serine/threonine-protein kinase PAR2.3 in chromosome III
 DE (EC 2.7.1.-).
 GN PAR2.3.
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
 OC Rhabditidae; Peloderinae; Caenorhabditis.
 OC NCBI_TaxID=6239;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Bristol N2;
 RX MEDLINE=94150718; PubMed=7906398;

RA Wilson R., Ainscough R., Anderson K., Baynes C., Berks M.,
 RA Bonfield J., Burton J., Connell M., Copey T., Cooper J., Coulson A.,
 RA Craxton M., Dear S., Du Z., Durbin R., Favello A., Fraser A.,
 RA Fulton L., Gardner A., Green P., Hawkins J., Hillier L., Jier M.,
 RA Johnston L., Jones M., Kershaw J., Kirsten J., Laister N.,
 RA Latreille P., Lightning J., Lloyd C., Mortimore B., O'Callaghan M.,
 RA Parsons J., Percy C., Rifkin L., Roopra A., Saunders D., Showkhen R.,
 RA Sims M., Smailson N., Smith A., Smith M., Sonnenhammer E., Staden R.,
 RA Sulston J., Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K.,
 RA Waterston R., Watson A., Wellstock L., Wilkinson-Sprat J.,
 RA Woldman P.,
 RA "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
 RT elegans."
 RL Nature 368:32-38(1994).

CC -1- SIMILARITY: Belongs to the Ser/Thr family of protein kinases.
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 CC or send an email to license@sib-sib.ch).
 CC -----
 CC EMBL; U00025; AAA50618.1; -.
 CC PIR; S44859; S44859.
 DR HSSP; 063450; 1A06.
 DR WormPep; PAR2.3; CE00847.
 DR InterPro; IPR000719; Prot. Kinase.
 DR InterPro; IPR008271; Ser Thr pkin AS.
 DR InterPro; IPR002290; Ser Thr pkinase.
 DR Pfam; PF00069; pkinase; 1.
 DR Prodom; PD000001; Prot_Kinase; 1.
 DR SMART; SM00220; S_TKc; 1.
 DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
 DR PROSITE; PS00108; PROTEIN KINASE ST; 1.
 DR PROSITE; PS00011; PROTEIN KINASE DOM; 1.
 KW Hypothetical protein; Transferase; Serine/threonine-protein kinase;
 KW ATP-binding.
 FT DOMAIN 24 276 PROTEIN KINASE.
 FT NP BIND 30 38 ATP (BY SIMILARITY).
 FT BINDING 53 53 ATP (BY SIMILARITY).
 FT ACT SITE 147 147 BY SIMILARITY.
 SQ SEQUENCE 622 AA; 69515 MW; D5F8155004B246 CRC64;

Query Match 33.2%; Score 894.5; DB 1; Length 622;
 Best Local Similarity 39.1%; Pred. No. 9.9e-56;
 Matches 208; Conservative 77; Mismatches 154; Indels 93; Gaps 12;

QY 7 GSGHSEALRNVLGRTIGITFGKVKIAEHLGHRVAIKINCRQMRNMEMEKAREF 66
 DB 15 GTGHK-IGNVIVETTGKAFVAVKRGTHIQYDVAIKILNGRKNGIGTVKNTNEI 73
 QY 67 KILKLFHPHILRYEVIYPTDIYVMEYCKYGEIPDYVEKGRLOEDERRIPQOIIIS 126
 DB 74 DNLQKLTHPHILRYEVIYPTDIYVMEYCKYGEIPDYVEKGRLOEDERRIPQOIIIS 133
 QY 127 GVEYCHRMNVHRDLKPENLILDSKYNVKLADFGLSNVMDGHFLKTSQSSPNYAAPEVI 186
 DB 134 GVSCHNMIVHRDLKPENLILDLANKNIKIADFGLSNVMTDGDLSTAQSPNYAAPELI 193
 QY 187 SGKYAAPPEVDVWSCGYIYALLCGTLPDDENIPNLFKIKKGIYTLPSHLALARDLI 246
 DB 194 SNKLYAPPEVDLWSCGYIYALLCGTLPDDQNPVTLFAKIKSGRYVPPSMERQADLI 253
 QY 247 PRMLVYEPKRIIRIREHQQFOIRLPRYLAVERPPTTQQAAMIDEDTLRDV----- 299
 DB 254 STMLOVDPYKADYKRIYVNSMFRIDLPYL---PECNESSTIVDIDVQSVAKETPPE 310
 QY 300 -----VNMGFKNHVCES-----LCSRLQNEATVAYLLLDNRFA----- 335
 DB 311 KIIFYIFRHLKEDVKEDEVGTALLAEDHHHFLCIAVRLVNHKRNADSSQVAMEDFW 370


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Qy 336 -----TSGLYADYQ-ESMDRLNQLASSSSSGTRNYPGSDPHSSGLRPPY 384
Dy 371 EIGTMKMGSTSLVGATTKSEKSERNAVKGFANVGKIL-----EGLKK-- 419
Qy 385 PVERK---WALGOSRAHREIWEVILKALQELNVRKQGNVCKWCPCGPEVNDTL 441
Dy 420 --EQKLTWNIGIRACLDPEVTMKHVFSLKSVDMEMVSLMYHIIYASKP--TPIN--- 472
Qy 442 DASNSFLDSTIMNDNDANGRLPTVIKPEPOLY-----KTQDKYLLMQRT 489
Dy 473 -----PDVVKVSLQLFALDKKXNKGYLDPKGLT 502

RESULT 13
MRKA_HUMAN STANDARD; PRT; 752 AA.
ID MRKA_HUMAN Q96J34; Q96YD8;
AC Q96J34; Q96YD8;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE MAP/microtubule affinity-regulating kinase 4 (EC 2.7.1.27)
DE (MAP/microtubule affinity-regulating kinase like 1).
DE MARK4 OR MARKL1 OR KIA1860.
GN Homo sapiens (Human).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP TISSUE=Brain;
RC TISSUE=Brain;
RA Drewes G., Mandelkow E.M.;
RT "MARK4, homologue of MARKL, MARK2 and MARK3.";
RL Submitted (SEP-2001) to the EMBL/Genbank/DBJ databases.
RN [2]
RP TISSUE=Brain;
RC TISSUE=Brain;
RA MEDLINE=2126021; PubMed=11326310;
RA Kato T., Satoh S., Okabe H., Kitahara O., Ono K., Kihara C.,
RA Tanaka T., Tanuda T., Yamada Y., Nakamura Y., Furukawa Y.;
RT "Isolation of a novel human gene, MARKL, homologous to MARK3 and its
RT involvement in hepatocellular carcinogenesis.";
RL Neoplasia 3:4-9(2001).
RN [3]
RP TISSUE=Brain;
RC TISSUE=Brain;
RA Beghini A., Magnani I., Roverei G., Piepoli T., Differlizi S.,
RA Pollo B., Conti A.M.F., Cowell J.K., Finocchiaro G., Latizza L.;
RT "Neutral progenitor-restricted isoform of MARKL gene is upregulated by
RT 19q13 amplification in human glioblastoma.";
RL Submitted (JUN-2002) to the EMBL/Genbank/DBJ databases.
RN [4]
RP TISSUE=Brain;
RC TISSUE=Brain;
RA MEDLINE=21245130; PubMed=11347906;
RA Nagase T., Nakayama M., Nakajima D., Kikuno R., Ohara O.;
RT "Prediction of the coding sequences of unidentified human genes. XX.
RT The complete sequences of 100 new cDNA clones from brain which code
RT for large proteins in vitro.";
RL DNA Res. 8:85-95(2001).
RN [5]
RP TISSUE=Thyroid;
RC TISSUE=Thyroid;
RA Itogai T., Ota T., Nishikawa T., Hayashi K., Otsuki T., Sugiyama T.,
RA Suzuki Y., Nagai K., Sugano S., Ishii S., Kawai-Hiro Y., Saio K.,
RA Yamamoto J., Wakamatsu A., Nakamura Y., Kojima S., Nagahara K.,
RA Hattori A., Okumura K., Iwayanagi T., Ninomiya K.;
RT "NDO human cDNA sequencing project.";
RL Submitted (MAR-2002) to the EMBL/Genbank/DBJ databases.
CC -1- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=1;

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CC IsoId=Q96J34-1; Sequence=Displayed;
CC Name=2; Synonyms=MARKL1S;
CC IsoId=Q96J34-2; Sequence=VSP_004946;
CC -1- TISSUE SPECIFICITY: Ubiquitous. Isoform 2 is brain-specific.
CC -1- SIMILARITY: Belongs to the Ser/Thr family of protein kinases. MARK
CC subfamily.
CC -1- SIMILARITY: Contains 1 kinase-associated (KAI) domain.
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CC -----
CC EMBL; AY057448; AAI23683.1; -.
CC EMBL; AB049127; BAB39380.1; -.
CC EMBL; AY120867; AAM55491.1; -.
CC EMBL; AK075272; BAC11510.1; -.
CC EMBL; AB058763; BAB47489.1; ALT_INIT.
CC HSSP; Q63450; 1A06.
CC Genew; HGNC:13538; MARK4.
CC MIM; 606495; -.
CC InterPro; IPR001772; Kinase Cterm.
CC InterPro; IPR000719; Prot Kinase.
CC InterPro; IPR008271; Ser_Thr_kin_AS.
CC InterPro; IPR001245; Tyr_kinase.
CC InterPro; IPR000449; UBA_domain.
CC Pfam; PF02149; KAI; 1.
CC Pfam; PF00069; Pkinase; 1.
CC Pfam; PF00627; UBA; 1.
CC PRINTS; PR00109; TYRKINASE.
CC PRODOM; PD000001; Prot_kinase; 1.
CC PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
CC PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
CC PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
CC PROSITE; PS50030; UBA; 1.
CC KW Transferrase; Serine/threonine-protein kinase; ATP-binding;
CC Alternative splicing.
CC KW DOMAIN 59 310 PROTEIN KINASE.
CC DOMAIN 324 368 UBA.
CC DOMAIN 703 752 KAI.
CC NP_BIND 65 73 ATP (BY SIMILARITY).
CC BINDING 88 88 ATP (BY SIMILARITY).
CC ACT_SITE 181 181 BY SIMILARITY.
CC VARSPLIT 628 752 ADEPERIGGEVTSCHLPMDOTETAPRLAPFMSVYKLTSSR
CC PPEALMALROATTAARCRQPOPFILACHGAGGPEPL
CC SHEFEVCOLEPRDLRGVLFRRVAGTALAFRTVTRLSNDL
CC EL -> TLDPSTKQNSNRVCVSGASLPGSKIRSGTNIRESG
CC DLREQVALIYIGIKKKPPGSGSDSPGV (In isoform
CC 2).
CC /FTId=VSP_004946.
CC F -> S (IN REF. 2).
CC QUERY SEQUENCE 752 AA; 82519 MW; 4B430FPD2B150E7A CRC64;
CC
CC Query Match 27.4%; Score 737.5; DB 1; Length 752;
CC Best Local Similarity 42.7%; Pred. No. 1.5e-44;
CC Matches 163; Conservative 52; Mismatches 122; Indels 45; Gaps 6;

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QY 196 VDWSGVLYALALCTLPFDENIPNLFKIKGITYLLPSHLAALDLIPRLVPEPM 255
 DB 237 VDMSGLVILVTLVSGSLPDSGHNKELERLARKKIVVFPWMSIDCSILRLFLVLP 296
 QY 236 KRITREIREHOFI-----RLPRYLAVPPPTTQQAAMIDEDTLRDVYVNGFNKHYC 310
 DB 297 KRCTLEQIMKRMWINGVEBELKEY-----TEPEEDFGDTKIEVWVGMYGTYREIK 349
 QY 311 ESLGRLNBEATVAAYLLLDNFRATSGYLGADVOESMDRNINOLA-----SSS 359
 DB 350 ESLISQKNEVATYLL-----LGKTEEGRGAPGALARVRAPSDTTNGT 397
 QY 360 SSSGSTRNVVPGSSDPHSSGLR 391
 DB 398 SSSKGT-----SHSKGR 410

RESULT 14
 SNL_HUMAN STANDARD; PRT; 786 AA.
 AC P57059;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Probable serine/threonine protein kinase SNF1LK (EC 2.7.1.-).
 GN SNF1LK.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID=9606;
 RP [1]
 RX MEDLINE=20289799; PubMed=10830953;
 RA Hatori M., Fujiyama A., Taylor T.D., Watanabe H., Yada T.,
 RA Park H.-S., Toyoda A., Ishii K., Totoki Y., Choi D.-K., Groner Y.,
 RA Soeda E., Ohtsuka M., Takagi T., Sakaki Y., Taudien S., Blechschmidt K.,
 RA Polley A., Menzel U., Delabar U., Kumpf K., Lehmann R., Patterson D.,
 RA Reichweid A., Rump A., Schillhabel M., Schudy A., Zimmermann W.,
 RA Rosenthal A., Kudoh J., Shibuya K., Kawasaki K., Asakawa S.,
 RA Shintani A., Saeki T., Nagamine K., Mitsuyma S., Antonarakis S.E.,
 RA Minoshima S., Shimizu N., Nordle G., Hornischer K., Brandt P.,
 RA Scharte M., Schoen O., Desario A., Reichelt J., Kauer G., Bloecher H.,
 RA Ransner J., Beck A., Klages S., Hennig S., Riesselmann L., Dagand E.,
 RA Wehrmeyer S., Borzym K., Gardiner K., Nizetic D., Francis F.,
 RA Lehrach H., Reinhardt R., Yaspo M.-L.;
 RA "The DNA sequence of human chromosome 21.";
 RL Nature 405:311-319(2000).
 CC -1- SIMILARITY: Belongs to the Ser/Thr family of protein kinases.
 CC SNF1 subfamily.
 CC -1- SIMILARITY: Contains 1 UBA domain.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; AP001751; BAA95536.1; -;
 DR HSSP; P24941; IAO1.
 DR GeneW; HGNC:11142; SNF1LK.
 DR MIM; 605705;
 DR InterPro; IPR000719; Prot_kinase.
 DR InterPro; IPR008271; Ser_thr_pkin_AS.
 DR InterPro; IPR002290; Ser_thr_pkinase.
 DR InterPro; IPR000449; UBA domain.
 DR Pfam; PF00069; Kinase_1.
 DR ProDom; PD000003; Prot_kinase; 1.
 DR SMART; SM00220; S_TKc; 1.
 DR SMART; SM00165; UBA; 1.
 DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.

DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
 DR PROSITE; PS50030; UBA; 1.
 KW Transferase; Serine/threonine-protein kinase; ATP-binding.
 FT DOMAIN 27 281 PROTEIN KINASE.
 FT NP BIND 306 346 UBA.
 FT BINDING 33 41 ATP (BY SIMILARITY).
 FT ACT SITE 56 56 ATP (BY SIMILARITY).
 FT ACT SITE 149 149 BY SIMILARITY.
 SQ SEQUENCE 786 AA; 85252 MW; P844EB7CAF87CB1A CnC64;
 Query Match 27.4%; Score 737.5; DB 1; Length 786;
 Best Local Similarity 36.3%; Pred. No. 1.6e-44;
 Matches 179; Conservative 75; Mismatches 164; Indels 75; Gaps 12;
 QY 2 DGSKSGHSEAL--NYNLTGRTIGTGFQVKAENHGTGRVAIKINCRQNMME 59
 DB 10 DPAGQGGQKPLVGVGFIDERTYKGFVAVVAKLRRHRYTVQVAKIKIDTRLDSSNL- 68
 QY 60 EKAREFKILKLFTHPIIRLYEVIYPTDIYVMEYCKYGLPDYIYEKRLQDEARR 119
 DB 69 EKIRYVQMLNHPHIIKLYQMETQDMLYITPAKNGEMFDYLSNGHLSSEARK 128
 QY 120 IFQIIISGVEXCHRMVVRDLKPEMLLDKRYVKLA--DFGLSNVMDGHFLKTS 176
 DB 129 KFWQILSAVEYCHDHHIVHRDLKTEMLLDGNDMDIKLAGTDFGFGNFKSGEPLSTW 188
 QY 177 SPNTAAPRVISGKIYAGPEVWVSCGYLYALLGTLFPDENIPNLFKIKGITYLPS 236
 DB 189 SPPTAAPPEVFGKYEYGFQDLIMSLGVLYLVGSGLPFDSPNPTLMQRVLGRFRFP 248
 QY 237 HSLAARDLIPRLVPEPMKRTITREIREHOFI-----RLPRYLAVPPPTTQQAAMID 292
 DB 249 FMSQDCESLIRMLVVPDARITTAQIRQHRMMAAPCLPSPAPAPSAHSYTNLGYD 308
 QY 293 EDTLRDVVWNGFNKNHVCESLCSRLQNEATVAYLLLDNFRATSGYLGADVOESMDRN 352
 DB 309 EQALGIMQTLGVDRQFVESHQNSYNHFAIYLLLE-----RL 348
 QY 353 NQLASSESSSG--TRNVVPGSSDPHSSGLRITYVERKMGALGSR-----AHPREI 403
 DB 349 KEYRNAQCARGPAPQPRRSSD--LSGLE--VPQE-----GLSTDPRPALCPQPTL 399
 QY 404 MVEYLKALQEL-----NYRWKKNGHYNYVC-----RWCPGPP 436
 DB 400 VQSLQAMDELDLSSQLMPLFPVVDASCSGVPRPRPVSSLDPTAISERAGPGLER 459
 QY 437 VNDTLDAANSFGL 449
 DB 460 EDDTQESLPSSTG 472

RESULT 15
 SNL_RAT STANDARD; PRT; 776 AA.
 AC Q9R1U5; Q9R081;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Probable serine/threonine protein kinase SNF1LK (EC 2.7.1.-) (Salt-
 DE inducible protein kinase) (Protein kinase KID2).
 GN SNF1LK OR SIK OR KID2.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RP [1]
 RX STRAIN=Soragae-Dawley; TISSUE=Adrenal gland;
 RX MEDLINE=99330184; PubMed=10403390;
 RA Wang Z., Takemori H., Halder S.K., Nonaka Y., Okamoto M.;
 RA "Cloning of a novel kinase (SIK) of the SNF1/AMPK family from high
 RA salt diet-treated rat adrenal.";
 RL FEBS Lett. 453:135-139(1999).

```
[2]
RN SEQUENCE FROM N.A.
RP Feldman J.D., Vician L., Crispino M., Hoe W., Baudry M.,
RA Herschman H.R.;
RT "The Kid2 gene encodes a protein kinase induced by depolarization in
   brain.";
RL Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Belongs to the Ser/Thr family of protein kinases. SNF1
   subfamily.
CC -1- SIMILARITY: Contains 1 UBA domain.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AB020480; BAA82673.1; -
DR EMBL; AF106937; AAF14191.1; -
DR HSSP; P24941; 1A01.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR008271; Ser_thr_pkin_AS.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR InterPro; IPR000449; UBA_domain.
DR Pfam; PF00069; pkinase; 1.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00220; S_TKc; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
DR PROSITE; PS50030; UBA; 1.
DR Transferase; Serine/threonine-protein kinase; ATP-binding.
FT DOMAIN 27 278 PROTEIN KINASE.
FT NP_BIND 303 343 UBA.
FT BINDING 33 41 ATP (BY SIMILARITY).
FT ACT_SITE 56 56 ATP (BY SIMILARITY).
FT ACT_SITE 149 149 BY SIMILARITY.
FT CONFLICT 473 473 R -> K (IN REF. 2).
SQ SEQUENCE 776 AA; 84908 MW; 7BF745AF28F17E6E CRC64;

Query Match 27.2%; Score 731.5; DB 1; Length 776;
Best local similarity 45.6%; Pred. No. 4.2e-44;
Matches 151; Conservative 56; Mismatches 115; Indels 9; Gaps 4;

QY 7 GSGHSEALR--NYNIGRTLIGTGGKVIAGHKLTHRAVAIKIINCROMNMEMEKAKR 64
DB 15 GQGQOKPLRVGVFVDEKRTGKGNFAVVKLAHRVTKTQVAIKIIDKRLDSSNL-EKIYR 73
QY 65 EFKIKLFIHPHITRIEVIYTPDIYVVMYCKYGEI.PDIYVEKGRLOEDEARRIFQOI 124
DB 74 EVQLMKLNHPHITRIEVIYTPDIYVVMYCKYGEI.PDIYVEKGRLOEDEARRIFQOI 133
QY 125 ISGVYCHRNWVHRDLKPENLIDSKYVXLADPGLSNVMDGHFLKTSQSPNYAPE 184
DB 134 LSAVEYCNHHIYHRDLKTEMLLDGNMDIKLADRGFNPFYKPGEPSTWCGSPYAPB 193
QY 185 VISGKLIVGPEVDWVSCGVIYALICGTLPPDENIPNLFFKIKIGITLPSHLSALARD 244
DB 194 VFEQGEYEGPOLDIWSLGVVLYLVCGSIPFGPNLPTLRORVLEGRPIPFMSQDCET 253
QY 245 LIPRLVVEPMKIRITIREIHEWFOIRLPRYLAVPDPDTQOAKM-----IDEDTLRDV 299
DB 254 LIRRLVVDPAKRITIAQROHRWQAD-PTLLQDDPAFMSQGTSTNLGDYNEQVLGIM 312
QY 300 VMGFKNHVCESLCSRLQNEATVAYVLLLD 330
DB 313 QALGIDRQRTVESLQNSSYNHFAIYVLLLE 343
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Search completed: July 7, 2004, 17:55:37

Job time : 18 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 7, 2004, 17:54:00 ; Search time 52 Seconds
(without alignments)
3046.990 Million cell updates/sec

Title: US-09-857-522B-4
Perfect score: 2693
Sequence: 1 MDSSKSGSHSEALRNYNLG.....GQPLFLDFCAFLTKLRVL 509

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1276540 seqs, 311283816 residues

Total number of hits satisfying chosen parameters: 1276540

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

Published Applications MA:*

- 1: /cgn2_6/ptodata/1/pubppaa/US07_PUBCOMB.pep:*
- 2: /cgn2_6/ptodata/1/pubppaa/PCT_NEW_PUB.pep:*
- 3: /cgn2_6/ptodata/1/pubppaa/US06_NEW_PUB.pep:*
- 4: /cgn2_6/ptodata/1/pubppaa/US06_PUBCOMB.pep:*
- 5: /cgn2_6/ptodata/1/pubppaa/US07_NEW_PUB.pep:*
- 6: /cgn2_6/ptodata/1/pubppaa/PCTUS_PUBCOMB.pep:*
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- 8: /cgn2_6/ptodata/1/pubppaa/US08_PUBCOMB.pep:*
- 9: /cgn2_6/ptodata/1/pubppaa/US09A_PUBCOMB.pep:*
- 10: /cgn2_6/ptodata/1/pubppaa/US09B_PUBCOMB.pep:*
- 11: /cgn2_6/ptodata/1/pubppaa/US09C_PUBCOMB.pep:*
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- 13: /cgn2_6/ptodata/1/pubppaa/US10A_PUBCOMB.pep:*
- 14: /cgn2_6/ptodata/1/pubppaa/US10B_PUBCOMB.pep:*
- 15: /cgn2_6/ptodata/1/pubppaa/US10C_PUBCOMB.pep:*
- 16: /cgn2_6/ptodata/1/pubppaa/US10_NEW_PUB.pep:*
- 17: /cgn2_6/ptodata/1/pubppaa/US60_NEW_PUB.pep:*
- 18: /cgn2_6/ptodata/1/pubppaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2693	100.0	509	12 US-10-183-687-236	Sequence 236, App
2	2693	100.0	513	12 US-10-425-114-58891	Sequence 58891, A
3	2422	89.9	509	12 US-10-183-687-401	Sequence 401, App
4	2422	89.9	509	16 US-10-437-963-152150	Sequence 152150, App
5	2411.5	89.5	508	16 US-10-437-963-152149	Sequence 152149, A
6	2411.5	89.5	525	12 US-10-425-114-49946	Sequence 49946, A
7	2378	88.3	531	12 US-10-183-687-256	Sequence 256, App
8	1977	73.4	505	12 US-10-183-687-402	Sequence 402, App
9	1977	73.4	505	16 US-10-437-963-183463	Sequence 183463, App
10	1974.5	72.9	514	12 US-10-183-687-248	Sequence 248, App
11	1963	72.9	504	12 US-10-183-687-407	Sequence 407, App
12	1958	72.7	570	12 US-10-183-687-240	Sequence 240, App
13	1945	72.2	549	12 US-10-425-114-63632	Sequence 63632, A
14	1939	72.0	515	12 US-10-183-687-252	Sequence 252, App
15	1937	71.9	545	12 US-10-425-114-62429	Sequence 62429, A

16	1931	71.7	579	12 US-10-183-687-238	Sequence 238, App
17	1922.5	71.4	482	12 US-10-425-114-52351	Sequence 52351, A
18	1890.5	70.2	523	12 US-10-183-687-258	Sequence 258, App
19	1881.5	69.9	514	12 US-10-183-687-408	Sequence 408, App
20	1748	64.9	330	12 US-10-425-114-47097	Sequence 47097, A
21	1654	61.4	515	12 US-10-424-599-180405	Sequence 180405, A
22	1462.5	54.3	356	12 US-10-424-599-181075	Sequence 181075, A
23	1462.5	54.3	552	9 US-09-824-735-4	Sequence 4, Appl1
24	1013.5	37.6	633	9 US-09-824-735-3	Sequence 3, Appl1
25	1013.5	37.6	633	9 US-09-801-368-338	Sequence 338, App
26	1013.5	37.6	633	15 US-10-369-493-1696	Sequence 1696, App
27	898	33.3	679	15 US-10-369-493-22764	Sequence 22764, A
28	894.5	33.2	622	15 US-10-369-493-5806	Sequence 5806, App
29	881.5	32.7	420	15 US-10-369-493-3864	Sequence 3864, App
30	802	29.8	438	15 US-10-437-963-196592	Sequence 196592, A
31	758	28.1	268	15 US-10-369-493-13344	Sequence 13344, A
32	749	27.8	783	9 US-09-815-915-2	Sequence 2, Appl1
33	749	27.8	783	14 US-10-393-316-2	Sequence 2, Appl1
34	749	27.8	826	12 US-10-425-114-54182	Sequence 54182, A
35	746	27.7	744	9 US-09-919-585-3	Sequence 3, Appl1
36	745	27.7	729	14 US-10-142-356-11	Sequence 11, Appl1
37	745	27.7	729	14 US-10-195-101-33	Sequence 33, Appl1
38	745	27.7	729	14 US-10-161-565-26	Sequence 26, Appl1
39	737.5	27.4	639	12 US-10-016-248-71	Sequence 71, Appl1
40	737.5	27.4	639	12 US-10-016-248-72	Sequence 72, Appl1
41	737.5	27.4	688	16 US-10-376-645-8	Sequence 8, Appl1
42	737.5	27.4	703	12 US-10-016-248-70	Sequence 70, Appl1
43	737.5	27.4	752	9 US-09-835-081-2	Sequence 2, Appl1
44	737.5	27.4	752	15 US-10-258-106-16	Sequence 16, Appl1
45	737.5	27.4	752	16 US-10-276-645-7	Sequence 7, Appl1

ALIGNMENTS

RESULT 1
US-10-183-687-236
Sequence 236, Application US/10183687
Publication No. US20030204870A1
GENERAL INFORMATION:
APPLICANT: Allen, Steve
APPLICANT: Allen, William B.
APPLICANT: Cahoon, Rebecca
APPLICANT: Epelbaum, Sabine
APPLICANT: Famodu, Omolayo O.
APPLICANT: Harvell, Leslie T.
APPLICANT: Jones, Todd
APPLICANT: Kinney, Tony
APPLICANT: Klein, Ted
APPLICANT: Li, Changliang
APPLICANT: Oliveira, Igor Cunha
APPLICANT: Sakai, Hajime
APPLICANT: Shen, Bo
APPLICANT: Tarczyński, Mitchell C.
TITLE OF INVENTION: Alteration Of Oil Traits In Plants
FILE REFERENCE: BRL458 US MA
CURRENT APPLICATION NUMBER: US/10/183,687
CURRENT FILING DATE: 2002-06-27
PRIOR APPLICATION NUMBER: 60/301,913
PRIOR FILING DATE: 2001-06-29
NUMBER OF SEQ ID NOS: 532
SOFTWARE: Microsoft Office 97
SEQ ID NO 236
LENGTH: 509
TYPE: PRT
ORGANISM: Zea mays
US-10-183-687-236

Query Match 100.0%; Score 2693; DB 12; Length 509;
Best local Similarity 100.0%; Pred. No. 2.9e-227;
Matches 509; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
1 MDSSKSGSHSEALRNYNLGRTIGIGTFGKYLAEHLTGHRVAIKINCRQNMNEMEE 60

Db 1 MDGSSKSGHSEALRNVLGRTLGIGTGKVKIAEHKLTGHRVAIKIINCORNMEMEE 60
Qy 61 KAKEFKLKLFIHPHIIIRLYEVYTPPDIVVMEYCKYGLFPIYVEKGLQDEARRI 120
Db 61 KAKEFKLKLFIHPHIIIRLYEVYTPPDIVVMEYCKYGLFPIYVEKGLQDEARRI 120
Qy 121 FOQIISGEVYCHRMNVVHRDLKPENLILDSKYNVKLADFGLSNVMDGHFLKTCGSPNY 180
Db 121 FOQIISGEVYCHRMNVVHRDLKPENLILDSKYNVKLADFGLSNVMDGHFLKTCGSPNY 180
Qy 181 AAEVVISGKLYAGEVDVWSCGVIYLLALCGTLPEPDENIPNLFKKIKGIIYTLPSHLA 240
Db 181 AAEVVISGKLYAGEVDVWSCGVIYLLALCGTLPEPDENIPNLFKKIKGIIYTLPSHLA 240
Qy 241 LARDLIPRLVVEPMKRTITREIHEHWFQIRLPRYLAAPPDPTQAKMIDEDTLRDV 300
Db 241 LARDLIPRLVVEPMKRTITREIHEHWFQIRLPRYLAAPPDPTQAKMIDEDTLRDV 300
Qy 301 NMGFKNHVCESLCSRLQNEATVAYLLDNRFRATSGYLADYQESMDRLNQLASSES 360
Db 301 NMGFKNHVCESLCSRLQNEATVAYLLDNRFRATSGYLADYQESMDRLNQLASSES 360
Qy 361 SSSGTRNVPGSSDPHSSGLRPYYPVERKVALGQSRAPREIWEVLKALQELNVRMK 420
Db 361 SSSGTRNVPGSSDPHSSGLRPYYPVERKVALGQSRAPREIWEVLKALQELNVRMK 420
Qy 421 NGHNVKRCMCPGPEVNDTLDAASNFLGDSITMDNDANGRLPTVIKFEFOLYKTKDK 480
Db 421 NGHNVKRCMCPGPEVNDTLDAASNFLGDSITMDNDANGRLPTVIKFEFOLYKTKDK 480
Qy 481 YLLDMQRTGTPQLFLDFCAAFITKLRVL 509
Db 481 YLLDMQRTGTPQLFLDFCAAFITKLRVL 509

RESULT 2
US-10-425-114-58891
; Sequence 58891, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jindong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Tongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 58891
; LENGTH: 513
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: 700473306_FLI.pep
US-10-425-114-58891

Query Match 100.0%; Score 2693; DB 12; Length 513;
Best Local Similarity 100.0%; Pred. No. 3e-227;
Matches 509; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 181 AAEVVISGKLYAGEVDVWSCGVIYLLALCGTLPEPDENIPNLFKKIKGIIYTLPSHLA 240
Db 185 AAEVVISGKLYAGEVDVWSCGVIYLLALCGTLPEPDENIPNLFKKIKGIIYTLPSHLA 244
Qy 241 LARDLIPRLVVEPMKRTITREIHEHWFQIRLPRYLAAPPDPTQAKMIDEDTLRDV 300
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Db 305 NMGFKNHVCESLCSRLQNEATVAYLLDNRFRATSGYLADYQESMDRLNQLASSES 364
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Db 365 SSSGTRNVPGSSDPHSSGLRPYYPVERKVALGQSRAPREIWEVLKALQELNVRMK 424
Qy 421 NGHNVKRCMCPGPEVNDTLDAASNFLGDSITMDNDANGRLPTVIKFEFOLYKTKDK 480
Db 425 NGHNVKRCMCPGPEVNDTLDAASNFLGDSITMDNDANGRLPTVIKFEFOLYKTKDK 484
Qy 481 YLLDMQRTGTPQLFLDFCAAFITKLRVL 509
Db 485 YLLDMQRTGTPQLFLDFCAAFITKLRVL 513

RESULT 3
US-10-183-687-401
; Sequence 401, Application US/10183687
; Publication No. US20030204870A1
; GENERAL INFORMATION:
; APPLICANT: Allen, Steve
; APPLICANT: Allen, William B.
; APPLICANT: Cahoon, Rebecca
; APPLICANT: Epelbaum, Sabine
; APPLICANT: Fomodu, Omolayo O.
; APPLICANT: Harwell, Leslie T.
; APPLICANT: Jones, Todd
; APPLICANT: Kinney, Tony
; APPLICANT: Klein, Ted
; APPLICANT: Li, Changjiang
; APPLICANT: Oliveira, Igor Cunha
; APPLICANT: Sakai, Hajime
; APPLICANT: Shen, Bo
; APPLICANT: Tarczyński, Mitchell C.
; TITLE OF INVENTION: Alteration of Oil Traits in Plants
; FILE REFERENCE: B81458 US NA
; CURRENT APPLICATION NUMBER: US/10/183,687
; CURRENT FILING DATE: 2002-06-27
; PRIOR APPLICATION NUMBER: 60/301,913
; PRIOR FILING DATE: 2001-06-29
; NUMBER OF SEQ ID NOS: 532
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 401
; LENGTH: 509
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION:
; OTHER INFORMATION: gi 4107001
US-10-183-687-401

Query Match 89.9%; Score 2422; DB 12; Length 509;
Best Local Similarity 88.6%; Pred. No. 1.7e-203;
Matches 451; Conservative 35; Mismatches 23; Indels 0; Gaps 0;

Qy 1 MDGSSKSGHSEALRNVLGRTLGIGTGKVKIAEHKLTGHRVAIKIINCORNMEMEE 60
Db 5 MDGSSKSGHSEALRNVLGRTLGIGTGKVKIAEHKLTGHRVAIKIINCORNMEMEE 64
Qy 61 KAKEFKLKLFIHPHIIIRLYEVYTPPDIVVMEYCKYGLFPIYVEKGLQDEARRI 120
Db 65 KAKEFKLKLFIHPHIIIRLYEVYTPPDIVVMEYCKYGLFPIYVEKGLQDEARRI 124

Qy 1 MDGSSKSGHSEALRNVLGRTLGIGTGKVKIAEHKLTGHRVAIKIINCORNMEMEE 60
Db 1 MEGNARCGHSEALKONVNLGRTLGIGTGKVKIAEHKLTGHRVAIKIINCORNMEMEE 60

```
Qy 61 KAKKEFKILKLFIPHIIRLYEVIYTPDIYVMEYCKGELFDYIVKGRLODEARRI 120
Db 61 KAKKEIKILRLFIPIHRIIRLYEVIYTPDIYVMEYCKGELFDYIVKGRLODEARRI 120
Qy 121 FQOIISGVEYCHRMVYVHRDLKPENLILDSKYNVKLADFGLSNVMHGHFLKTS CGSPNY 180
Db 121 FQOIISGVEYCHRMVYVHRDLKPENLILDSKYNVKLADFGLSNVMHGHFLKTS CGSPNY 180
Qy 181 AAPVISGKLYAGBEVDVMSCGVILYALCGTLPPDDENIPNLFKKIKGSIYTLPSHLSA 240
Db 181 AAPVISGKLYAGBEVDVMSCGVILYALCGTLPPDDENIPNLFKKIKGSIYTLPSHLSA 240
Qy 241 LARLIPRMIVPEMKRITITREIREHOWFOIRLPRYLAAPPPTDQAOKMIDEDTLDDVV 300
Db 241 LARLIPRMIVPEMKRITITREIREHOWFOIRLPRYLAAPPPTDQAOKMIDEDTLDDVV 300
Qy 301 NMGNKXHVCESLCSRLONEATVAYYLLDNRFRAATSGYLADYQESMDRNLNOLASSES 360
Db 301 NLGYEKHVCESLNRLONEATVAYYLLDNRFRAATSGYLADYQESLERNLNFASSES 360
Qy 361 SSSGTRNVPGSSDPHSGRLPRYPYVERKVALGLQSRAPREIWEVLKALQELNVKMK 420
Db 361 ASSNTRHYLPSSSDPHASGLRPHYVERKVALGLQSRAPREIWEVLKALQELNVKMK 420
Qy 421 NGHYNVKCRMCPPPEVNDTLSDASNFLGDSITMDNDANGRLPTVIKEEFOLYKTDK 480
Db 421 NGQYNMKCRMSVGPQATMDLVNHSFVDSIIMDNGDVNGRLPAVTKFBIQLYKSRDEK 480
Qy 481 YLDMQRTVGQQLFLDFCAAFITKLRVL 509
Db 481 YLDMQRTVGQQLFLDFCAAFITKLRVL 509

RESULT 4
US-10-437-963-152150
; Sequence 152150, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437, 963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 152150
; LENGTH: 509
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_52229C.1.pcp
US-10-437-963-152150

Query Match 89.9%; Score 2422; DB 16; Length 509;
Best Local Similarity 88.6%; Pred. No. 1.7e-203;
Matches 451; Conservative 35; Mismatches 23; Indels 0; Gaps 0;
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```
Qy 1 MDGSSKSGHSEALRNVLGRTLGIFGKVIKIAEHKLTGHRVAIKIINCROMNMEME 60
Db 1 MEGNARGGHSEALKNVNLGRTLGISGKVIKIAEHKLTGHRVAIKIINRQRMNMEME 60
Qy 61 KAKKEFKILKLFIPHIIRLYEVIYTPDIYVMEYCKGELFDYIVKGRLODEARRI 120
Db 61 KAKKEIKILRLFIPIHRIIRLYEVIYTPDIYVMEYCKGELFDYIVKGRLODEARRI 120
Qy 121 FQOIISGVEYCHRMVYVHRDLKPENLILDSKYNVKLADFGLSNVMHGHFLKTS CGSPNY 180
Db 121 FQOIISGVEYCHRMVYVHRDLKPENLILDSKYNVKLADFGLSNVMHGHFLKTS CGSPNY 180
Qy 181 AAPVISGKLYAGBEVDVMSCGVILYALCGTLPPDDENIPNLFKKIKGSIYTLPSHLSA 240
Db 181 AAPVISGKLYAGBEVDVMSCGVILYALCGTLPPDDENIPNLFKKIKGSIYTLPSHLSA 240
Qy 241 LARLIPRMIVPEMKRITITREIREHOWFOIRLPRYLAAPPPTDQAOKMIDEDTLDDVV 300
Db 241 LARLIPRMIVPEMKRITITREIREHOWFOIRLPRYLAAPPPTDQAOKMIDEDTLDDVV 300
Qy 301 NMGNKXHVCESLCSRLONEATVAYYLLDNRFRAATSGYLADYQESMDRNLNOLASSES 360
Db 301 NLGYEKHVCESLNRLONEATVAYYLLDNRFRAATSGYLADYQESLERNLNFASSES 360
Qy 361 SSSGTRNVPGSSDPHSGRLPRYPYVERKVALGLQSRAPREIWEVLKALQELNVKMK 420
Db 361 ASSNTRHYLPSSSDPHASGLRPHYVERKVALGLQSRAPREIWEVLKALQELNVKMK 420
Qy 421 NGHYNVKCRMCPPPEVNDTLSDASNFLGDSITMDNDANGRLPTVIKEEFOLYKTDK 480
Db 421 NGQYNMKCRMSVGPQATMDLVNHSFVDSIIMDNGDVNGRLPAVTKFBIQLYKSRDEK 480
Qy 481 YLDMQRTVGQQLFLDFCAAFITKLRVL 509
Db 481 YLDMQRTVGQQLFLDFCAAFITKLRVL 509
```

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Qy 121 FQOIISGVEYCHRMVYVHRDLKPENLILDSKYNVKLADFGLSNVMHGHFLKTS CGSPNY 180
Db 121 FQOIISGVEYCHRMVYVHRDLKPENLILDSKYNVKLADFGLSNVMHGHFLKTS CGSPNY 180
Qy 181 AAPVISGKLYAGBEVDVMSCGVILYALCGTLPPDDENIPNLFKKIKGSIYTLPSHLSA 240
Db 181 AAPVISGKLYAGBEVDVMSCGVILYALCGTLPPDDENIPNLFKKIKGSIYTLPSHLSA 240
Qy 241 LARLIPRMIVPEMKRITITREIREHOWFOIRLPRYLAAPPPTDQAOKMIDEDTLDDVV 300
Db 241 LARLIPRMIVPEMKRITITREIREHOWFOIRLPRYLAAPPPTDQAOKMIDEDTLDDVV 300
Qy 301 NMGNKXHVCESLCSRLONEATVAYYLLDNRFRAATSGYLADYQESMDRNLNOLASSES 360
Db 301 NLGYEKHVCESLNRLONEATVAYYLLDNRFRAATSGYLADYQESLERNLNFASSES 360
Qy 361 SSSGTRNVPGSSDPHSGRLPRYPYVERKVALGLQSRAPREIWEVLKALQELNVKMK 420
Db 361 ASSNTRHYLPSSSDPHASGLRPHYVERKVALGLQSRAPREIWEVLKALQELNVKMK 420
Qy 421 NGHYNVKCRMCPPPEVNDTLSDASNFLGDSITMDNDANGRLPTVIKEEFOLYKTDK 480
Db 421 NGQYNMKCRMSVGPQATMDLVNHSFVDSIIMDNGDVNGRLPAVTKFBIQLYKSRDEK 480
Qy 481 YLDMQRTVGQQLFLDFCAAFITKLRVL 509
Db 481 YLDMQRTVGQQLFLDFCAAFITKLRVL 509

RESULT 5
US-10-437-963-152149
; Sequence 152149, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437, 963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 152149
; LENGTH: 508
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_52228C.1.pcp
US-10-437-963-152149

Query Match 89.5%; Score 2411.5; DB 16; Length 508;
Best Local Similarity 89.0%; Pred. No. 1.4e-202;
Matches 453; Conservative 29; Mismatches 26; Indels 1; Gaps 1;
```

```
Qy 1 MDGSSKSGHSEALRNVLGRTLGIFGKVIKIAEHKLTGHRVAIKIINCROMNMEME 60
Db 1 MDGNAKGGHSEALKVNLGRTLGISGKVIKIAEHKLTGHRVAIKIINRQRMNMEME 60
Qy 61 KAKKEFKILKLFIPHIIRLYEVIYTPDIYVMEYCKGELFDYIVKGRLODEARRI 120
Db 61 KAKKEIKILRLFIPIHRIIRLYEVIYTPDIYVMEYCKGELFDYIVKGRLODEARRI 120
Qy 121 FQOIISGVEYCHRMVYVHRDLKPENLILDSKYNVKLADFGLSNVMHGHFLKTS CGSPNY 180
Db 121 FQOIISGVEYCHRMVYVHRDLKPENLILDSKYNVKLADFGLSNVMHGHFLKTS CGSPNY 180
Qy 181 AAPVISGKLYAGBEVDVMSCGVILYALCGTLPPDDENIPNLFKKIKGSIYTLPSHLSA 240
Db 181 AAPVISGKLYAGBEVDVMSCGVILYALCGTLPPDDENIPNLFKKIKGSIYTLPSHLSA 240
```

Db 181 AAEVISGKLYAGEVDVWSCGVLVLLCGTLPEFDENIPNLFKKIKGGIYTLPSHLSA 240
Qy 241 LARDLIPRMLVVEPMKRTITREIREHOFQIRLPRYLAAPPDDTQAQKMIDEDTLADV 300
Db 241 LARDLIPRMLVVDPMKRTITREIREHOFQIRLPRYLAAPPDDTQAQKMIDEDTLADV 300
Qy 301 NMGNKHNVCESLCSRLQNEATVAYLLLDNRFPATSGYLADYQESMDRLNQLASSES 360
Db 301 NLGCKDHVCESLNRLQNEATVAYLLLDNRFPATSGYLADYQESMDRLNQLASSES 360
Qy 361 SSSGTRNVYVGGSSDPHSSGRLPYYPVERKVALGQSRAPREIVEYLKALQELANVWK 420
Db 361 ASSNTRHYLPSSDPHSSGRLPYYPVERKVALGQSRAPREIVEYLKALQELANVWK 420
Qy 421 NGHNVKCRMCPCPEPEVNDTLDASNSFLGDSITMDNDANGRLPTVYKFEQLYKTDDK 480
Db 421 NGQYNNKCRMSVG-TQATMDLDVNNSFVDDSIIMDNGDVNGRLPAVYKFEIQLYKTRDEK 479
Qy 481 YLLDMQRTVGPQLLFLDFCAFLTKLRYL 509
Db 480 YLLDMQRTVGPQLLFLDFCAFLTKLRYL 508

RESULT 6
US-10-425-114-49946
; Sequence 49946, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jindong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(5313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 49946
; LENGTH: 525
; TYPE: PRT
; ORGANISM: Oryza sativa nipponbare
; OTHER INFORMATION: Clone ID: LIB3477-009-G7_FLI.pcp
; US-10-425-114-49946

Query Match 89.5%; Score 2411.5; DB 12; Length 525;
Best Local Similarity 89.0%; Pred. No. 1.5e-202;
Matches 453; Conservative 29; Mismatches 26; Indels 1; Gaps 1;
Qy 1 MDGSSKSGSHSEALRNVLGRTLGIGFGKVIKAEHKL TGHRAVAKIINCRQNNMEMEE 60
Db 18 MDGNAKGGSHSEALKNVNLGRTLGIGSGKVIKAEHKL TGHRAVAKIINCRQNNMEMEE 77
Qy 61 KAKREFKILKLFHPHRIIRLYEVITYPTDIYVMEYCKYGELEFDYIYEKRLQDEARRI 120
Db 78 KAKREIKILRLFIHPHRIIRLYEVITYPTDIYVMEYCKYGELEFDYIYEKRLQDEARRI 137
Qy 121 FQOIIISGEVYCHRNVAHRDLKPENLILDSKYNVKLA DFGLSNVMDHGHFLKTS CGSPNY 180
Db 138 FQOIIISGEVYCHRNVAHRDLKPENLILDSKYNVKLA DFGLSNVMDHGHFLKTS CGSPNY 197
Qy 181 AAEVISGKLYAGEVDVWSCGVLVLLCGTLPEFDENIPNLFKKIKGGIYTLPSHLSA 240
Db 198 AAEVISGKLYAGEVDVWSCGVLVLLCGTLPEFDENIPNLFKKIKGGIYTLPSHLSA 257
Qy 241 LARDLIPRMLVVEPMKRTITREIREHOFQIRLPRYLAAPPDDTQAQKMIDEDTLADV 300
Db 258 LARDLIPRMLVVDPMKRTITREIREHOFQIRLPRYLAAPPDDTQAQKMIDEDTLADV 317

Qy 301 NMGNKHNVCESLCSRLQNEATVAYLLLDNRFPATSGYLADYQESMDRLNQLASSES 360
Db 318 NLGCKDHVCESLNRLQNEATVAYLLLDNRFPATSGYLADYQESMDRLNQLASSES 377
Qy 361 SSSGTRNVYVGGSSDPHSSGRLPYYPVERKVALGQSRAPREIVEYLKALQELANVWK 420
Db 378 ASSNTRHYLPSSDPHSSGRLPYYPVERKVALGQSRAPREIVEYLKALQELANVWK 437
Qy 421 NGHNVKCRMCPCPEPEVNDTLDASNSFLGDSITMDNDANGRLPTVYKFEQLYKTDDK 480
Db 438 NGQYNNKCRMSVG-TQATMDLDVNNSFVDDSIIMDNGDVNGRLPAVYKFEIQLYKTRDEK 496
Qy 481 YLLDMQRTVGPQLLFLDFCAFLTKLRYL 509
Db 497 YLLDMQRTVGPQLLFLDFCAFLTKLRYL 525

RESULT 7
US-10-183-687-256
; Sequence 256, Application US/10183687
; Publication No. US20030204870A1
; GENERAL INFORMATION:
; APPLICANT: Allen, Steve
; APPLICANT: Allen, William B.
; APPLICANT: Cahoon, Rebecca
; APPLICANT: Epelbaum, Sabine
; APPLICANT: Ramodu, Omolayo O.
; APPLICANT: Harvell, Leslie T.
; APPLICANT: Jones, Todd
; APPLICANT: Kinney, Tony
; APPLICANT: Klein, Ted
; APPLICANT: Li, Changliang
; APPLICANT: Oliveira, Igor Cunha
; APPLICANT: Sakai, Hajime
; APPLICANT: Shen, Bo
; APPLICANT: Tarczyński, Mitchell C.
; TITLE OF INVENTION: Alteration Of Oil Traits In Plants
; FILE REFERENCE: BB1458 US NA
; CURRENT APPLICATION NUMBER: US/10/183,687
; CURRENT FILING DATE: 2002-06-27
; PRIOR APPLICATION NUMBER: 60/301,913
; PRIOR FILING DATE: 2001-06-29
; NUMBER OF SEQ ID NOS: 532
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 256
; LENGTH: 531
; TYPE: PRT
; ORGANISM: Triticum aestivum
; US-10-183-687-256

Query Match 88.3%; Score 2378; DB 12; Length 531;
Best Local Similarity 86.8%; Pred. No. 1.3e-199;
Matches 442; Conservative 34; Mismatches 33; Indels 0; Gaps 0;
Qy 1 MDGSSKSGSHSEALRNVLGRTLGIGFGKVIKAEHKL TGHRAVAKIINCRQNNMEMEE 60
Db 23 MGNTRCGGSHSDALKNVNLGRTLGIGFGKVIKAEHKGTHKAVAKIINCRQNNMEMEE 82
Qy 61 KAKREFKILKLFHPHRIIRLYEVITYPTDIYVMEYCKYGELEFDYIYEKRLQDEARRI 120
Db 83 KAKREIKILRLFIHPHRIIRLYEVITYPTDIYVMEYCKYGELEFDYIYEKRLQDEARRI 142
Qy 121 FQOIIISGEVYCHRNVAHRDLKPENLILDSKYNVKLA DFGLSNVMDHGHFLKTS CGSPNY 180
Db 143 FQOIIISGEVYCHRNVAHRDLKPENLILDSKYNVKLA DFGLSNVMDHGHFLKTS CGSPNY 202
Qy 181 AAEVISGKLYAGEVDVWSCGVLVLLCGTLPEFDENIPNLFKKIKGGIYTLPSHLSA 240
Db 203 AAEVISGKLYAGEVDVWSCGVLVLLCGTLPEFDENIPNLFKKIKGGIYTLPSHLSA 262
Qy 241 LARDLIPRMLVVEPMKRTITREIREHOFQIRLPRYLAAPPDDTQAQKMIDEDTLADV 300
Db 263 LARDLIPRMLVVDPMKRTITREIREHOFQIRLPRYLAAPPDDTQAQKMIDEDTLADV 322


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Qy 301 NMGEFNKHCESLCSRLQNEATVAYLLDNRFRATSGYLQADYQESMDRNLQJLASS 360
Db 298 NMGEFNKHCESLCSRLQNEATVAYLLDNRFRATSGYLQADYQESMDRNLQJLASS 357
Qy 361 SSSGTRNVPGSSDPHSSGRLPYYPVERKMGALQSRAPREIWEVVKALQELNVW 420
Db 358 PMSATDRHOGHMSPGFGLRHFAADRKMALGLQSRAPREIWEVVKALQELNVW 417
Qy 421 NGHNVVCRWCPGPEVNDLTDANSFLGDSITMDNDANRLPTVYKFEFOLKTKDOK 480
Db 418 IGHNMKCRWSPSPSHESMNNHNGFASALILETDSKSTHTV-KPEIQLYKTDK 476
Qy 481 YLDMORVTPGQLFLDFCAAFITKLRVL 509
Db 477 YLDDLQVSGPQLFLDFCAAFITKLRVL 505

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RESULT 10

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US-10-183-687-248
; Sequence 248, Application US/10183687
; Publication No. US20030204870A1
; GENERAL INFORMATION:

```

```

; APPLICANT: Allen, Steve
; APPLICANT: Allen, William B.
; APPLICANT: Cahoon, Rebecca
; APPLICANT: Epelbaum, Sabine
; APPLICANT: Famodu, Omolayo O.
; APPLICANT: Harvell, Leslie T.
; APPLICANT: Jones, Todd
; APPLICANT: Kinney, Tony
; APPLICANT: Klein, Ted
; APPLICANT: Li, Changjiang
; APPLICANT: Oliveira, Igor Cunha
; APPLICANT: Sakai, Hajime
; APPLICANT: Shen, Bo
; APPLICANT: Tarczyński, Mitchell C.
; TITLE OF INVENTION: Alteration Of Oil Traits In Plants
; FILE REFERENCE: B01458 US NA
; CURRENT APPLICATION NUMBER: US/10/183,687
; CURRENT FILING DATE: 2002-06-27
; PRIOR APPLICATION NUMBER: 60/301,913
; PRIOR FILING DATE: 2001-06-29
; NUMBER OF SEQ ID NOS: 532
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 248
; LENGTH: 514
; TYPE: PRT
; ORGANISM: Glycine max
; US-10-183-687-248

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Query Match 73.3%; Score 1974.5; DB 12; Length 514;
Best Local Similarity 74.0%; Pred. No. 3e-164;
Matches 382; Conservative 49; Mismatches 76; Indels 9; Gaps 3;

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```

Qy 1 MDGSS--KSGSHSALRNYNLGRITGTFGKVIKAEHLTGRHVAIKIINCROMNMEM 58
Db 1 MDGAGAGGAGLMDLFLPYKIGKTLGSGFGKVIKAEHLTGRHVAIKIINCROMNMEM 60
Qy 59 EEKAKREKIKLFIHPHILRYEVIYTPDIYVMEYCKGELFDYIVKGRLOEDBAR 118
Db 61 EEKARREKIKLFIHPHILRYEVIYTPDIYVMEYCKGELFDYIVKGRLOEDBAR 120
Qy 119 RIPOIISGVEYCHRNWVHBDLPENLLDSKXNVKADFGLSNWMHGHFLKTSQSP 178
Db 121 NFPOIISGVEYCHRNWVHBDLPENLLDSKXNVKADFGLSNWMHGHFLKTSQSP 180
Qy 179 NYAAPVVISGLVYAGPEVWVSCGVITLALCGTLPPDENIPNLFFKIKIGIYTLPSHL 238
Db 181 NYAAPVVISGLVYAGPEVWVSCGVITLALCGTLPPDENIPNLFFKIKIGIYTLPSHL 240
Qy 239 SALARDLIPMLVVEPMKRTITREIRHWFQIRLPRYLAVPPDTTQOAMIDEDTLRD 298

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Db 241 SPGARDLIPMLVVEPMKRTITREIRHWFQIRLPRYLAVPPDTTQOAKKIDEEILOE 300
Qy 299 VVNMGEFNKHCESLCSRLQNEATVAYLLDNRFRATSGYLQADYQESMDRNLQJLASS 358
Db 301 VVNMGEFNKHCESLCSRLQNEATVAYLLDNRFRATSGYLQADYQESMDRNLQJLASS 360
Qy 359 SSSGTRNVPGSSDPHSSGRLPYYPVERKMGALQSRAPREIWEVVKALQELNVW 418
Db 361 ELASVVGNFPGMEYVGVSGRQGFVERKMGALQSRAPREIWEVVKALQELNVW 420
Qy 419 KRGHNVVCRWCPGPEVNDLTDANSFLGDSITMDNDANRLPTVYKFEFOLKTKDOK 473
Db 421 KGI GHVNMKCRWAGIPGHHEGVNANNVSHNHFGDSNLTENDAVS--TSNVKCEVOL 478
Qy 474 YKTKDDEYLDLMORVTPGQLFLDFCAAFITKLRVL 509
Db 479 YKTRBKYLDDLQVSGPQLFLDFCAAFITKLRVL 514

```

RESULT 11

```

US-10-183-687-407
; Sequence 407, Application US/10183687
; Publication No. US20030204870A1
; GENERAL INFORMATION:

```

```

; APPLICANT: Allen, Steve
; APPLICANT: Allen, William B.
; APPLICANT: Cahoon, Rebecca
; APPLICANT: Epelbaum, Sabine
; APPLICANT: Famodu, Omolayo O.
; APPLICANT: Harvell, Leslie T.
; APPLICANT: Jones, Todd
; APPLICANT: Kinney, Tony
; APPLICANT: Klein, Ted
; APPLICANT: Li, Changjiang
; APPLICANT: Oliveira, Igor Cunha
; APPLICANT: Sakai, Hajime
; APPLICANT: Shen, Bo
; APPLICANT: Tarczyński, Mitchell C.
; TITLE OF INVENTION: Alteration Of Oil Traits In Plants
; FILE REFERENCE: B01458 US NA
; CURRENT APPLICATION NUMBER: US/10/183,687
; CURRENT FILING DATE: 2002-06-27
; PRIOR APPLICATION NUMBER: 60/301,913
; PRIOR FILING DATE: 2001-06-29
; NUMBER OF SEQ ID NOS: 532
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 407
; LENGTH: 504
; TYPE: PRT
; ORGANISM: Cucumis sativus
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION:
; OTHER INFORMATION: gi 1743009
; US-10-183-687-407

```

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Query Match 72.9%; Score 1963; DB 12; Length 504;
Best Local Similarity 74.8%; Pred. No. 3e-163;
Matches 374; Conservative 53; Mismatches 65; Indels 8; Gaps 4;

```

```

Qy 16 NYNIGRTLGITGFGKVIKAEHLTGRHVAIKIINCROMNMEMEEKAKREKIKLFIHP 75
Db 7 NYKLGITGIGSGFGKVIKAEHLTGRHVAIKIINCROMNMEMEEKAKREKIKLFIHP 66
Qy 76 HIIRLYEVITTPDIYVMEYCKGELFDYIVKGRLOEDBARIPQIISGVEYCHRM 135
Db 67 HIIRLYEVITTPDIYVMEYCKGELFDYIVKGRLOEDBARIPQIISGVEYCHRM 126
Qy 136 VVNRDLKPEMLLDSKXNVKADFGLSNWMHGHFLKTSQSPNYAAPVVISGLVYAGPE 195
Db 127 VVNRDLKPEMLLDSKXNVKADFGLSNWMHGHFLKTSQSPNYAAPVVISGLVYAGPE 186
Qy 196 VDVWVSGVITLALCGTLPPDENIPNLFFKIKIGIYTLPSHLALARDLIPMLVVEPM 255

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Db 187 VDWMSCGILYVALLCGTLPEDDENIPNLFKIKGITYLPSHLSGARELPSMLVVDPM 246
Qy 256 KRITREIREHOMFOIRLPRYLAVPPDDTQOAKMIDEDTLADVNMGNKKNHVESLCS 315
Db 247 KRITPEIRQHFHFAHLPRLYLAAPPDDTMOAKKIDEDTLQSVKMGDRQLVESLBN 306
Qy 316 RLQNEATVAYVYLLDNRFATSGYLADVQESMDRNLQNLASSSESSGSTRYVVGSSDP 375
Db 307 RLQNEATVAYVYLLDNRFVSSGILGAEFOETMETGPNRHPSDPTNPAVGHRLPGYNDY 366
Qy 376 HSSGLRPYVVERKVALGQSRAPREIWEVYKALQELINVMKXGNHNVKCRWCPGP 435
Db 367 QGMGRAPQFVYERKVALGQSRAPREIWEVYKALRELINVMKKGHYNMKCRWLPGP 426
Qy 436 -----EVNDTLASNSFLGCD-STINDNDANGRLPTVYKEFQLYKTADKTLDMQY 489
Db 427 GHHEGMINPVH-SNHYFGDKSTIENDGV-VKSPNVIKFEVQLYKTREKYLTLDRVQ 484
Qy 490 GPQLFLDPCAFLLTKRLV 509
Db 485 GPQLFLDPCAFLLTKRLV 504

```

RESULT 12

```

US-10-183-687-240
; Sequence 240, Application US/10183687
; Publication No. US20030204870A1
; GENERAL INFORMATION:
; APPLICANT: Allen, Steve
; APPLICANT: Allen, William B.
; APPLICANT: Cahoon, Rebecca
; APPLICANT: Epelbaum, Sabine
; APPLICANT: Famodu, Omolayo O.
; APPLICANT: Harvell, Leslie T.
; APPLICANT: Kinney, Tony
; APPLICANT: Klein, Ted
; APPLICANT: Li, Changjiang
; APPLICANT: Oliveira, Igor Cunha
; APPLICANT: Sakai, Hajime
; APPLICANT: Shen, Bo
; APPLICANT: Tarczyński, Mitchell C.
; TITLE OF INVENTION: Alteration Of Oil Traits In Plants
; FILE REFERENCE: B01458 US NA
; CURRENT FILING DATE: 2002-06-27
; PRIOR APPLICATION NUMBER: 60/301,913
; PRIOR FILING DATE: 2001-06-29
; NUMBER OF SEQ ID NOS: 532
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 240
; LENGTH: 570
; TYPE: PRT
; ORGANISM: Zea mays
US-10-183-687-240

```

Query Match 72.7%; Score 1958; DB 12; Length 570;
 Best Local Similarity 74.8%; Pred. No. 9.7e-163;
 Matches 382; Conservative 48; Mismatches 67; Indels 14; Gaps 6;

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Qy 1 MDSSKSGHSEALRNVLGRTIGTGGKVKIAEHKLTGHRVAKIINCQNMNME 60
Db 72 MEGAGK--DGNPLNRYIGKTLGSGFGKVIASHISTGHVAKILNRKIKGEMEE 128
Qy 61 KAKEEFILKLFIPHIIRLYEVYTPDIYVWMEYCKGELFDYIVKGRLODEAR 120
Db 129 KVKREIKILRLFPMPHIIRLYEVIDTPADIVWMEYVCGELFDYIVKGRLODEAR 188
Qy 121 FOQIISGVEYCHRMVVRDLKPENLILDSKYNVCLADFGLSNVMHDGFLKTS 180
Db 189 FOQIISGVEYCHRMVVRDLKPENLILDSKYNVCLADFGLSNVMHDGFLKTS 248

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Qy 181 AAEVISGKLYAGPEVDVWSCGVLVALLCGTLPEDDENIPNLFKIKGITYLPSHLSA 240
Db 249 AAEVISGKLYAGPEVDVWSCGVLVALLCGTLPEDDENIPNLFKIKGITYLPSHLSG 308
Qy 241 LARDLIPMLVVEPMKRTITREIREHOMFOIRLPRYLAVPPDDTQOAKMIDEDTL 300
Db 309 AARDLIPMLVVDPMKRTITREIREHOMFOIRLPRYLAVPPDDTQOAKMIDEDTL 368
Qy 301 NMGFKNHVSLSCLRQNEATVAYVYLLDNRFATSGYLADVQESMDRNLQNLASSE- 359
Db 369 GMDYDKNLVBSIQRLQNEATVAYVYLLDNRLFTTSGYLAECQEAQSSFSNLSYET 428
Qy 360 -SSSGSTRNYPVSSDPHSSGLRPYVYERKVALGQSRAPREIWEVYKALQELINVM 418
Db 429 PSSARGNQOIFMES--PVGLRPHLPARKMALGQSRAPKEMSVVYKALQELINVM 485
Qy 419 KKNGHYVNCWCPGPEVNDTLASNSFLGDSSTINDNDANGRLPTVYKEFQLYKT 478
Db 486 KKGHYNMKCRWSPGFA--QIHNNHVSAGS--IETDSLSERL-SLIKFEIDLYKTRD 539
Qy 479 DKYLLDMQRYVGPQLFLDPCAFLLTKRLV 509
Db 540 EKYLLDMQRYVGPQLFLDPCAFLLTKRLV 570

```

RESULT 13

```

US-10-425-114-63632
; Sequence 63632, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(5313)B
; CURRENT FILING DATE: US/10/425,114
; PRIOR FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 63632
; LENGTH: 549
; TYPE: PRT
; ORGANISM: Zea mays subsp. mexicana
; FEATURE:
; OTHER INFORMATION: Clone ID: UC-ZMFLTEOSINTE089A07_FLI.pep
US-10-425-114-63632

```

Query Match 72.2%; Score 1945; DB 12; Length 549;
 Best Local Similarity 73.3%; Pred. No. 1.3e-161;
 Matches 373; Conservative 54; Mismatches 76; Indels 6; Gaps 3;

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Qy 1 MDSSKSGHSEALRNVLGRTIGTGGKVKIAEHKLTGHRVAKIINCQNMNME 60
Db 47 MEGAGK--DGNPLNRYIGKTLGSGFGKVIASHISTGHVAKILNRKIKGEMEE 103
Qy 61 KAKEEFILKLFIPHIIRLYEVYTPDIYVWMEYCKGELFDYIVKGRLODEAR 120
Db 104 KVKREIKILRLFPMPHIIRLYEVIDTPADIVWMEYVCGELFDYIVKGRLODEAR 163
Qy 121 FOQIISGVEYCHRMVVRDLKPENLILDSKYNVCLADFGLSNVMHDGFLKTS 180
Db 164 FOQIISGVEYCHRMVVRDLKPENLILDSKYNVCLADFGLSNVMHDGFLKTS 223
Qy 181 AAEVISGKLYAGPEVDVWSCGVLVALLCGTLPEDDENIPNLFKIKGITYLPSHLSA 240
Db 224 AAEVISGKLYAGPEVDVWSCGVLVALLCGTLPEDDENIPNLFKIKGITYLPSHLS 283
Qy 241 LARDLIPMLVVEPMKRTITREIREHOMFOIRLPRYLAVPPDDTQOAKMIDEDTL 300
Db 284 SARDLIPMLVVDPMKRTITREIREHOMFOIRLPRYLAVPPDDTQOAKMIDEDTL 343

```

QY 301 NMGNKHCVCESLCSRLQNEATVAYLLDNRFRATSGYLQADYQESMDRLNLQJASSES 360
DB 344 KMGDRKQQLIESLQNRQNEATVAYLLDNRFRATSGYLQADYQESMDRLNLQJASSES 402
QY 361 SSSGTRNVYVPGSSDPHSSGLRPPYVVERKVALGLQSRAPREIWEVYKALQELNVKWK 420
DB 403 PTAATLROHGFSSPSGGLRQHFPAERKVALGLQSRAPREIWEVYKALQELNVKWK 462
QY 421 NGHNVYCRWCPGEPFENVDTLDANSFLGSDTIMDNDANGLRPTVYKEEFOLKTKDDK 480
DB 463 IGHVNMKCRWSPGGLRQHFPAERKVALGLQSRAPREIWEVYKALQELNVKWK 520
QY 481 YLLDMORYTGPOLLFLDFCAFLTKLRVL 509
DB 521 YLLDLQRYVSSHLFLDLCSAFLTKLRVL 549

RESULT 14

US-10-183-687-252

Sequence 252, Application US/10183687
Publication No. US20030204870A1

GENERAL INFORMATION:

APPLICANT: Allen, Steve
APPLICANT: Allen, William B.
APPLICANT: Cahoon, Rebecca
APPLICANT: Epelbaum, Sabine
APPLICANT: Farnodu, Omolayo O.
APPLICANT: Harvell, Leslie T.
APPLICANT: Jones, Todd
APPLICANT: Kliney, Tony
APPLICANT: Kliney, Ted
APPLICANT: Li, Changjiang
APPLICANT: Oliveira, Igor Cunha
APPLICANT: Sakai, Hajime
APPLICANT: Shen, Bo
APPLICANT: Tarczyński, Mitchell C.
TITLE OF INVENTION: Alteration Of Oil Traits In Plants
FILE REFERENCE: B01458 US NA
CURRENT APPLICATION NUMBER: US/10/183,687
CURRENT FILING DATE: 2002-06-27
PRIOR FILING DATE: 2001-06-29
PRIOR FILING DATE: 2001-06-29
NUMBER OF SEQ ID NOS: 532
SOFTWARE: Microsoft Office 97
SEQ ID NO 252
LENGTH: 515
TYPE: PRT
ORGANISM: Glycine max
US-10-183-687-252

Query Match 72.0%; Score 1939; DB 12; Length 515;

Best Local Similarity 72.1%; Pred. No. 3.9e-161; Indels 10; Gaps 4;

Matches 373; Conservative 58; Mismatches 76;

QY 1 MDGSS-KSGSGS--EALRNVNLGRTLGITGFKVYKIAEHKLTGHRVAIKIINCRQNRME 57
DB 1 MDRSTGRGCGSVMLFANVYKLGITGSGFKVYKIAEHKLTGHRVAIKIINCRQNRME 60
QY 58 MEKAKREFFKILKLFHPHIIIRLYEVITYPTDIYVMEYCKYBELFDYIYKGRLODBEA 117
DB 61 MEKAKREFFKILKLFHPHIIIRLYEVITYPTDIYVMEYCKYBELFDYIYKGRLODBEA 120
QY 118 RRIQOIIISGVYCHRMNVVRDLKPENLILDSKYNVLADEPGISNVVMDHGFILKTSQGS 177
DB 121 RHFPQOIIISGVYCHRMNVVRDLKPENLILDSKYNVLADEPGISNVVMDHGFILKTSQGS 180
QY 178 PNYAAPVYISGLYAGPEVDWVSCGVIYALLCGTLPPDDENIPNLFFKIKIGGIYTLPSH 237
DB 181 PNYAAPVYISGLYAGPEVDWVSCGVIYALLCGTLPPDDENIPNLFFKIKIGGIYTLPSH 240
QY 238 LSLALRDLIPMLVVEPKRITIRIRHQPQIRLPRYLAVPPDDTQAKMIDEDTTLR 297

DB 241 LSPGARDLIPRMLVDEPKRMTIPEIRQHPWFOVHLPRYLAVPPDDTQAKMIDEDTTLR 300
QY 298 DVNMGFNKHCVCESLCSRLQNEATVAYLLDNRFRATSGYLQADYQESMDRLNLQJASSES 357
DB 301 EVNMGFDNRQQLIESLQNRQNEATVAYLLDNRFRATSGYLQADYQESMDRLNLQJASSES 360
QY 358 SSSGTRNVYVPGSSDPHSSGLRPPYVVERKVALGLQSRAPREIWEVYKALQELNVKWK 417
DB 361 GEVASPVAGHSTGYMDYQGVGMKQFPVERKVALGLQSRAPREIWEVYKALQELNVKWK 420
QY 418 WKRGHNVYCRWCPGEPFENVDTLDANSFLGSDTIMDNDANGLRPTVYKEEFOLKTKDDK 472
DB 421 WKRGHNVYCRWCPGEPFENVDTLDANSFLGSDTIMDNDANGLRPTVYKEEFOLKTKDDK 478
QY 473 LYTKDDKXVLLDMQRYTGPOLLFLDFCAFLTKLRVL 509
DB 479 LYTKREKXVLLDMQRYTGPOLLFLDFCAFLTKLRVL 515

RESULT 15

US-10-425-114-62429

Sequence 62429, Application US/10425114
Publication No. US20040034888A1

GENERAL INFORMATION:

APPLICANT: Liu, Jingdong
APPLICANT: Zhou, Yihua
APPLICANT: Kovalic, David K.
APPLICANT: Screen, Steven E.
APPLICANT: Tabaska, Jack E.
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
FILE REFERENCE: 38-21(5313)B
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 62429
LENGTH: 545
TYPE: PRT
ORGANISM: Zea mays
OTHER INFORMATION: Clone ID: 700204782_FLI.pep
US-10-425-114-62429

Query Match 71.9%; Score 1937; DB 12; Length 545;

Best Local Similarity 72.8%; Pred. No. 6.3e-161; Indels 16; Gaps 5;

Matches 374; Conservative 56; Mismatches 68;

QY 1 MDGSSKSGSGSEALRNVNLGRTLGITGFKVYKIAEHKLTGHRVAIKIINCRQNRME 60
DB 43 MEGAGR--DANPLGGRYRIGITGSGFKVYKIAEHKLTGHRVAIKIINCRQNRME 99
QY 61 KAKEFFKILKLFHPHIIIRLYEVITYPTDIYVMEYCKYBELFDYIYKGRLODBEAR 120
DB 100 KAKEFFKILKLFHPHIIIRLYEVITYPTDIYVMEYCKYBELFDYIYKGRLODBEAR 159
QY 121 FOQIIISGVYCHRMNVVRDLKPENLILDSKYNVLADEPGISNVVMDHGFILKTSQGS 180
DB 160 FOQIIISGVYCHRMNVVRDLKPENLILDSKYNVLADEPGISNVVMDHGFILKTSQGS 219
QY 181 AAPVYISGLYAGPEVDWVSCGVIYALLCGTLPPDDENIPNLFFKIKIGGIYTLPSH 240
DB 220 AAPVYISGLYAGPEVDWVSCGVIYALLCGTLPPDDENIPNLFFKIKIGGIYTLPSH 279
QY 241 LARDLIPRMLVVEPKRITIRIRHQPQIRLPRYLAVPPDDTQAKMIDEDTTLR 300
DB 280 SARDLIPRMLVVEPKRITIRIRHQPQIRLPRYLAVPPDDTQAKMIDEDTTLR 339
QY 301 NMGNKHCVCESLCSRLQNEATVAYLLDNRFRATSGYLQADYQESMDRLNLQJASSES 359
DB 340 KMGDRKQQLIESLQNRQNEATVAYLLDNRFRATSGYLQADYQESMDRLNLQJASSES 399
QY 360 SSSGTRNVYVPGSSDPHSSGLRPPYVVERKVALGLQSRAPREIWEVYKALQELNVKWK 415

Db	400	TSATEHROHVFTESPG-----SGLRQHFASERKWAIGLQSRAPRRIISEVLKALQELN	453
Qy	416	VRMKNGHYNKCRWCPCFPPEVNDTLDASNSFLGDSITMDNDANGRLPTVIKPEFQLYK	475
Db	454	VYWKKGHYNKCRWSPGCL--SMMHNCDFSAESALIIETDULAKSTRIVKEFIQLYK	511
Qy	476	TKDDXYLLDMQRYTGPOLLFLDFCAFLTKLRYL	509
Db	512	TRDEKYLIDLQRVSGPOLFLFDLCSAFLTLQLYL	545

Search completed: July 7, 2004, 17:58:14
 Job time : 54 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - nucleic search, using frame_p2n model

Run on: July 9, 2004, 11:24:34 ; Search time 629 Seconds
(without alignments)
3437.731 Million cell updates/sec

Title: US-09-857-522B-4
Perfect score: 2693
Sequence: 1 MDGSSKSGHSEALRYNLG.....GPOLLPFDCAAFYTKLRVL 509

Scoring table:
BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 337363 seqs, 212409041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

-MODEL=frame+g2n.model -DEV=x1h
-Q=/cgn2_1/USPTO.epool/US09857522/runat_07072004_161356_1862/app_query.fasta_1.647
-DB=N.GeneSeq 29Jan04 -QMT=fastcap -SUFFIX=p2n.rng -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MTN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pct -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USBR=US09857522.QCGN_1_1470@runat_07072004_161356_1862 -NCPU=6 -ICPU=3
-NO MMAP -LARGESUBSTRY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

N.GeneSeq_29Jan04:*
1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002as:*
7: geneseqn2003as:*
8: geneseqn2003bs:*
9: geneseqn2003cs:*
10: geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2693	100.0	1948	3	AAAS2768
2	2693	100.0	1948	7	AAAS2768
3	2378	88.3	1899	7	ACC00753
4	1974.5	73.3	2123	3	AAAS2772
5	1974.5	73.3	2123	3	AAAS2772
6	1969.5	73.1	1539	6	ABZ14852
7	1942	72.1	2052	7	ACC00745
8	1939	72.0	2543	3	AAAS2774

9	1939	72.0	2543	7	ACC00751	ACC00751 Glycine m
10	1937.5	71.9	1929	4	AAAF6201	AAAF6201 Tomato le
11	1931	71.7	2107	7	AAAS2769	AAAS2769 Corn puta
12	1931	71.7	2107	7	ACC00744	ACC00744 Zea mays
13	1923	71.4	1536	6	AAQ47789	AAQ47789 SHP gene
14	1903.5	70.7	1539	6	ABZ12357	ABZ12357 Arabidops
15	1903.5	70.7	1792	3	AAAC4825	AAAC4825 Arabidops
16	1899.5	70.5	1825	6	AAI46639	AAI46639 A thalian
17	1891.5	70.2	1825	6	AAI46642	AAI46642 A thalian
18	1890.5	70.2	2006	3	AAAS2777	AAAS2777 wheat put
19	1890.5	70.2	2006	7	ACC00754	ACC00754 Triticum
20	1869.5	69.4	1539	6	AAI71048	AAI71048 Arabidops
21	1545.5	57.4	1485	3	AAAC4606	AAAC4606 Arabidops
22	1537	57.1	3550	6	AAI46640	AAI46640 A thalian
23	1529	56.8	3550	6	AAI46641	AAI46641 A thalian
24	1267	47.0	944	9	ADCT5707	ADCT5707 DNA homol
25	1187.5	44.1	817	3	AAAS2776	AAAS2776 wheat put
26	1148	42.6	1783	2	AAQ76198	AAQ76198 CDNA of h
27	1144	42.5	2761	2	AAQ76197	AAQ76197 CDNA of r
28	1139	42.3	3079	4	AAAS60973	AAAS60973 Human can
29	1119	41.6	1647	9	ADB52890	ADB52890 Primary r
30	1115	41.4	1647	2	AAAT85925	AAAT85925 Mammalian
31	1109	41.2	2663	4	ABL05573	ABL05573 Drosophila
32	1101.5	40.9	1698	9	ADB61362	ADB61362 Clone of
33	1013.5	37.6	1902	7	ACC60983	ACC60983 Gene sequ
34	1004.5	37.3	5277	4	ABL05572	ABL05572 Drosophila
35	971	36.1	915	9	ADCO7761	ADCO7761 Rice DNA
36	817.5	30.4	986	6	ABN98495	ABN98495 Arabidops
37	773	28.7	2000	9	ADCO8538	ADCO8538 Rice DNA
38	749	27.8	2352	4	AAI66823	AAI66823 Human pro
39	749	27.8	2968	4	AAI66822	AAI66822 Human pro
40	749	27.8	4699	5	AAH76213	AAH76213 Human kin
41	746	27.7	2193	7	AAAS1406	AAAS1406 Human mic
42	746	27.7	2271	6	AAAD30396	AAAD30396 Human PAR
43	746	27.7	2632	3	AAAX82952	AAAX82952 Human ker
44	745	27.7	2190	4	AAAF4654	AAAF4654 Novel pro
45	745	27.7	2698	2	AAV03002	AAV03002 Human Twe

ALIGNMENTS

RESULT 1	AAAS2768	standard; CDNA; 1948 BP.
AAAS2768		
AC	AAAS2768;	
DT	03-JAN-2001	(first entry)
XX		Corn putative catabolite repression protein SNF1 coding sequence #2.
XX		Corn; carbon catabolite repression; sucrose non-fermenting protein 1;
KW	SNF1; plant growth; ss.	
XX		
OS	Zea mays.	
XX		
FT	Key	Location/Qualifiers
FT	CDS	173..1702
FT		/*tag= a
FT		/product= "SNF1"
XX		
PN	MO200036115-A2.	
PD	22-JUN-2000.	
XX		
PF	15-DEC-1999;	99MO-US029824.
XX		
PR	16-DEC-1998;	98US-0112563P.
XX		
PA	(DUPO) DU PONT DE NEMOURS & CO E I.	
XX		
PI	Allen SM, Heppard EP, Sakai H, Weng Z, Helentjaris TG, Macool DJ, Miao G;	

XX WPI: 2000-431593/37.
DR p-PSDB: AAB03416.

XX New nucleic acids encoding sucrose non-fermenting 1 (SNF1) proteins
PT involved in carbon catabolite repression in plants and seeds, useful for
PT controlling carbon and nitrogen partitioning pathways during plant growth
PT and development.

XX Claim 2, Page 34-35, 59pp; English.

XX The present sequence is a putative sucrose non-fermenting protein SNF1
CC coding sequence from corn. The sequence was isolated by searching a corn
CC tassel shoot cDNA library for sequences similar to those encoding SNF1 in
CC Arabidopsis thaliana, Cucumis sativus, Glycine max and Oryza sativa. The
CC protein is involved in carbon catabolite repression, and so the gene and
CC protein can be used in plants to control the nitrogen and carbon
CC partitioning pathways during plant growth and development. They can also
CC be used to alter the accumulation of carbohydrates, lipids and proteins
CC during plant growth

XX Sequence 1948 BP: 572 A; 380 C; 461 G; 535 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	1,38e-264	Length:	1948
Score:	2693.00	Matches:	509
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	3	Gaps:	0

US-09-857-522B-4 (1-509) x AAAS2768 (1-1948)

Qy	1	MetAspGlySerSerIySGlySerGlyVhiSserGluAlaLeuArgAsnTyrAsnLeuGly	20
Db	173	ATGATGGAAGTAAAGGAGGAGGCGATTCGAAGCATTAAGAACTACAACTGAG	232
Qy	21	ArgThrLeuGlyIleGlyThrPheGlyVhiSValIySleIaGluHsiSlyLeuThrGly	40
Db	233	AGAACTTTAGTATCGGTACCTTTGGAAAAGTGAAGATTCAGAGCATTAAGCTTAC	292
Qy	41	HisArgValAlaIleIySleIleAsnCySArgGlnMetArgAsnMetGluMetGlu	60
Db	293	CATAGCGTTCATTAAGATCATCACTGCCCAATGAAATATGAAATGGAAGAG	352
Qy	61	LysAlaIySArgGluPheIySleIleuIySleuPheIleHsiProHsiIleIaArgLeu	80
Db	353	AAAGCAAGAGAGATTCAGATATGAAATGATTCACCCCATATCATTCGCTT	412
Qy	81	TyrGluValIleIyThrProThrAspIleTyrValIaMetGluTyrCySlySleTyrGly	100
Db	413	TATAGGTCATATACACCTACAGATATATGTGTGATGAGATATGTAATATAGGC	472
Qy	101	GluLeuPheAspTyrIleValGluIySlyValArgLeuGlnIaAspGluIaArgArgIle	120
Db	473	GAGTATATTTGATTCATTTGAGAAAGGAGATTAACAGAAATGAAAGCTCGTCAATC	532
Qy	121	PheGlnGlnIleIleSerGlyValGluTyrCySHisArgAsnMetValIaHsiArgAsp	140
Db	533	TTCCAGAGATCATATCTGGCGTCAATTCGCCATACAAACAGATGTGTCCACCGTAC	592
Qy	141	LeuIySProGluAsnLeuLeuAspSerIySArgAsnValIySLeuAlaAspPheGly	160
Db	593	CTAAGCGGAAACTTCTTACTTGATTCAAAGTATATGTAATAAATCTGGCGATTTGGT	652
Qy	161	LeuSerAsnValMetHisAspGlyVhiSleuIySThrSerCySlySerProAsnTyr	180
Db	653	CTGAGCAATGTCAATGATGATGCGCATTTCTGAAGATTAAGTGGAGTCCCAACAT	712
Qy	181	AlaAlaProGluValIleSerGlyIySleuTyrIaGlyProGluValAspValTyrSer	200
Db	713	GCTGCTCCAGAGGATATATCTGTAACTATATGCTGAGCTGAGGTGATGAGT	772

Qy	201	CysGlyValIleLeuTyrAlaLeuLeuCySglyThrLeuProPheAspGluAsnIle	220
Db	773	TGTGGGTGATTTCTTATGCTCTTCTTGTGGAACCTTCCATTTGATGATGAAATATT	832
Qy	221	ProAsnLeuPheIySlyIleIySlyGlyIleTyrThrLeuProSerHisLeuSerAla	240
Db	833	CCCAATCTGTTCAAAAAAATTAAGGGGATATCTACACACTTCCAGTCAATTTGTGCT	892
Qy	241	LeuAlaArgAspLeuIleProArgMetLeuValIaGluProMetCysArgIleThrIle	260
Db	893	TTGGCCAGGATTTGATCCAGAAATGCTTTGTTGATGACCTTGAAGAAATACAAATT	952
Qy	261	ArgGluIleArgGluHsiGlnTyrPheGlnIleArgLeuProArgTyrIleAlaValPro	280
Db	953	AGGAAATTCGGGAGATCAATGATTCAGATTCGCTTCCAGTTACTTGGCAGTGCCT	1012
Qy	281	ProProAspThrThrGlnGlnAlaIySMeIleAspGluAspThrLeuAspArgValIa	300
Db	1013	CCACCAATACGACACAAAGCCAAATGATGATGAAATACACTTCAGATGTGTT	1072
Qy	301	AsnMetGlyPheAsnIySValCySlySerLeuCySserArgLeuGlnAsnGlu	320
Db	1073	AAATGGGATTTTAACAGAAACATGTGTGAAATCACTGTGACGACACTTCAAAATGAG	1132
Qy	321	AlaThrValAlaTyrTyrLeuLeuLeuAspAsnArgPheArgAlaThrSerGlyTyrLeu	340
Db	1133	GCAACTGTTCATATTTACTATTGACCAATCGGTTTGAAGCAACTAATGAGCTATCTT	1192
Qy	341	GlyAlaAspTyrGlnGluSerMetAspArgAsnLeuAsnGlnIleuAlaSerSerGluSer	360
Db	1193	GGGGCAATTAATCAAGATCAATGACAGCAAAATTAATCAAGCTGGGTCATCTGAATCA	1252
Qy	361	SerSerSerGlyThrArgAsnTyrValProGlySerSerAspProHisSerSerGlyLeu	380
Db	1253	TCTAGTCTGTGACAGAAATTTATGTTCCAGAAAGCATATCTCTACACATGCTTGG	1312
Qy	381	ArgProTyrTyrProValGluArgIySValIaLeuGlnIleuGlnSerArgAlaHsiPro	400
Db	1313	CGGCATATTAATCTGTTGAAAGAAATGGCGCTTGAATTCAGTCTCGGGCCCACTT	1372
Qy	401	ArgGluIleMetValGluValIleuIySValIaLeuGlnIleuLeuAsnValaTyrPlySlyS	420
Db	1373	CGTGAATTAATGTTGAGTCTTAAAGCACTTCMAAATTAACGTCAGATGGAAGAG	1432
Qy	421	AsnGlyHisTyrAsnValIySArgTyrCySProGlyPheProGluValaAsnAspThr	440
Db	1433	AAATGGCACTACAAACGAAATGCAATGTGCTCCAGAGCTTCTCTGAAGTTATGACAG	1492
Qy	441	LeuAspAlaSerAsnSerPheLeuGlyAspSerThrIleMetAspAsnAspAspAlaAsn	460
Db	1493	TTAGATGCCAGCAACAGCTTCTTGGTGAATCACTACATCATGATATGATGATGCTAAT	1552
Qy	461	GlyArgLeuProThrValIleIySValIaLeuGlnIleuIySValIaLeuAspAspIyS	480
Db	1553	GGGAGGCTACCTCTGTGATCAAGTTGAATTCAGCTTTACAAAGAGAAAGAGACAG	1612
Qy	481	TyrLeuLeuAspMetGlnArgValIleThrGlyProGlnIleuLeuPheLeuAspPheCysAla	500
Db	1613	TACCTCTTAATATGCAAGAGATTAATCTGACCTCAAGCTGCTCTTCTGCTGCGC	1672
Qy	501	AlaPheLeuThrIySLeuArgValLeu	509
Db	1673	GCTTCTTACCAAGCTTAGGTTCTA	1699

RESULT 2
ACC00743 standard; cDNA; 1948 BP.
ACC00743;
ACC00743;
16-MAY-2003 (first entry)
Zea mays oil trait related cDNA sequence SEQ ID NO:235.

XX Plant; oil trait; oil phenotype; altered lipid profile; MAP kinase;
KM receptor-like protein kinase; mitogen activated protein kinase; oil;
KM LIP15-like transcription factor caleosin; ATP citrate lyase; SNI;
KM CKC-like transcription factor; antisense inhibition; co-suppression;
transgenic plant; gene; ss.
XX
OS Zea mays.
XX
PN WO2003002751-A2.
XX
PD 09-JAN-2003.
XX
PF 27-JUN-2002; 2002WO-US020152.
XX
PR 29-JUN-2001; 2001US-0301913P.
XX
PA (DUPO) DU PONT DE NEMOURS & CO E I.
XX (PION-) PIONEER HI-BRED INT INC.
PI Allen SM, Allen WB, Cahoon RE, Epelbaum S, Farnodu OO, Harvell LT,
PI Jones TJ, Kinney AJ, Klein TM, Li C, Oliveira IC, Sakai H, Shen B,
PI Tarczynski MC;
XX
XX WPI; 2003-201509/19.
DR P-PSDB; ABR40708.
XX
XX Novel nucleotide fragment encoding polypeptides having receptor-like
PT protein kinase activity, caleosin-like activity, useful for altering oil
PT phenotypes in plants such as sunflower, coconut, soybean, wheat and rice.
XX
PS Claim 18; Page 272-273; 542pp; English.
XX
XX The present invention describes an isolated nucleotide fragment (I)
CC comprising a nucleic acid sequence (NS) chosen from a NS encoding a
CC polypeptide (PP) having receptor-like protein kinase activity, mitogen
CC activated protein (MAP)-kinase activity, LIP15-like transcription factor
CC activity, caleosin-like activity, ATP citrate lyase activity, SNI-like
CC activity and CKC-like transcription factor activity. Also described: (1)
CC complement (II) of (I); (2) a chimeric construct (III) comprising (I) or
CC (II), operably linked to a regulatory sequence; (3) a plant (IV)
CC comprising (III) in its genome; (4) seeds (V) obtained from (IV); and (5)
CC oil obtained from (V). (I) or its part can be used in antisense
CC inhibition or co-suppression in a transformed plant. (III) is useful for
CC altering the oil phenotype in a plant such as corn, soybean, wheat, rice,
CC canola, Brassica, sorghum, sunflower or coconut. (III) is also useful for
CC creating transgenic plants having altered lipid profiles. (I) can also be
CC used as a hybridisation probe. ACC00626 to ACC00868 and ABR40591 to
CC ABR40879 represent sequences used in the exemplification of the present
CC invention
XX
SQ Sequence 1948 BP; 572 A; 380 C; 461 G; 535 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 1,38e-264 Length: 1948
Score: 2693.00 Matches: 509
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 7 Gaps: 0

US-09-857-522B-4 (1-509) x ACC00743 (1-1948)
QY 1 MetAspGlySerSerLysGlySerGlyHisSerGluAlaLeuArgAsnTyrAsnLeuGly 20
Db 173 ATGATGAGACAGTAAAGGAGAGTGCGCATTCGTAAGCATTAAGGACCTTAACCTGGGA 232
QY 21 ArgThrLeuGlyIleGlyThrPheGlyLysValIleAlaGluHisLeuThrGly 40
Db 233 AGAACCTTTAGGATCGGATCTTGGAAGGAGGATTGCGAGCATTAAGCTTAAGCTGGA 292
QY 41 HisArgValAlaIleLysIleLeuAsnCyArgGlnMetArgAsnMetGluMetGluGlu 60
|||

Db 293 CATAGGGTGCTATAAGATCATCATCGCCGCAAAATGAAATATGAAATGGAAGAG 352
QY 61 LysAlaLysAsnGluPheLysIleLeuLysLeuPheIleHisProHisIleIleArgLeu 80
Db 353 AAACCAAGAGAGAAATCAAAATTTGAAGTTGTCATTCACCCCAATCATTCGGGTT 412
QY 81 TyrGluValIleTyrThrProThrAspIleTyrValIleMetGluTyrCysLeuTyrGly 100
Db 413 TATAGGTCATATACACACCTTACGATATATATGTTGATGAGAAATATGATATGCG 472
QY 101 GluLeuPheAspTyrIleValGluLysGlyArgLeuGlnIleAspGluAlaArgArgIle 120
Db 473 GAGTTATTGATTCATTTGATTTGAGAAAGCAGATTACAGAAATGAAAGCTCGTGAATC 532
QY 121 PheGlnGlnIleIleSerGlyValGlyTyrCysHisArgAsnMetValIleHisArgAsp 140
Db 533 TTCAGCAGATCATATCTGGGGTGAATATCGCATGAAACATGATTTGCCACCGTAC 592
QY 141 LeuLysProGluAsnLeuLeuLeuAspSerLysTyrAsnValLysLeuAlaAspPheGly 160
Db 593 CTAAAGCCGGAACCTTGTCTTATCTGATTCAAAGTATATGTAACCTTGGGATTTGCT 652
QY 161 LeuSerAsnValMetHisAspGlyHisPheLeuLysThrSerCysGlySerProAsnTyr 180
Db 653 CTGAGCAATGTCATGATGATGCGCATTTCTGAAGATCTGCTGGAGTCCGAATCAT 712
QY 181 AlaAlaProGluValIleSerGlyLysLeuTyrAlaGlyProGluValAspValTyrSer 200
Db 713 GCTCTCCAGAGGATTAATATCTGTAACCTATATCTGAGCCTGAGCGATGATGAGT 772
QY 201 CysGlyValIleLeuTyrAlaLeuLeuCysGlyThrLeuProPheAspAspGluAsnIle 220
Db 773 TGTGGGGATTTCTTATGCTCTTCTTGTGGAACCTTCCATTTGATGATGAGAAATTT 832
QY 221 ProAsnLeuPheLysLysIleLysGlyGlyIleTyrThrLeuProSerHisLeuSerAla 240
Db 833 CCNATCTGTTCAAAAAATTAAGGAGGATCTACACACTTCCAGATCATTTGTGCT 892
QY 241 LeuAlaArgAspLeuIleProArgMetLeuValValGluProMetLysArgIleThrIle 260
Db 893 TTGGCCAGGGATTTGATCCACGATCTGTTGTGAGCTTAAGAAAGATACAAATT 952
QY 261 ArgGluIleArgGluHisGlnThrPheGlnIleArgLeuProArgTyrLeuAlaValPro 280
Db 953 AGGAAATTCGGGACATCATATGTTCCAGATTTGCCCTTCCACTTACTTGGCGATGCT 1012
QY 281 ProProAspThrThrGlnGlnAlaLysMetIleAspGluAspThrLeuArgAspValVal 300
Db 1013 CCACGAGTACAGACAAACCAAGCAAAATGATGATGATGATGATGATGATGATGATGAT 1072
QY 301 AsnMetGlyPheAsnLysAsnHisValCysGluSerLeuCysSerArgLeuGlnAsnGlu 320
Db 1073 AATATGGATTTTAAACAAGAACCATGTGTGTAATCATCTGTCACAGACTTCAAAATGAG 1132
QY 321 AlaThrValAlaTyrTyrLeuLeuLeuAspAsnArgPheArgAlaThrSerGlyTyrLeu 340
Db 1133 GCAACTGTTGCATATTTATTTATCTTTGACATATGCTTTAGAGCAACTATGCTATCTT 1192
QY 341 GlyAlaAspTyrGlnGlnIleSerMetAspArgAsnLeuAsnGlnLeuAlaSerSerGluSer 360
Db 1193 GGGCAGATTTATCAAGATCATGATGACAGGAATTTAATCATGCTGCGCTCATCTGAATCA 1252
QY 361 SerSerSerGlyThrArgAsnTyrValProGlySerSerAspProHisSerSerGlyLeu 380
Db 1253 TCTAGTTCTGTGTACAGAAATTAATGTTCCAGGAAGCAGTGAATCTCTATAGCAGGTTTG 1312
QY 381 ArgProTyrTyrProValGluArgLysTyrAlaLeuGlyLeuGlnSerArgAlaHisPro 400
Db 1313 CGGCCATATTTATCTGTTGGAAGAAATGGCGCTTGGACTTCAGTCTTGGGCCACCT 1372
QY 401 ArgGluIleMetValGluValIleLysAlaLeuGlnIleLeuAsnValArgTyrLysLys 420
Db 1373 CGTGAATTAATGTTGAGGCTTATTAAGCACTTCAAGAAATTAACGTCAATGGAAGAAG 1432

QY 421 AsnGlyHisTyrAsnValIysCysArgTrpCysProGlyPheProGluValAsnAspThr 440
CC altering the oil phenotype in a plant such as corn, soybean, wheat, rice,
CC canola, Brassica, sorghum, sunflower or coconut. (iii) is also useful for
CC creating transgenic plants having altered lipid profiles. (ii) can also be
CC used as a hybridisation probe. ACC00626 to ACC00868 and ABR40591 to
CC ABR40879 represent sequences used in the exemplification of the present
CC invention
XX
QY 441 LeuAspAlaSerAsnSerPheLeuGlyAspSerThrIleMetAspAsnAspAlaAsn 460
Db 1493 TTATATGCACCAACAGCTTTCTTGTCATCTCAATCATGATGATGATGATGATGAT 1552
QY 461 GlyArgLeuProThrValIleIysPheGluPheGluLeuTyrIleTyrIysAspAlaLys 480
Db 1553 GGGGAGCTACTACTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1612
QY 481 TyrLeuLeuAspMetGlnArgValThrGlyProGluLeuLeuPheLeuAspPheCysAla 500
Db 1613 TACCTCTTAATGATGACAGAGCTTACTGACCTGACCTGCTCTTCTTGACTCTGTCG 1672
QY 501 AlaPheLeuThrIysLeuArgValIleu 509
Db 1673 GCCTTCCTTACCAAGCTTAGGTTCTA 1699
RESULT 3
ID ACC00753 standard; cDNA; 1899 BP.
AC C00753;
XX ACC00753;
DT 16-MAY-2003 (first entry)
XX
XX Triticum aestivum oil trait related cDNA sequence SEQ ID NO:255.
XX
XX Plant; oil trait; oil phenotype; altered lipid profile; MAP kinase;
XX receptor-like protein kinase; mitogen activated protein kinase; oil;
XX LIP5-like transcription factor caleosin; ATP citrate lyase; SNF1;
XX CKC-like transcription factor; anticense inhibition; co-suppression;
XX transgenic plant; gene; ss.
XX
XX Triticum aestivum.
XX
XX WO2003002751-A2.
XX
XX 09-JAN-2003.
XX
XX 27-JUN-2002; 2002WO-US020152.
XX
XX 29-JUN-2001; 2001US-0301913P.
XX
XX (DUPO) DU PONT DE NEMOURS & CO E I.
XX (PION-) PIONEER HI-BRED INT INC.
XX
XX Allen SM, Allen WB, Cahoon RE, Epelbaum S, Famodu OO, Harveyll LT;
XX Jones TJ, Kinney AJ, Klein TM, Li C, Oliveira IC, Sakai H, Shen B;
XX Tarczynski MC;
XX
XX WPI; 2003-201509/19.
XX
XX P-PSDB; ABR40718.
XX
XX Novel nucleotide fragment encoding polypeptides having receptor-like
XX protein kinase activity, caleosin-like activity, useful for altering oil
XX phenotypes in plants such as sunflower, coconut, soybean, wheat and rice.
XX
XX Claim 18; Page 296; 542pp; English.
XX
XX The present invention describes an isolated nucleotide fragment (i)
XX comprising a nucleic acid sequence (NS) chosen from a NS encoding a
XX polypeptide (PP) having receptor-like protein kinase activity, mitogen
XX activated protein (MAP)-kinase activity, LIP5-like transcription factor
XX activity, caleosin-like activity, ATP citrate lyase activity, SNF1-like
XX activity and CKC-like transcription factor activity. Also described: (1)
XX complement (ii) of (i); (2) a chimeric construct (iii) comprising (i) or
XX (ii), operably linked to a regulatory sequence; (3) a plant (iv)
XX comprising (iii) in its genome; (4) seeds (v) obtained from (iv); and (5)
XX oil obtained from (v). (i) or its part can be used in antisense

CC inhibition or co-suppression in a transformed plant. (iii) is useful for
CC altering the oil phenotype in a plant such as corn, soybean, wheat, rice,
CC canola, Brassica, sorghum, sunflower or coconut. (iii) is also useful for
CC creating transgenic plants having altered lipid profiles. (ii) can also be
CC used as a hybridisation probe. ACC00626 to ACC00868 and ABR40591 to
CC ABR40879 represent sequences used in the exemplification of the present
CC invention
XX
SQ Sequence 1899 BP; 572 A; 364 C; 462 G; 501 T; 0 U; 0 Other;
Alignment Scores:
Pred. No.: 1.93e-232 Length: 1899
Score: 2378.00 Matches: 442
Percent Similarity: 93.52% Conservative: 34
Best Local Similarity: 86.84% Mismatches: 33
Query Match: 88.30% Indels: 0
D5: Gaps: 0
US-09-857-522B-4 (1-509) x ACC00753 (1-1899)
QY 1 MetAspGlySerSerIysGlySerGlyHisSerGluAlaLeuArgAsnTyrAsnLeuGly 20
Db 67 ATGGAAGGAAACACTAGAGAGAGGTGGCATTTGACCATTTAAAGAACTACATGTCGGC 126
QY 21 ArgThrLeuGlyIleGlyThrPheGlyIysValIysIleAlaGluHisIysLeuThrGly 40
Db 127 AGAACATTAGGTATAGGCACATTGGAAAGTAGATTCAGAGCATAGCATACAGCGG 186
QY 41 HisArgValAlaIleIysIleIleAsnCysArgGlnMetArgAsnMetGluMetGluGlu 60
Db 187 CATTAAGTCTCTTAAAGATTGAAACCGTCGCAATGAACTAGAAATGAGAGAG 246
QY 61 LysAlaIysArgGluPheIysIleLeuIysLeuPheIleHisProHisIleIleArgLeu 80
Db 247 AAAGCAAGAGAGAGACCAAGATTTGAGGTTGTCATCCACCTCATATCATCCGGCTT 306
QY 81 TyrGluValIleTyrThrProThrAspIleTyrValIaMetGluTyrCysIysTyrGly 100
Db 307 TATGAGGTCAATTAAACACCTACAGATATATTTGTTGATGAAATTCCAAGTATGCT 366
QY 101 GluLeuPheAspTyrIleValIleGluIysGlyIysGluGlnGluAspGluIleArgArgIle 120
Db 367 GAGCTATTGACATGCACTTGTGAGAAAGGCGGTTCAGAGAAATGAGGCTCGTCGATC 426
QY 121 PheGlnGlnIleIleSerGlyValIleGluTyrCysHisArgAsnMetValIleHisArgAsp 140
Db 427 TTCAGCAATTTATATTTGCTGTTGATCTGCACAGAAACATGCTGCTCATCGAT 486
QY 141 LeuIysPheGluAsnLeuLeuLeuAspSerIysTyrAsnValIysLeuAlaAspPheGly 160
Db 487 CTAAAGCCAGAGAACTGTTACTTGATTCCAATATACATGTGAACCTTGCCGACTTGGG 546
QY 161 LeuSerAsnValMetHisAspGlyHisPheLeuIysPheIysSerProAsnTyr 180
Db 547 TTAAATATGATGACATGATGATGATGATGATGATGATGATGATGATGATGATGAT 606
QY 181 AlaAlaProGluValIleSerGlyIysLeuTyrAlaGlyProGluValAspValTyrSer 200
Db 607 GCTGCACCAAGGATTAATCTGACGTAATTAATTAATTAATTAATTAATTAATTAAT 666
QY 201 CysGlyValIleLeuTyrAlaLeuLeuCysGlyThrLeuProPheAspAspGluAsnIle 220
Db 667 TGCGGGGTGATTAATTTGCTCTTCTTGTCGCACTTTCATTTGATGATGATGATGAT 726
QY 221 ProAsnLeuPheIysValIleIysGlyIleTyrThrLeuProSerHisLeuSerAla 240
Db 727 CCCAACTGTTCAAAAAGATTAAGGGGAGATCATATCTTCCAAATCATTTATCTGCT 786
QY 241 LeuAlaArgAspLeuIleProArgMetLeuValIysGluProMetIysArgIleThrIle 260
Db 787 CTTCGAAGGATTTGATCCCAAGAAATCTGTTGTTGATCTCTATGAAGAGATACAAAT 846
QY 261 ArgGluIleArgGluHisGlnTyrPheGlnIleArgLeuProArgTyrLeuAlaValPro 280


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Db      847  CGTGAATTCGAGAACACCCATGCTTTCAGAAATCGCTTCCTGCTCACTGGCAGTGCCT
Qy      281  ProProbAerThrThngInglAlaIyMetIleAspGluAerThrLeuAAspValVal
Db      907  CCACGACGACGCGGCGACCAAGCCAAATGATGTGAAGATACCTTAAGAGATTGTC
Qy      301  AsnMetGlyPheAsnLysAsnHisValCysGluSerLysCysSerArgLeuGlnAsnGlu
Db      967  AACCTGGATATGATTAAGACCATGTGTGATATTTGTGCAATAGGCTGCANAAATGAG
Qy      321  AlaThrValAlaIyTyTyLeuLeuLeuAspAsnArgPheArgAlaThrSerGlyTyTyLeu
Db      1027  GCAACTGTGATATTACTTACTTCTTGACATAGGTTCCGGGCGCAGTAGGGCATTTTG
Qy      341  GlyAlaAspTyTyGlnGluSerMetCAspArgAsnLeuAsnGlnLeuAlaSerSerGluSer
Db      1087  GGGGCTGACTATCTACATCAATGAGGTGAGAGTTTAACTGATTCACTTATGGAAATCA
Qy      361  SerSerSerGlyThrArgAsnTyValProGlySerSerArgProHisSerSerGlyLeu
Db      1147  GCAAGCCCAAGTACCGGACAGTATCTTCAGACAGCAATGATTTCTAAGGCGATGGCTTG
Qy      381  ArgProTyTyTyProValGluArgTyTyPalaLeuGlyLeuGlnSerArgAlaHisPro
Db      1207  CGGCAATATTACCCCGTTGAAAGAAATGGGCTCTGGGGCTCCAGTCTCGAGCTCAACT
Qy      401  ArgGluIleMetValGluValLeuLysValLeuGlnGluLeuAsnValArgTyTyLys
Db      1267  CGTAGAATATGATCGAGGTCTTAAGGCACTTCAGAAATTAATATGCTGCTGGAAAG
Qy      421  AsnGlyHisTyAsnValLysCysArgTyTyCysProGlyPheProGluValAsnAspThr
Db      1327  AATGACACTTCAACATATAATGCAAGTGGTGCTGCTGCTTCTTCAGGTCAAGTATATG
Qy      441  LeuAspAlaSerAsnSerPheLeuGlyAspSerThrIleMetAspAsnAspAlaAsn
Db      1387  TTAGATGCAACACACAGCTTTGTGATGACTTACCATCAAGATTAACGGGATGCTAT
Qy      461  GlyArgLeuProThrValIleLysPheGluPheGlnLeuTyTyTyTyLysAspLys
Db      1447  GGGAGGCTACCTGCGGTGATCAAGTTTGAATCCAGCTTTCACAGACCAAGATGACAA
Qy      481  TyrLeuLeuAspMetGlnArgValThrGlyProGlnLeuLeuPheLeuAspPheCysAla
Db      1507  TACCTGCTAGATATGACAGAGATTACGTGACCTCCTCTCTGGAATTTTGGCGG
Qy      501  AlaPheLeuThrLysLeuArgValLeu
Db      1567  GCCTTCCTTACCAACCTTAGGGTTCTA

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PD      22-JUN-2000.
XX      15-DEC-1999; 99WO-US029824.
XX      16-DEC-1998; 98US-0112563P.
XX      (DUPO ) DU PONT DE NEMOURS & CO E. I.
PI      Allen SM, Heppard EP, Sakai H, Weng Z, Helencjariis TG, Maccoll DJ,
PI      Miao G;
XX      WPI: 2000-431593/37.
DR      P-PSDB; AAB03420.
XX      New nucleic acids encoding sucrose non-fermenting 1 (SNF1) proteins
PT      involved in carbon catabolite repression in plants and seeds, useful for
PT      controlling carbon and nitrogen partitioning pathways during plant growth
PT      and development.
XX      Claim 2; Page 42-43; 59pp; English.
XX      The present sequence is a putative sucrose non-fermenting protein SNF1
CC      coding sequence from the soybean. The sequence was isolated by searching
CC      a pod DNA library for sequences similar to those known to encode SNF1 in
CC      Arabidopsis thaliana, Cucumis sativus, Glycine max and Oryza sativa. The
CC      protein is involved in carbon catabolite repression, and so the gene and
CC      protein can be used in plants to control the nitrogen and carbon
CC      partitioning pathways during plant growth and development. They can also
CC      be used to alter the accumulation of carbohydrates, lipids and proteins
CC      during plant growth
XX      SQ      Sequence 2123 BP; 593 A; 395 C; 477 G; 658 T; 0 U; 0 Other;
Alignment Scores:
Pred. No.: 3,59e-191 Length: 2123
Score: 1974.50 Matches: 382
Percent Similarity: 83.53% Conservative: 49
Best Local Similarity: 74.03% Mismatches: 76
Query Match: 73.32% Indels: 9
DB: Gaps: 3
US-09-857-522B-4 (1-509) x AAAS2772 (1-2123)
Qy      1 MetAspGlySerSer-----LysGlySerGlyHisSerGluAlaLeuAAspTyrAsn 18
Db      123 ATGATGACCAAGCTGGCCGACGATGCTGGCTGACATGTTCTTACCAAAATTATATAA 182
Qy      19 LeuGlyArgThrLeuGlyIleGlyThrPheGlyLysValLysIleAlaGlnHisLysLeu 38
Db      183 TTGGGAAAAACACCTCGGGAATTGATCTTTGGCAAGTGAATAATTGCAAGAACATGTTTG 242
Qy      39 ThrGlyHisArgValAlaIleLysIleIleAsnCysArgGlnMetCysArgAsnMetGluMet 58
Db      243 ACTGGCCATTAAGTTGGATCAAGATCCTTAACCGAAGCAATGAAGAAATGCAAGATG 302
Qy      59 GluGluLysAlaLysArgGluPheLysIleLeuLysLeuPheIleHisProHisIleIle 78
Db      303 GAAGAAAAAGTGAAGAAAGAAATCAAAATTTAAGATTGTTCAATGCAATCCTCAATTATT 362
Qy      79 ArgLeuTyTyGluValIleTyTyThrProThrAspIleTyTyValIleMetGluTyTyCysLys 98
Db      363 CGACTTTATAGCATAGCAATGAACCTCCAACTGACATATATTTGTCATGAGATATGAG 422
Qy      99 TyTyGlyLeuLeuPheAspTyTyIleValGluLysGlyArgLeuGlnGluAspGluAlaArg 118
Db      423 TCTGGAGAGCTTTTCCATATCATATGATGAGAGAGGTGTGTCAGGAAGATGAAGCTCGT 482
Qy      119 ArgIlePheGlnGlnIleIleSerGlyValGluTyTyCysHisArgAsnMetValIleHis 138
Db      483 AATTTTTCAGCAGATTAATCTCTGGGGTGAAGTCACTGACAGGAATATGATGCTTCAT 542
Qy      139 ArgAspLeuLysProGluLeuLeuLeuLeuAspSerLysTyTyAsnValLysLeuAlaAsp 158

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Db 543 AGAGATTGAGCCTGAGAAATTACTTTTGACATCCAAATGTAATGTCAGATTGCTGAT 602
 Qy PheGlyLeuSerAsnValMetHisAspGlyHisPheLeuLysThrSerCysGlySerPro 178
 Db 603 TTTGGCTTGAACCAATCATTCGATGCTACCTTTCTTAAACAAGTTGGGAAGCCCT 662
 Qy AsnTyrAlaAlaProGluValIleSerGlyLysLeuTyrAlaGlyProGluValAspVal 198
 Db 663 AACTATGACAGCTCTGAGATTATCTGAGAAATTTGATAGCTGAGACCTGAAATGATGTC 722
 Qy TrpSerCysGlyValIleLeuTyrAlaLeuLeuCysGlyThrLeuProPheAspAspGlu 218
 Db 723 TGGAGCTGTGTGTAATTTTATATAGCCCTCTTTGTGGCACCCCTCTTTGATGATGAA 782
 Qy AsnIleProAsnLeuPheLysValIleLeuGlyGlyIleTyrThrLeuProSerHisLeu 238
 Db 783 AATATTCGAATCTCTTCAGAAATTAAGGGTGGGATTTACACTCTTCCAGTCATCTA 842
 Qy SerAlaLeuAlaArgAspLeuIleProArgMetLeuValGluProMetLysArgIle 258
 Db 843 TCACCCGGTGTGATAGATTGATACAGGAGATGCTTGCGTTGACCCATAGAGAGATG 902
 Qy ThrIleArgGluIleArgGluHisGlnTrpPheGlnIleArgLeuProArgTyrLeuAla 278
 Db 903 ACCATACCTGAGATCCGTCACACCCATGTTCCAGCTCCACTTCCACGTTATTTAGCT 962
 Qy ValProProAspThrThrGlnGlnAlaLysMetIleAspGluAspThrLeuArgAsp 298
 Db 963 GTGCGACACACAGATACAGATCAACAGCCAAAGATTGATGAGAGATCTTCAGAGAA 1022
 Qy ValValAsnMetGlyPheAsnLysAsnHisValCysGlySerLeuCysSerArgLeuGln 318
 Db 1023 GTGGTGAATAAGGATTTGACAGAAATCAATGGTTGATCTCTGGGAACAGATACAA 1082
 Qy AsnGluAlaThrValAlaTyrTyrLeuLeuLeuAspAsnArgPheAlaThrSerGly 338
 Db 1083 AATAGAGGTACTGTGGCATACTATTTTATTTGACAAACCATTTTCGTTTCAGTGGC 1142
 Qy TyrLeuGlyAlaAspTyrGlnGluSerMetAspArgAsnLeuAsnGlnLeuAlaSerSer 358
 Db 1143 TATCTTGGAGCTGAGTTTCAGAGAACCATGATCCGGTTTAAATCAATGATCTCCAGT 1202
 Qy GluSerSerSerSerGlyThrArgAsnTyrValProGlySerSerAspProHisSerSer 378
 Db 1203 GAACCTGCTCTTCAGTTGTTGAAACCGCTTCCAGGCTCATGAGAAATATCCAGAGTA 1262
 Qy GlyLeuArgProTyrTyrProValGlnArgLysTrpAlaLeuGlyLysGlnSerArgAla 398
 Db 1263 GGATCGAGGCAACAGTCCCTGTTGAAAGAAATGGGCCCTTGGGCTTCAGTTCGAGCC 1322
 Qy HisProArgGluIleMetValGluValLeuLysAlaLeuGlnGluLeuAsnValArgTrp 418
 Db 1323 CATCTGCTGAAATTAAGTACTGAGGTTCTTAAAGCTTTGCAAGAAATTAATGTTTGTGG 1382
 Qy LysLysAsnGlyHisTyrAsnValLysCysArgTrpCysProGlyPhePro----- 435
 Db 1383 AAGAAAGTTGCTCACTCAACATGAGTGAAGTGGTGGTGGCATTCCTGTCACACAC 1442
 Qy 436 -----GluValAsnAspThrLeuAspAlaSerAsnSerPheLeuGlyAspSerThrIle 453
 Db 1443 GAAAGAAATGTTAAACATTAAGTCAATGATATCACTTACCTTGGAGATGATTCACAAT 1502
 Qy MetAspAsnAspAspAlaAsnGlyArgLeuProThrValIleLysPheGluPheGluLeu 473
 Db 1503 ATTGAGATGATGCTGTTCT-----ACTTCAATGATGTCAGAAAGTTGAAAGTCAGCTT 1556
 Qy TyrIleThrLysAspAspLysTyrLeuLeuLysPheGlnArgValThrGlyProGlnLeu 493
 Db 1557 TACAAACCCCGGAAGAAAGATATCTGCTGATCTTCAAGAGGTCAGAGGTCACAGATT 1616
 Qy LeuPheLeuAspPheCysAlaAlaPheLeuThrLysLeuArgValLeu 509
 Db 1617 CTTTCTTGTGATCTATGCTGCTTCTTCCACAGCTTCGTGTCCTC 1664

RESULT 5
 ACC00749
 ID ACC00749 standard; cDNA; 2123 BP.
 XX
 AC ACC00749;
 DT
 XX 16-MAY-2003 (first entry)
 DE Glycine max oil trait related cDNA sequence SEQ ID NO:247.
 XX
 KW Plant; oil trait; oil phenotype; altered lipid profile; MA kinase;
 KW receptor-like protein kinase; mitogen activated protein kinase; oil;
 KW LIPID-1-like transcription factor caleosin; ATP citrate lyase; SNF1;
 KW CKC-like transcription factor; antisense inhibition; co-suppression;
 KW transgenic plant; gene; ss.
 XX
 OS Glycine max.
 PN
 XX W02003002751-A2.
 PN
 XX 09-JAN-2003.
 XX
 XX 27-JUN-2002; 2002W0-US020152.
 XX
 XX 29-JUN-2001; 2001US-0301913P.
 PR
 PA (DUPLO) DU PONT DE NEMOURS & CO E I.
 PA (PION-) PIONEER HI-BRED INT INC.
 XX
 PI Allen SM, Allen WB, Cahoon RE, Epelbaum S, Famodu OO, Harvell LT, B;
 PI Jones TJ, Kinney AJ, Klein TM, Li C, Oliveira IC, Sakai H, Shen B;
 PI Tarczyński MC;
 XX
 DR WPI: 2003-201509/19.
 DR P-PSDB; ABR40714.
 XX
 PT Novel nucleotide fragment encoding polypeptides having receptor-like
 PT protein kinase activity, caleosin-like activity, useful for altering oil
 PT phenotypes in plants such as sunflower, coconut, soybean, wheat and rice.
 XX
 PS Claim 18; Page 286-287; 542pp; English.
 XX
 CC The present invention describes an isolated nucleotide fragment (I)
 CC comprising a nucleic acid sequence (NS) chosen from a NS encoding a
 CC polypeptide (PP) having receptor-like protein kinase activity, mitogen
 CC activated protein (MAP)-kinase activity, LIPID-1-like transcription factor
 CC activity, caleosin-like activity, ATP citrate lyase activity, SNF1-like
 CC activity and CKC-like transcription factor activity. Also described: (1)
 CC complement (II) of (I); (2) a chimeric construct (III) comprising (I) or
 CC (II), operably linked to a regulatory sequence; (3) a plant (IV)
 CC comprising (III) in its genome; (4) seeds (V) obtained from (IV); and (5)
 CC oil obtained from (V). (I) or its part can be used in antisense
 CC inhibition or co-suppression in a transformed plant. (III) is useful for
 CC altering the oil phenotype in a plant such as corn, soybean, wheat, rice,
 CC canola, Brassica, sorghum, sunflower or coconut. (III) is also useful for
 CC creating transgenic plants having altered lipid profiles. (I) can also be
 CC used as a hybridisation probe. ACC00626 to ACC00686 and ABR40591 to
 CC ABR40879 represent sequences used in the exemplification of the present
 CC invention.
 XX
 SQ Sequence 2123 BP; 593 A; 395 C; 477 G; 658 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 3,59e-191 Length: 2123
 Score: 1974.50 Matches: 382
 Percent Similarity: 83.53% Conservative: 49
 Best Local Similarity: 74.03% Mismatches: 76
 Query Match: 73.32% Indels: 9
 DB: Gaps: 3

US-09-857-522B-4 (1-509) x ACC00749 (1-2123)

QY 1 MetaspGlySerSer-----LysGlySerGlyHisSerGluAlaLeuArgAsnTyrAsn 18
DB 123 ATGATGGAACCAAGCGCGGAGGTGGTGGCTGGACATGTTCTTCAAAATTAATAA 182
QY 19 LeuGlyArgThrLeuGlyIleGlyThrPheGlyLysValIleIleAlaGluHisLysLeu 38
DB 183 TTGGGAAAAACACTCGGATTTGGATCTTTTGGCAAGGTGAATAATGCAAGACATGTGTG 242
QY 39 ThrGlyHisArgValAlaIleLeuIleIleLeuAsnGlySerGluMetArgAsnMetCys 58
DB 243 ACTGGCCATAAGTTGCGATCAAGATCCCTTAACCCAGCCAGATTAAGAAACATGGAATG 302
QY 59 GluGlyLysAlaLysArgGluPheLysIleLeuLysLeuPheIleHisProHisIleIle 78
DB 303 GAAGAAAAAGTGAAGAAAGAAATCAAAATTTTAATTTGTTCAATGATCTTCACTTATT 362
QY 79 ArgLeuTyrGluValIleTyrThrProThrAspIleTyrValIleMetGluTyrCysLys 98
DB 363 CGACTTATGAAGTATGAATAAATCTCAACTGACATATATGTGTGATGAGTATGTGAAG 422
QY 99 TyrGlyGluLeuPheAspTyrIleValGluLysGlyArgLeuGluAlaAspGluAlaArg 118
DB 423 TCTGAGAGCTTTTGCATTACATAGTGAAGAGGTGAGGTGACAGAAAGATGAAGCTGCT 482
QY 119 ArgIlePheGluGluIleIleSerGlyValGluTyrCysHisArgAsnMetValIleHis 138
DB 483 AATTTTTCACGACATATATCTTGGGGTGAAGTACTGTCAAGAAATATGTGTGTTTAT 542
QY 139 ArgAspLeuLysProGluAsnLeuLeuLeuAspSerLysTyrAsnValIleLysLeuAlaAsp 158
DB 543 AGAGATTTGAAGCCGGAATAATTACTTTTGACCTCAATGATATGATGATGATGATGAT 602
QY 159 PheGlyLeuSerAsnValMetHisAspGlyHisPheLeuLysPheSerCysGlySerPro 178
DB 603 TTTGGCTTGACCAATCATGATGATGATGATGATGATGATGATGATGATGATGATGAT 662
QY 179 AsnTyrAlaAlaProGluValIleIleSerGlyLysLeuTyrAlaGlyProGluValAlaAspVal 198
DB 663 AACATGACAGCTCTGAGATTTATCTCTGGAAATTTGATGCTGACCTGAAATGAGATGTC 722
QY 199 TrpSerCysGlyValIleLeuTyrAlaLeuLeuCysGlyThrLeuProPheAspAspGlu 218
DB 723 TGGAGCTGTGGTATATTATATATCCCTTCTTGTGCAACCTTCTTGTGATGATGATA 782
QY 219 AsnIleProAsnLeuPheLysLysIleLysGlyLysIleTyrThrLeuProSerHisLeu 238
DB 783 AATATTTCCAAATCTTCAAGAAATAAAGGTGGATTTACACTTCCCAAGTCATCTTA 842
QY 239 SerAlaLeuAlaArgAspLeuIleProArgMetLeuValIleGluProMetLysArgIle 258
DB 843 TCACCCCGGTCTAGAGATTTGATACAGAGATGCTTGTGGTTGACCTTAAGAGAAATG 902
QY 259 ThrIleArgGluIleArgGluHisGluIleTrpPheGluIleArgLeuProArgTyrIleAla 278
DB 903 ACCATACCTGAGATCCGTCACAACCCCATGTTCCAACTGCACTTCCAGTTATTTACT 962
QY 279 ValProProProAspThrThrGluGluAlaLysMetIleAspGluAspThrLeuArgAsp 298
DB 963 GTGCACACCAAGATACAAATGCAACAGGCAAAAAGATTTGAGAGAAATCTTCCAGAA 1022
QY 299 ValValAsnMetGlyPheAsnLysAsnHisValCysGluSerLeuCysSerArgLeuGlu 318
DB 1023 GTGGTGAATAATGGATTTGACAGCAATCAATTTGGTTGAATCTTTGGAAACAGATACAA 1082
QY 319 AsnGluAlaThrValAlaTyrTyrIleLeuLeuAspAsnArgPheArgAlaThrSerGly 338
DB 1083 AATAGGGTACTGTGGCATACTATTGTTATTTGCAACCATTTTGGTTTCCAGTGGC 1142
QY 339 TyrLeuGlyAlaAspTyrGluGluSerMetAspArgAsnLeuAsnGluLeuAlaSerSer 358
DB 1143 TATTTTGGAGCTGTGATCAAGAGCAATGATATCCCGTTTAAATCAATTCATTTCCAGT 1202
QY 359 GluSerSerSerSerGlyThrArgAsnTyrValProGlySerSerAspProHisSerSer 378

DB 1203 GAACCTGCTTCTTCAAGTTGTTGAACCCGCTTCCAGGCTCATGAAATATCCAGAGTA 1262
QY 379 GlyLeuArgProTyrTyrProValGluArgLysTrpAlaLeuGlyLysGluSerArgAla 398
DB 1263 GGATCGAGGCAACAGTTCCCTGTTGAAAGAAATGGGCGCTTGGGCTTCACTTCGAGCC 1322
QY 399 HisProArgGluIleMetValGluValLeuLysValIleGluGluIleLeuAsnValArgTrp 418
DB 1323 CATCTCGTAATAATATGACTGAGGTTCTTAAAGCTTTGCAAGAAATTAATGTTGTGG 1382
QY 419 LysLysAsnGlyHisTyrAsnValLysCysArgTrpCysProGlyPhePro----- 435
DB 1383 AAGAAGATTTGCTCACTCAACAATGAAAGTGAAGTGGTGGTGGCATTCCTGTCACAC 1442
QY 436 -----GluValAsnAspThrLeuAspAlaSerAsnSerPheLeuGlyAspSerThrIle 453
DB 1443 GAAGCAATGCTTAACAATTAATGTCATATGATATCTTGTGAGATGATGATCCAAACATT 1502
QY 454 MetAspAsnAspAspAlaAsnGlyArgLeuProThrValIleLysPheGluPheGluLeu 473
DB 1503 ATGGAATGATGCTGTTCT------ACTTCAATGTGTCAGAGTTGAAGTGCAGCTT 1556
QY 474 TyrIleThrLysAspAspLysTyrLeuLeuAspMetGluArgValIleGlyProGluLeu 493
DB 1557 TCAAAACCCCGGAAGAAATATATCTGTTGATCTTCAAGAGTGCAGGTCACAGTTT 1616
QY 494 LeuPheLeuAspPheCysAlaAlaPheLeuThrLysLeuArgValLeu 509
DB 1617 CTTTCTTGGATCTATGCTGCTTCTTCTTCCACAGCTTCGTGTCCTC 1664

RESULT 6

ID ABZ14852 standard; DNA; 1539 BP.

AC ABZ14852;

DT 21-JAN-2003 (first entry)

DE Arabidopsis thaliana stress regulated gene SEQ ID NO 2657.

KW Arabidopsis thaliana; plant; gene; stress; transgenic; ds.

OS Arabidopsis thaliana.

FN W0200216655-A2.

PD 28-FEB-2002.

PE 24-AUG-2001; 2001WO-US026685.

PR 24-AUG-2000; 2000US-0227866P.

PR 26-JAN-2001; 2001US-0264647P.

PR 22-JUN-2001; 2001US-0300111P.

PA (SCRI) SCRIPS RES INST.

PA (SYGN) SYNGENTA PARTICIPATIONS AG.

PI Harper JF, Kreps J, Wang X, Zhu T,

PX WPI; 2002-304127/34.

PT Identifying a stress condition to which a plant cell has been exposed and

PT producing plants with increased tolerance to these abiotic stresses.

CC Claim 144; SEQ ID NO 2657; 577bp + Sequence Listing; English.

CC The invention relates to identifying a stress condition to which a plant

CC cell has been exposed, comprising: (a) contacting nucleic acid

CC representative of expressed polynucleotides in the plant cell with an

CC array of probes representative of the plant cell genome; and (b)

CC detecting a profile of expressed polynucleotides in the plant cell

CC characteristic of a stress response. The method is useful in the

CC production of transgenic plants, cells and seeds and in producing plants
 CC with increased tolerance to abiotic stress. The present sequence is that
 CC of an Arabidopsis thaliana stress regulated gene (AB212196-AB217574) used
 CC in methods of the invention. Note: The sequence data for this patent is
 CC not represented in the printed specification but is based on sequence
 CC information supplied to Derwent by the European Patent Office

XX Sequence 1539 BP; 432 A; 313 C; 381 G; 413 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 7,33e-191 Length: 1539
 Score: 1969.50 Matches: 377
 Percent Similarity: 82.82% Conservative: 52
 Best Local Similarity: 72.78% Mismatches: 74
 Query Match: 73.13% Indels: 15
 Gaps: 4

US-09-857-522b-4 (1-509) x AB214852 (1-1539)

QY 1 MetAspGlySerSerLySGly-----SerGlyHisSerGluAlaLeuArgAsnTyrAsn 18
 Db 1 ATGATGATGATGAGCAGCAGCAGTGAAGTGGGTGAATGATCTTACCAATTTACAG 60
 QY 19 LeuGlyArgThrLeuGlyLeGlyThrPheGlyLysValLysIleAlaGluHisLysLeu 38
 Db 61 CTGGGAGAACTCTTGATTTGGTTCCTTGGTGAAGGATAGCTGACATGACATG 120
 QY 39 ThrGlyHisArgValAlaIleLysIleLeuAsnCySarGlnMetArgAsnMetGluMet 58
 Db 121 ACAGACATCAATGAGTGTCTATCAAGATCCTCAATCGTCCAAACCAAGAAATGAGAGT 180
 QY 59 GluGluLysAlaLysArgGluPheLysIleLeuLysLeuPheIleHisProHisIle 78
 Db 181 GAGAGAAAGTGAAGAGAGATCAAAATCTTGACATTTATGATCTCCACATGATC 240
 QY 79 ArgLeuTyrGluValIleTyrThrProThrAspIleTyrValAlaMetGluTyrCysLys 98
 Db 241 CGTCTCATGAGTTATGAGACTCCCAAGATATTTATCTTGATGAGATGATGAC 300
 QY 99 TyrGlyGluLeuPheAspTyrIleValGluLysGlyArgLeuGlnLysAspGluAlaArg 118
 Db 301 TCTGTGAGCTATTGATATATTGTTGAGAAAGGTGATGACAGAGATGAGCCGAG 360
 QY 119 ArgIlePheGlnGlnIleLeuSerGlyValGluTyrCysHisArgAsnMetValAlaHis 138
 Db 361 AACCTTTTTCAGCATATATATCAGAGTGAATCTCCATCGAAACATGTTGTTAC 420
 QY 139 ArgAspLeuLysProGluAsnLeuLeuAspSerLysTyrAsnValLysLeuAlaAsp 158
 Db 421 AGAGACCTCAAGCCGAAACCTGCTTTGACCTTAATCAATGTMAAGATTGCTGAT 480
 QY 159 PheGlyLeuSerAsnValMetHisAspGlyHisPheLeuLysThrSerCysGlySerPro 178
 Db 481 TTGGCTGAGACAAATATGACAGATGCTATTTTGAAGACAAGTTGGAGAGTCCA 540
 QY 179 AsnTyrAlaAlaProGluValIleSerGlyLysLeuTyrAlaGlyProGluValAlaAspVal 198
 Db 541 AATTATGCGCGTCCAGAGTAAATTCGGGCAAGTTATATGCTGGCCCGAAGTAGATTC 600
 QY 199 TyrSerCysGlyValIleLeuTyrAlaLeuLeuCysGlyThrLeuProPheAspAspGlu 218
 Db 601 TGGAGCTGTGTGATCTCAACCTCTCTCTGTGGAGACGCTTCCATTGATGATGAA 660
 QY 219 AsnIleProAsnLeuPheLysLysIleLysGlyGlyIleTyrThrLeuProSerHisLeu 238
 Db 661 AACATTTCCCAACTTTTAAAGATMAAGGAGGATATACACATTACCTAGCCATTTA 720
 QY 239 SerAlaLeuAlaArgAspLeuIleProArgMetLeuValAlaGluProMetLysArgIle 258
 Db 721 TCTCTGTGTGATGATTTGATCCCGGATGCTGTGAGTTGACCCATGAACGAGTA 780
 QY 259 ThrIleArgGluIleArgLysGlnIleTyrPheGlnIleArgLeuProArgTyrLeuAla 278

Db 781 ACCATCCCTGAGATCCGGCAACCCCTTGCTTCAAGCTCATCTCCGAGTATTAGCT 840
 QY ValProProAspThrThrGlnAlaLysMetIleAspGluAspThrLeuArgAsp 298
 Db 841 GTTCTCTCCAGATCTGTCGACAGGCAAAAAGATTACAGAGAGATTTCTCAAGAA 900
 QY ValValAsnMetGlyPheAsnLysAsnHisValCysGluSerLeuCysSerArgLeuGln 318
 Db 901 GTTATCAATATGGGATTGTGACAGAAACCACTCATGCAATCGCTCCGCAACCAACCA 960
 QY 319 AsnGluAlaThrValAlaTyrTyrLeuLeuLeuAspAsnArgPheArgAlaThrSerGly 338
 Db 961 AATGATGACACTGAGACGTCTATCTGATCTGACATGATGTTTCCGTGCTTATGAGT 1020
 QY 339 TyrLeuGlyAlaAspTyrGlnGluSerMetAspArgAsnLeuAsnGlnLeuAlaSerSer 358
 Db 1021 TATCTGGGGCTGAGTTTCAAGACCATGGA---GATCTCCCTCATGATCCAGCA 1077
 QY 359 GluSerSerSerSerGlyThrArgAsnTyrValProGlySerSerAspProHisSerSer 378
 Db 1078 GAAAGCGTTCCTTCACTGTTAGCATCGGCTTCCAGACCTGATGAAATCAAGAGATT 1137
 QY 379 GlyLeuArgProTyrTyrProValGluArgLysThrAlaLeuGlyLysGlnSerArgAla 398
 Db 1138 GGCCTTGAGATCTCAATTCCTGTTGAGAGAAATGGGCTCTTGACCTTCAGTCTCGGGCT 1197
 QY 399 HisProArgGluIleMetValGluValLeuLysValLeuGlnGluLeuAsnValArgTyr 418
 Db 1198 CATCCCGTGAATATATGACGAAAGTCTTAAGCCCTGCAAGATTTGAATGATGTTGG 1257
 QY 419 LysLysAsnGlyHisTyrAsnValLysCysArgTyrCysProGlyPheProGluValAsn 438
 Db 1258 AAGAAATAGAGGCACTCAACATGAAGTCAGATGGGTTCT-----AAC 1302
 QY 439 AspThrLeuAspAla-----SerAsnSerPheLeuGlyAspSer 451
 Db 1303 AGCAGCCCAATGATGATGCTCACTAATCGATGACACATCAACTTGGAGAGAG 1362
 QY 452 ThrIleMetAspAsnAspAspAlaAsnGlyArgLeuProThrValIleLysPheGluPhe 471
 Db 1363 TCCAGCATATATAGAAAGCAAGCAGCTGTTAAAGTCCCAATGTTGCAAGTTTGAAT 1422
 QY 472 GlnLeuTyrLysThrLysAspAspLysTyrLeuLeuAspMetGlnArgValThrGlyPro 491
 Db 1423 CAGTTGTATAAACTCGGAGACGACAACTATCTCTGATTTGACAGAGATCAAGGTCT 1482
 QY 492 GlnLeuLeuPheLeuAspPheCysAlaAlaPheLeuThrLysLeuArgValLeu 509
 Db 1483 CAGTTCTGTGTTGATCTGTGTGCTTTTCTTCTGCTGAGCTCCGAGTCTC 1536

RESULT 7
 ACC00745
 ID ACC00745 standard; cDNA; 2052 BP.
 AC ACC00745;
 XX
 XX
 XX
 XX
 DE 16-MAY-2003 (first entry)
 XX
 XX
 XX
 XX
 XX
 XX
 XX
 OS Zea mays.
 XX
 XX
 PN MO2003002751-A2.
 XX
 XX
 PD 09-JAN-2003.
 XX
 XX
 PF 27-JUN-2002; 2002MO-US020152.

Zea mays oil trait related cDNA sequence SEQ ID NO:239.
 Plant; oil trait; oil phenotype; altered lipid profile; MAP kinase;
 receptor-like protein kinase; mitogen activated protein kinase; oil;
 lipid-like transcription factor callosin; ATP citrate lyase; SNF1;
 CRC-like transcription factor; antisense inhibition; co-suppression;
 transgenic plant; gene; ss.

Db 1620 GAGAAATACCTCCCGATTTTGCAAGAGTCACTGGGCACAGCTCTTCTTGACTTG 1679
Qy 499 GysAlaAlaPheLeuThrLysLeuArgValIeu 509
Db 1680 TGGCGGCGCTTTCTTACTCACTGAGAGTCTT 1712
RESULT 8
AAA52774
ID AAA52774 standard; cDNA; 2543 BP.
XX AAA52774;
AC
XX
DT 03-JAN-2001 (first entry)
XX Soybean putative catabolite repression protein SNF1 coding sequence #4.
DE Soybean; carbon catabolite repression; sucrose non-fermenting protein 1;
KM SNF1; plant growth; ss.
XX Glycine max.
OS
XX
FH Key Location/Qualifiers
FT CDS 73..1620
FT /*tag= a
FT /product= "SNF1"
XX MO200036115-A2.
PN 22-JUN-2000.
XX
XX 15-DEC-1999; 99WO-US029824.
PF
XX 16-DEC-1998; 98US-0112563P.
PR
XX (DUPO) DU PONT DE NEMOURS & CO E I.
PA
PI Allen SM, Heppard EP, Sakai H, Weng Z, Helentjaris TG, Macool DJ;
FI Miao G;
XX WPI; 2000-431593/37.
DR P-PSDB; AAB03422.
DR
XX New nucleic acids encoding sucrose non-fermenting 1 (SNF1) proteins
PT involved in carbon catabolite repression in plants and seeds, useful for
PT controlling carbon and nitrogen partitioning pathways during plant growth
PT and development.
XX
PS Claim 2; Page 47-48; 59pp; English.
XX
CC The present sequence is a putative sucrose non-fermenting protein SNF1
CC coding sequence from the soybean. The sequence was isolated by searching
CC a seed cDNA library for sequences similar to those known to encode SNF1
CC in Arabidopsis thaliana, Cucumis sativus, Glycine max and Oryza sativa.
CC The protein is involved in carbon catabolite repression, and so the gene
CC and protein can be used in plants to control the nitrogen and carbon
CC partitioning pathways during plant growth and development. They can also
CC be used to alter the accumulation of carbohydrates, lipids and proteins
CC during plant growth
XX
SQ Sequence 2543 BP; 740 A; 477 C; 557 G; 769 T; 0 U; 0 Other;
Alignment Scores:
Pred. No.: 1.96e-187 Length: 2543
Score: 1939.00 Matches: 373
Percent Similarity: 83.37% Conservative: 58
Best Local Similarity: 72.15% Mismatches: 76
Query Match: 72.00% Indels: 10
DB: 3 Gaps: 4
US-09-857-522B-4 (1-509) x AAA52774 (1-2543)
Qy 1 MetAspGlySerSer---LysGlySerGlyHisSer-----GluAlaLeuArgAsnTyr 17

Db 73 ATGACAGATCACTGGCCGTGGTGGTGAAGTGTGCACATGTTTCTCCCAAAATTAT 132
Qy 18 AsnLeuGlyArgThrLeuGlyIleGlyThrPheGlyValIleValIleAsnIleLys 37
Db 133 AAGTGGGAAAACACCTGGCATTTGGCTCTTGGCAAGGTGAATAATGCTGAGCATGA 192
Qy 38 LeuThrGlyHisArgValAlaIleLysIleIleAsnGlySerGlyMetArgAsnMetGlu 57
Db 193 CGGACTGTGTCATAAAGTGTCTATTAAGATCTTAAACCGCCACAAGTTAAACATGGAA 252
Qy 58 MetGluGluLysAlaLysArgGluPheLysIleLeuLysLeuPheIleHisProHisIle 77
Db 253 ATGGAAGAAAAGTTGAAGAGAAATCAAAATTTTAAGATTGTTATGCAATCATCAT 312
Qy 78 IleArgLeuThrGluValIleIleThrProThrAspIleThrValIleMetGluTyrCys 97
Db 313 ATTAAGACTATATAGAGTTGTAGAAACCCCAACAGACATATATGTTATGAGATATGTG 372
Qy 98 LysTyrGlyGluLeuPheAspTyrIleValGluLysGlyArgLeuGlnIleAspGluAla 117
Db 373 AAATCTGGAGAGCTCTTTGATTTACATATAGAGAGGTGGCTGCCAAGAGATGAAGCC 432
Qy 118 ArgArgIlePheGlnGlnIleIleSerGlyValGluTyrCysHisArgAsnMetValVal 137
Db 433 CGTCATTTTTCAGCAGATTAATTTCTGTGTGAGTACGTCAAGAAATATGTGTT 492
Qy 138 HisArgAspLeuLysProGluAsnLeuLeuLeuAspSerLysTyrAsnValLysLeuAla 157
Db 493 CATAGAGACCTGAAGCCTGAAGATTATCTGTGACCTCAAAATTTAATCATCAAGATTTGCT 552
Qy 158 AspPheGlyLeuSerAsnValMetHisAspGlyHisPheLeuLysThrSerCysGlySer 177
Db 553 GATTTGGGTTGAGCAACATCATCCGATGTCATCTTTTAAGACAATTTGTGGAAGC 612
Qy 178 ProAsnTyrAlaAlaProGluValIleSerGlyLysLeuTyrAlaGlyProGluValAsp 197
Db 613 CTTAATTATCGGGCTCCAGAGGTATCTTGAAAATTTGATGTGGACCAAGAGTATGAT 672
Qy 198 ValThrSerCysGlyValIleLeuTyrAlaLeuLeuLysGlyThrLeuProPheAsp 217
Db 673 GTCTGAGAGCTGTGTGAATTTATATATGCTCTCTGTGGCATCTTCTTTGAGAT 732
Qy 218 GluAsnIleProAsnLeuPheLysLysIleLysGlyGlyIleTyrThrLeuProSerHis 237
Db 733 GAAACATTTCCCATCTCTTCAAAAAATAAAGGTGGATATACATCTTCCATGAT 792
Qy 238 LeuSerAlaLeuAlaArgAspLeuIleProArgMetLeuValValGluProMetLysArg 257
Db 793 CTATCACCTGGTGTAGAGATTGTGATACCAAGATGCTGTGGATCCCATGACAGAG 852
Qy 258 IleThrIleArgGluIleArgGluHisGlnThrPheGlnIleArgLeuProArgTyrLeu 277
Db 853 ATGACCACTACCTGAGTAACGCAACACCACTGTTCCAGATTCATCAACCGCTTATTTA 912
Qy 278 AlaValProProAspThrThrGlnGlnAlaLysMetIleAspGluAspThrLeuArg 297
Db 913 GCACTGGCAACCAACGATACCTGCAACAGCCAAAAGATGATGAGAGATCTTCAG 972
Qy 298 AspValValAsnMetGlyPheAsnLysAsnHisValCysGluSerLeuCysSerArgLeu 317
Db 973 GAACTGTTAATATAGGATTTGACAGAAATCAATGATTGATTCTTCAAGACAGATA 1032
Qy 318 GluAsnGluAlaThrValAlaIleTyrThrLeuLeuAspAsnArgPheArgAlaThrSer 337
Db 1033 CAAATATAGGGTACTGTACACTACTATTGTTATGGAACAACCGTTTCGTGTTCTAAGT 1092
Qy 338 GlyTyrLeuGlyAlaAspTyrGlnGlnLysMetAspArgAsnLeuAsnGlnLeuLysSer 357
Db 1093 GGTATATCTTGAGCTGAATTTCAAGACAAATGATTCGTGTTTAAACCGATGCATTC 1152
Qy 358 SerGluSerSerSerGlyThrArgAsnTyrValProGlySerSerAspProHisSer 377

Db 1153 GCCGAGTTCCTTCACGTTGTTGGACACGACGAGGATATGATATTCAGGG 1212
 Qy 378 SerGlyLeuAsgProTyrTyrProValGluArgLysThrAlaLeuGlyLeuGlnSerArg 397
 Db 1213 GTAGAGATGCGGACAGCTCCCTGTTGAGGAAATGGCCCTTGAGCTTCAGCTCGA 1272
 Qy 398 AlaHisProArgGluIleMetValGluValLeuLysAlaLeuGlnGluLeuAsnValArg 417
 Db 1273 GCCCAGACAGCTGAATATATGACGAGGCTCTTAAGCTCTACAAAGATTAAGTTTGT 1332
 Qy 418 TrpLysLysAsnGlyHisTyrAsnValLysCysArgTyrCysProGlyPhePro----- 435
 Db 1333 TGGAGAGAGATTGGACACTATATACATGAGATGGATGGTGGCGACATGCTGTCAT 1392
 Qy 436 -----GluValAsnAspThrLeuAspAlaSerAsnSerPheLeuGlyAspSerThr 452
 Db 1393 CATGAGAGATGATTACAAATCTCTGCATGATATCATCTTGGAAATGATTCGGC 1452
 Qy 453 IleMetAspAsnAspAlaAsnGlyArgLeuProThrValIleLysPheGluPheGln 472
 Db 1453 ATTATGAAATGAGAGCTGTTCT-----AAGTCAATGTGCTGCAAGTTTGAAGTCAG 1506
 Qy 473 LeuTyrLysThrLysAspAspLysTyrLeuLeuAspMetGlnArgValThrGlyProGln 492
 Db 1507 CTTTACAAAACCTCGTGAAGAGAAATATCTGCTTGAATTTCAAGGGCTCAGGCCACAG 1566
 Qy 493 LeuLeuPheLeuAspPheCysAlaAlaPheLeuThrLysLeuValLeu 509
 Db 1567 TTTCTTTCTTGAGATGTGTGCGCTGCTTCTTTCACAGCTACGTTCTC 1617
 RESULT 9
 ID ACC00751 standard; cDNA; 2543 BP.
 AC ACC00751;
 DT 16-MAY-2003 (first entry)
 XX Glycine max oil trait related cDNA sequence SEQ ID NO:251.
 DE Glycine max oil trait related cDNA sequence SEQ ID NO:251.
 XX Plant; oil trait; oil phenotype; altered lipid profile; MAP kinase;
 KW receptor-like protein kinase; mitogen activated protein kinase; oil;
 KW LIP15-like transcription factor caleosin; ATP citrate lyase; SNF1;
 KW CKC-like transcription factor; antisense inhibition; co-suppression;
 KW transgenic plant; gene; ss.
 OS Glycine max.
 XX
 OS WO2003002751-A2.
 PN 09-JAN-2003.
 XX
 PD 27-JUN-2002; 2002WO-US020152.
 XX
 PF 29-JUN-2001; 2001US-0301913P.
 PR
 XX (DUPO) DU PONT DE NEMOURS & CO E I.
 PA (PION-) PIONEER HI-BRED INT INC.
 XX
 PI Allen SM, Allen WB, Cahoon RE, Epelbaum S, Famodu OO, Harvell LT;
 PI Jones TJ, Kinney AJ, Klein TM, Li C, Oliveira IC, Sakai H, Shen B;
 PI Tarczynski MC;
 PI
 XX WPI; 2003-201509/19.
 DR P-PSDB; ABR40716.
 XX
 XX Novel nucleotide fragment encoding polypeptides having receptor-like
 PT protein kinase activity, caleosin-like activity, useful for altering oil
 PT phenotypes in plants such as sunflower, coconut, soybean, wheat and rice.
 PS Claim 18; Page 291-292; 542pp; English.
 XX
 CC The present invention describes an isolated nucleotide fragment (I)

CC comprising a nucleic acid sequence (NS) chosen from a NS encoding a
 CC polypeptide (PP) having receptor-like protein kinase activity, mitogen
 CC activated protein (MAP)-kinase activity, LIP15-like transcription factor
 CC activity, caleosin-like activity, ATP citrate lyase activity, SNF1-like
 CC activity and CKC-like transcription factor activity. Also described: (1)
 CC complement (II) of (I); (2) a chimeric construct (III) comprising (I) or
 CC (II), operably linked to a regulatory sequence; (3) a plant (IV)
 CC comprising (III) in its genome; (4) seeds (V) obtained from (IV); and (5)
 CC oil obtained from (V). (I) or its part can be used in antisense
 CC inhibition or co-suppression in a transformed plant. (III) is useful for
 CC altering the oil phenotype in a plant such as corn, soybean, wheat, rice,
 CC canola, Brassica, sorghum, sunflower or coconut. (III) is also useful for
 CC creating transgenic plants having altered lipid profiles. (I) can also be
 CC used as a hybridisation probe. ACC00626 to ACC00868 and ABR40591 to
 CC ABR40879 represent sequences used in the exemplification of the present
 CC invention
 CC
 XX
 XX Sequence 2543 BP; 740 A; 477 C; 557 G; 769 T; 0 U; 0 Other;
 Alignment Scores:
 Pred. No.: 1.96e-187 Length: 2543
 Score: 1939.00 Matches: 373
 Percent Similarity: 83.37% Conservative: 58
 Best Local Similarity: 72.15% Mismatches: 76
 Query Match: 72.00% Indels: 10
 DB: 7 Gaps: 4
 US-09-857-522B-4 (1-509) x ACC00751 (1-2543)
 Qy 1 MetAspGlySerSer---LysGlySerGlyHisSer-----GluAlaLeuArgAsnTyr 17
 Db 73 ATGACAGATCAACCTGCGCGTGTGAGTGAAGTGGACATGTTCTCCGAATATAT 132
 Qy 18 AsnLeuGlyArgThrLeuGlyIleGlyThrPheGlyLysValLysIleAlaGluHisLys 37
 Db 133 AAGTTGGAAAAACACCTCGCATTTGGCTCTTGGCAAGGTGAATAATGCTGAGCAATGTA 192
 Qy 38 LeuThrGlyHisArgValAlaIleLysIleLeuAsnCysArgGlnMetArgAsnMetGlu 57
 Db 193 CGGACTGTCTATTAAGTTGCTATTAAGATCTTAAACCCGACCAAGATTAAACATGAA 252
 Qy 58 MetGluLysAlaLysArgGluPheLysIleLeuLysLeuPheIleHisProHisIle 77
 Db 253 ATGAAAGAAAAGTTAAAGAAATCAAAATTTTAAGATTGTTATGACATCATCAT 312
 Qy 78 IleArgLeuTyrGluValIleTyrThrProThrAspIleTyrValValMetGluTyrCys 97
 Db 313 ATTAAGACTATATGAGTTGTAGAAACCCCAACAGACATATATGTTGTTATGAGATATGTG 372
 Qy 98 LysTyrGlyLysLeuPheAspTyrIleValGluLysGlyArgLeuGlnGluAspGluAla 117
 Db 373 AAATCTGAGAGCTCTTGTGATTAATGATGAGAGAGGCTGCGTCAAGAGATGAAGCC 432
 Qy 118 ArgArgIlePheGlnGlnIleIleSerGlyValGluTyrCysHisArgAsnMetValVal 137
 Db 433 CGTCATTTTTCACGAGATTAATTTCTGCTGTGAGATCTGACAGGAATATGCTGT 492
 Qy 138 HisArgAspLeuLysProGluAsnLeuLeuAspSerLysTyrAsnValLysLeuAla 157
 Db 493 CATGAGACCTGGAAGCCTGGAATTTACTCTTGACCTCAAAATTTAACATCAAGATTGCT 552
 Qy 158 AspPheGlyLeuSerAsnValMetHisAspGlyHisPheLeuLysThrSerCysGlySer 177
 Db 553 GATTTTGGTTGAGCAACATCATGCGTGAATGCTCATCTTTAAGACAAATGTTGGAAGC 612
 Qy 178 ProAsnTyrAlaAlaProGluValIleSerGlyLysLeuTyrAlaGlyProGluValAsp 197
 Db 613 CTRPATTAATCGGCTCCAGAGTTATCTTGAAATTTGATGCTGACAGAAAGTATGAT 672
 Qy 198 ValTyrSerCysGlyValIleLeuTyrAlaLeuLeuCysGlyThrLeuProPheAspAsp 217
 Db 673 GTCGAGCTGTGTGTAATTTATATATGCTCTCTGTGCACTCTTCTTTGATGAT 732

QY	218	GIuSen1lePrhoSenPheUlsy1lelysg1ygl1y1eTyrThleuProSerSis	237
Db	733	GAAAAcATTCcCAAcTCTTcCAAAAAATTAAGGGTGGAAATAcAcTCTTCAAGTAT	792
QY	238	LeuSerAlaLeuAlaArgAspLeu1leProArgMetLeuVala1GluProMetLysArg	257
Db	793	CTATACCTGGTGGTGAAGATTGATACCAAGATGCTTGTTGGTGGATCCCATGAAGGG	852
QY	258	1leThr1leArgGlu1leArgGlu1leSgIntPheGln1leArgLeuProArgTyrLeu	277
Db	853	ATGACCAATACCTGAATAGCCAAcCAcCATGTTCCAAGTTCATCTACCGGTTATTTA	912
QY	278	AlaVal1ProProProAspThrThrGlnGlnAlaLysMet1leAspGluAspThrLeuArg	297
Db	913	GCAGTGCACCAcCCAGATACACTGCAcCAAGcCAAAAAAGATTGAAGAGATTCCTTACG	972
QY	298	AspVal1ValAsnMetG1yPheAsnLysAsn1leVal1CySg1userLeuCySerArgLeu	317
Db	973	GAAAGGTGTAATATGGATTGACAGGAATCAATTGTTGAATCTCTTAAGCAcAGATTA	1033
QY	318	GlnAsnGlnAla1aThrValAla1aTyrTyrLeuLeuLeuAspAsnArgPheArgAlaAsnSer	337
Db	1033	CAAAATGAGCGTACCTGAACATACATATTGTTATTGGAcCAcCGGTTTCGTGTTCTAGT	1092
QY	338	G1yTyrLeuG1yAlaAspTyrGlnG1userNetAspArgAsnLeuAsnGlnLeuAlaSer	357
Db	1093	GGTATCTCTTGGAGCTGAATTCACAGACAAATGGATTCGTGTTTAAcCGATGATTCc	1152
QY	358	SerG1userSerSerSerG1yThrArgAsnTyrVal1ProG1ySerSerAspProHisSer	377
Db	1153	GGCGAAGTTGCTTTCcCAcGTTGGACACCAcCAcCAcGAGGTATATGATATTCAAGG	1212
QY	378	SerG1yLeuArgProTyrTyrProValGluArgLysTTPAlaLeuG1yLeuGlnSerArg	397
Db	1213	GTAAGAAATCGGGCAcAGTTCCTCTGTGAAGAAATAGGGCCCTTGCGCTCAGTCTGA	1272
QY	398	AlaHisProArgGln1leMetVal1GluVal1LeuLysAlaLeuGlnGlnLeuAsnValArg	417
Db	1273	GCCCAcCAcCAcCGAATATATGACTGAGGTCCTTAAAGCTCTTACAAGAATTAAATGTTGT	1332
QY	418	TP1yLysLysAsnG1yHisTyrAsnVal1ySgYsaGTPCySProG1yPhePro-----	435
Db	1333	TGGAAGAAAGATTGACACTATACATGAAGTCAATGGGTTGCTGGCACTGCTGTCAT	1392
QY	436	-----GluValAsnAspThrIleuAspAlaSerAsnSerPheLeuG1yAspSerThr	452
Db	1393	CATGAAGAAATGATTATACATCTCTCGCATACTATCATTACTTTGGAAATGATTCcCGGC	1455
QY	453	1leMetAspAsnAspAlaAsnG1yArgLeuProThrVal1leLysPheGlnPheGln	472
Db	1453	ATTATTGAAAAATGAAGCTGTTTCT-----AAGTCAAAATGTGTCAAGTTGAAcGTGACG	1508
QY	473	LeuTyrLysThrLysAspAspLysTyrLeuLeuAspMetGlnArgVal1ThG1yProGln	492
Db	1507	CTTTACAAAACCTCGAGAGAGAAATATGCTTGATCTTCAAAAGGCTCCAGGcCCACAG	1566
QY	493	LeuLeuPheLeuAspPheCysAla1aPheLeuThrLysLeuArgValLeu	509
Db	1567	TTTCTTTTCTTGATCTGTGCGCTCTTCTTCTTCAcAGTACGATTCCTC	1617
RESULT 10			
AAf62011			
ID	AAf62011	standard; DNA; 1929 BP.	
XX	AAf62011;		
AC			
DT	02-MAY-2001	(first entry)	
XX			
DE	Tomato LesNFI (sucrose nonfermenting yeast homologue) gene.		
XX	Sucrose non-fermenting; SNF-4; SNF-1; tomato; sugar metabolism; seed;		
KM	source-sink; fruit; enhanced quality; sugar accumulation; LesNFI;		
KW	stress resistance; transgenic plant; germination stimulation; ds.		

XX	Lycopersicon esculentum.
OS	WO200107570-A1.
PN	01-FEB-2001.
XX	21-JUL-2000; 2000MO-US019981.
PD	21-JUL-1999; 99US-00359161.
XX	(REGC) UNIV CALIFORNIA.
PA	Bradford KJ, Peetambar D, Yang H, Cooley M, Downie B, Gee OH;
XX	WPI; 2001-168545/17.
DR	New sucrose non-fermenting (SNF1) and SNF4 polynucleotides and expression
PT	cassettes containing the polynucleotides for modulating source-sink
PT	relationships in plants and enhancing yield or quality of harvested plant
PT	products.
XX	Claim 19; Page 39; 43pp; English.
PS	This invention relates to polynucleotide sequences encoding plant sucrose
CC	non-fermenting SNF-4 or SNF-1 polypeptides. Specifically included in the
CC	invention are tomato LeSNF-4 and LeSNF-1 polynucleotide sequences. A
CC	recombinant expression vector comprising SNF-4 or SNF-1 polynucleotide
CC	sequences is useful for modulating sugar metabolism in a plant. The
CC	recombinant expression cassette comprising the DNA sequence is useful for
CC	modulating source-sink relationships in plants and therefore enhances
CC	yield or quality of harvested plant products, such as fruit. SNF-4 and
CC	SNF-1 DNA can be used to enhance sink activity or starch or lipid
CC	accumulation in seeds. Also they can be used to enhance sugar
CC	accumulation in fruits. The expression cassettes can also be used to
CC	enhance responsiveness to stress conditions in plants. Enhanced
CC	expression of SNF1 and SNF4 polynucleotides or polypeptides is used to
CC	alter expression of sugar related genes or to enhance resistance to
CC	stresses. Inhibition of endogenous SNF1 or SNF4 genes modulates the
CC	activity of enzymes associated with sugar metabolism. In seeds,
CC	inhibition of SNF4 expression can be used to break dormancy and stimulate
CC	germination. The present sequence represents the tomato LeSNF-1 gene
XX	
SQ	Sequence 1929 BP; 546 A; 384 C; 442 G; 557 T; 0 U; 0 Other;
Alignment Scores:	
Pred. No.:	1,88e-187 Length: 1929
Score:	1937.50 Matches: 375
Percent Similarity:	85.08% Conservative: 64
Best Local Similarity:	72.67% Mismatches: 68
Query Match:	71.95% Indels: 10
DB:	Gaps: 4 6
US-09-857-522B-4 (1-509) x AAF62011 (1-1929)	
QY	1 MetAspGlySerSer---LysGlySerGlyHisSerGluAlaA--LeuArgenTyArgan 18
Dd	33 ATGACGGGAACAAGTCGTCTCAAGANTTTTAATCGTGAATAATACCTAAACTATTAA 92
Dd	19 LeuGIYAArgThleuGIYLllegIYhrrPheGIYLYseValIyLIlelaGluHlsylau 38
QY	93 CTCGGGAAAAACCTTGGCATTGATGCTTCCTGGCAAAGTTAAATACCTGAACATACGTTA 152
QY	39 ThrGIYHISArgValAlaIleLysIIleIeaNCysArGIuMeCArgasMetGIumeE 58
Dd	153 ACAAGGCCAACAAAGTTCGTCTCAAGANTTTTAATCGTGAATAATACGAAATATGACATG 212
QY	59 GluGIuLYseAlILysArGIuPhelysIIleuLYseLeuPhelIleIsProhisIIelle 78
Dd	213 GAGGAGAAGATCCGATGAGAAATCAAAAATATGAGATTGTCATGCATCTCATATTATA 272
QY	79 ArgLeuTYrGIuValIIleTYrThrProTHrAPilleyValValMetGIuTYrCySLvs 98


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Db      273 CGGCTTTATGAGTCATAGACAGACACCATATATATGTTGTGATGAGTATGTGAAA 332
Qy      99 TyrGIuLeuPheAspTyrIleValIGluysgIyATgLeuGluAspGluIaArg 118
Db      333 TCTGGCGAGTATTTGATTACATGTGTGAGAGGGCAGATTGACAGAGATGAACCTGCT 392
Qy      119 ArgIlePheGlnGlnIleIeSerGIyValGIuTyrCySHiEArgAsmValIaHis 138
Db      393 AACTTTTTCACCAATATTTCTGTGTGAGTACTGCCATKGAACATGTTGTTTCAAT 452
Qy      139 ArgAspLeuysPProGluAsnLeuLeuAspSerIyEyrAsnValIyLeuIaAsp 158
Db      453 AGAGACCTTAAGCCTGAAAACTCTCTGCACTCCAATGGAATGTGAAGATCCAGAT 512
Qy      159 PheGIyLeuSerAsnValMetHiSaPgiYHiSPhelEuysThSerCySgIySerPro 178
Db      513 TTTGGTTTGAGCAATATCATGCGCATGTCTCTCTGAGCAACCAAGTTGCGAGGCCCA 572
Qy      179 AsnTyrAlaAlaPProGIuValIleSerGIyLySLeuTyrAlaGIyProGIuValaAspVal 198
Db      573 AACTATGCTGCCCGACAGGTTTATCAGGTAAATTTGATGCTGGCCCTGAGGTAGATGTA 632
Qy      199 TrpSerCySgIyValIleLeuTyrAlaLeuLeuCySgIyThLeuProPheAspGlu 218
Db      633 TGAAGCTGTGGTATTCTTATCTTATGCTCTCTGAGCAACCTCCGTTTGACATGA 692
Qy      219 AsnIleProAsnLeuPheIyLeuIySgIyIleTyrThLeuProSerHiSLeu 238
Db      693 AACATATCCCAATCTTTTAAAGAAATAAAGGTGAAATATATCTCCGCCGCAATTTA 752
Qy      239 SerAlaLeuAlaArgAspLeuIleProArgMetLeuValaGIuProMetLySArgIle 258
Db      753 TCAAGTGTGCGAGGATTTGATTCGAGAGTCTTATATGATGACCCCAATGAAGGAATG 812
Qy      259 ThrIleArgGluIleArgGluHiSgIIntPheGlnIleArgLeuProArgTyrIleuAla 278
Db      813 ACTATTTCTGAGATTGCGCTGCAACCTTGTTCCAAAGTCATTTGCCAGCTATTGGCC 872
Qy      279 ValProProProAspThrThrGlnGlnAlaIySmetIleAspGluAspThrLeuArgAsp 298
Db      873 GTGCTCCACCAAGATACCAACCCCAACCAAGAAATCGAAGAAATCTTCCTCAAG 932
Qy      299 ValIaAsnMetGlyPheAsnLySAsnHiSAsnIyCySgIySerIyCySgIyArgLeu 318
Db      933 GTGCTTAAGATGGATTGACAGAAACAACCTTACTGAGTCTCTTCGCAATATGATTCAA 992
Qy      319 AsnGluAlaThrValaIaIaTyrTyrLeuLeuLeuAspAsnArgPheArgAlaThrSerGIy 338
Db      993 AATGAGGACACTGTGTGATATCTGCTGCTCGCAATCGCCATCGTGTTCACACTGGC 1052
Qy      339 TyrLeuGIyAlaAspTyrGlnIySerMetAspArgAsnLeuAsnGlnLeuAlaSerSer 358
Db      1053 TATCTTGAAGCTGATTTCAAGAGTCCATGAAATGTGTTACMAACCGATCAATTTCTAT 1112
Qy      359 GluSerSerSerSerGIyThArgAsnTyrValProGIySerSerAspProHisSerSer 378
Db      1113 GAACCCGCTGCTTCCCTGTTGGTCAACGTTTCCAGAAATATATGATTAACAGAACCT 1172
Qy      379 GlyLeuArgProTyrTyrProValGIuArgIySTPAlaLeuGIyLeuGlnSerArgAla 398
Db      1173 GGTGCAAGA---CAAGTCCCACTGAAAGAAATGGGCTCTGGCCCTCAAGTCTGACGG 1229
Qy      399 HisProArgGluIleMetValGluValLeuLeuYsAlaLeuGlnGlnLeuAsnValaArgTrp 418
Db      1230 CATCACGCTGAATATATAGTCAAGATTTTGAAGCTTCGCAAGAACTGAATGTAATTGGG 1289
Qy      419 LysIySaenGIyHiSTyrAsnValIyCySargTrpCySPProGIyPheProGIuValaAsn 438
Db      1290 AAAAGATT-GGTCAATATACATGAATGTGATGGTCTTCAAGTTCACCTGTCATCAT 1348
Qy      439 AspThrLeuAspAlaSer-----AsnSerPheLeuGIy--AspSerThrIle 453
Db      1349 GAAGCATGGGTGTTAATTCATGATGAGGAATCAGTTCTTTGAGATGATTCATCATC 1408

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Qy      454 MetAspAsnAspAlaAsnGIyArgLeuProThrValIleYsPheGluPheGlnLeu 473
Db      1409 ATTGAAATGATGGGCCACAC---AAGTTTAACAATATGTGTCAGATTGAAGTTCAAGCTT 1465
Qy      474 TyrIySThrLySAspAspLySTyrIleLeuAspMetGlnArgValThnGIyProGlnLeu 493
Db      1466 TACAAACACAGAGAGAACTACTTGTCTTACCTTCAGACACTTCAGAGGTCCCAATTC 1525
Qy      494 LeuPheLeuAspPheCySAlaAlaPheLeuThrIySLeuArgValLeu 509
Db      1526 CTTTCTCGATCTCTGTGCTGCTTTCTTCTGTCAGCTTCAGATCACTT 1573

RESULT 11
AAA52769
ID      AAA52769 standard; cDNA; 2107 BP.
XX
AC      AAA52769;
XX
DT      03-JAN-2001 (first entry)
XX
DE      Corn putative catabolite repression protein SNF1 coding sequence #3.
XX
KW      Corn; carbon catabolite repression; sucrose non-fermenting protein 1;
KM      SNF1; plant growth; ss.
XX
OS      Zea mays.
XX
FH      Key      Location/Qualifiers
FT      CDS      2..1739
FT      FT      /*tag= a
FT      FT      /product= "SNF1"
FT      FT      /partial

XX      W0200036115-A2.
XX      22-JUN-2000.
XX
PF      15-DEC-1999; 99MO-US029824.
XX
PR      16-DEC-1998; 98US-0112563P.
XX
PA      (DUP0 ) DU PONT DE NEMOURS & CO E. I.
XX
PI      Allen SM, Heppard EP, Sakai H, Weng Z, Helenjaris TG, Macool DJ;
PI      Miao G;
XX
DR      WPI; 2000-431593/37.
XX
DR      P-PSDB; AAB03417.
XX
FT      New nucleic acids encoding sucrose non-fermenting 1 (SNF1) proteins
FT      involved in carbon catabolite repression in plants and seeds, useful for
FT      controlling carbon and nitrogen partitioning pathways during plant growth
FT      and development.
XX
PS      Claim 2; Page 37; 59pp; English.
XX
CC      The present sequence is a putative sucrose non-fermenting protein SNF1
CC      coding sequence from corn. The sequence was isolated by searching a corn
CC      stem cDNA library for sequences similar to those encoding SNF1 in
CC      Arabidopsis thaliana, Cucumis sativus, Glycine max and Oryza sativa. The
CC      protein is involved in carbon catabolite repression, and so the gene and
CC      protein can be used in plants to control the nitrogen and carbon
CC      partitioning pathways during plant growth and development. They can also
CC      be used to alter the accumulation of carbohydrates, lipids and proteins
CC      during plant growth
XX
SQ      Sequence 2107 BP: 578 A; 454 C; 484 G; 591 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:      9,81e-187      Length:      2107
Score:      1931.00      Matches:      372
Percent Similarity:      83.69%      Conservative:      54

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DK WPI; 2003-201303/13.
DR P-PSDB; ABR40709.

Pl. Jaraczynski MC;
XX

Pl. Jaraczynski MC;
XX

PT Novel nucleotide fragment encoding polypeptides having receptor-like
PT protein kinase activity, callosein-like activity, useful for altering oil
XX phenotypes in plants such as sunflower, coconut, soybean, wheat and rice.
PS Claim 18; Page 274-275; 542pp; English.

CC The present invention describes an isolated nucleotide fragment (I)
CC comprising a nucleic acid sequence (NS) chosen from a NS encoding a
CC polypeptide (PP) having receptor-like protein kinase activity, mitogen
CC activated protein (MAP) kinase activity, LIP15-like transcription factor
CC activity, callosein-like activity, ATP citrate lyase activity, SNF1-like
CC activity and CKC-like transcription factor activity. Also described: (1)
CC complement (II) of (I); (2) a chimeric construct (III) comprising (I) or
CC (II), operably linked to a regulatory sequence; (3) a plant (IV) or
CC comprising (III) in its genome; (4) seeds (V) obtained from (IV); and (5)
CC oil obtained from (V). (I) or its part can be used in antisense
CC inhibition or co-suppression in a transformed plant. (III) is useful for
CC altering the oil phenotype in a plant such as corn, soybean, wheat, rice,
CC canola, Brassica, sorghum, sunflower or coconut. (III) is also useful for
CC creating transgenic plants having altered lipid profiles. (I) can also be
CC used as a hybridisation probe. ACC00626 to ACC00868 and ABR40591 to
CC ABR40879 represent sequences used in the exemplification of the present
CC invention
CC
CC
XX
SQ Sequence 2107 BP; 578 A; 454 C; 484 G; 591 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 9.81e-187 Length: 2107
Score: 1931.00 Matches: 372
Percent Similarity: 83.69% Conservative: 542
Best Local Similarity: 73.08% Mismatches: 77
Query Match: 71.70% Indels: 6
DB: 7 Gaps: 3

US-09-857-522B-4 (1-509) x ACC00744 (1-2107)

QY 1 MetaspGlySerSerLeGlySerGlyHisSerGluAlaLeuArgAsnTyPAsnLeuGly 20
DB 230 ATGAGGAGAGCGCGGAGAG-----GATGCCAACCTTTGAGGGGTTACAGAAATTGGC 280
QY 21 ArgThrLeuGlyIleGlyThrPheGlyLysValLysIleAlaGluHisLysLeuThrGly 40
DB 281 AAAACCCGCGGAAATGGGTGCGTCCGTGAAGTGAAGATCGCGAATCATATATGACTGCT 340
QY 41 HisArgValAlaIleLysIleLeuAsnCySarGlnMetArgAsnMetGluMetGluGlu 60
DB 341 CATAGGAGGCGGATCAAGATTCATATGCAATGCAAGAGATCAAGATGATGATGAAAG 400
QY 61 LysAlaLysArgGluPheLysIleLeuLysLeuPheIleHisProHisIleIleArgLeu 80
DB 401 AAAGTTAAGAGAGAAATCAAGTACTGATTTATTTATGCAATCCATATCATACGCTT 460
QY 81 TyrGluValIleTyrThrProThrAspIleTyrValValMetGluTyrCysLysTyrGly 100
DB 461 TATAGGAGTATAGATATACACTGCTGATATCTGTGTTTATGAGTATGTTAAATCTGA 520
QY 101 GluLeuPheAspTyrIleValGluLysGlyArgLeuGlnGluAspGluAlaArgArgIle 120
DB 521 GAGTTGTTTGAATTCATGTTGAGAGAGGAGGATCAACGAAAGGAGAGCCGACACTTT 580
QY 121 PheGlnGlnIleIleSerGlyValGluTyrCysHisArgAsnMetValHisArgAsp 140
DB 581 TTTGAGGAGATCATATCTGCTGTTGAAATATGTCCTATGGAACATGCTGTCACCGTAT 640
QY 141 LeuLysProGluAsnLeuLeuLysAspSerLysTyrAsnValLysLeuAlaAspPheGly 160
DB 641 TTTAAGCCAGAGAAATCTCTTTTGATTCAAATATGCAATGTTAAGATTCGCAATTTGGC 700
QY 161 LeuSerAsnValMetHisAspGlyHisPheLeuLysThrSerCysGlySerProAsnTyr 180
DB 701 TTAAGTATATATATGCGTATGATGTCATCTTCTTAAGAGAGATGTTGGTACCGAATTTAT 760
QY 181 AlaAlaProGluValIleSerGlyLysLeuTyrAlaGlyProGluValAlaAspValTrpSer 200

DB 761 GCACACCTAGAGGATCATATCTGTAATATATCTGCTGTAAGTGAAGTCTGAGC 820
QY 201 CysGlyValIleLeuTyrAlaLeuLeuCysGlyThrLeuProPheAspGluAsnIle 220
DB 821 TGTGAGATATATCTTATATGCTCTTTTGTGGCACTCTCCATTTGACGATGAAATAT 880
QY 221 ProAsnLeuPheLysIleLysGlyGlyTyrLeuThrLeuProAsnHisLeuSerAla 240
DB 881 CCAACCTTTCAAGAAATTAAGAGGAGATATATACCTTCTGATCATTTGTCACT 940
QY 241 LeuAlaArgAspLeuIleProArgMetLeuValGluProMetLysArgIleThrIle 260
DB 941 TCACGAGGAGATCTGATTTCCAGAAATCTGCTGTTTATTCATCAAGAAAGATTAACA 1000
QY 261 ArgGluIleArgGluHisGlnTyrPheGlnIleArgLeuProArgTyrLeuAlaValPro 280
DB 1001 CGTGAATATCCGTGAACATGTGTGTTCAAGATCCGACTTCGCGCTATTTGGCTGTC 1060
QY 281 ProProAspThrThrGlnGlnAlaLysMetIleAspGluAspThrLeuArgAspVal 300
DB 1061 CTTCAAGACACTGCTCAACAAATTAAGAGTCAACAGAGAACTTTAATGATGATTA 1120
QY 301 AsnMetGlyPheAsnLysAsnHisValCysGluSerLeuCysSerArgLeuGlnAsnGlu 320
DB 1121 AAGATGGGTTTGAACAAGATCAAGTAAATGAAATCTTCGCAAAACAGATTCAGAA 1180
QY 321 AlaThrValAlaTyrTyrLeuLeuLeuAspAsnArgPheArgAlaThrSerGlyTyrLeu 340
DB 1181 GCAACAGATGGCTATTTATTTACTTGTGACAAATGAGCTTGTCACACAGTGTATCTT 1240
QY 341 GlyAlaAspTyrGlnGlnGlnSerMetAspArgAsnLeuAsnGlnLeuAlaSerSerGluSer 360
DB 1241 GGAATCAATTTCAAGATCATGAGACTCATCTTGTCTCAAGTAATC--GCTGAACA 1297
QY 361 SerSerSerGlyThrArgAsnTyrValProGlySerSerAspProHisSerSerGlyLeu 380
DB 1298 CCAACTTCAGACACTGAACCTTCGACAGATGGGTTTCAAGATTCAGAGTTCGCTTG 1357
QY 381 ArgProTyrTyrProValGluArgLysTrpAlaLeuGlnLysLeuGlnSerArgAlaHisPro 400
DB 1358 AGCAGACATTTTGGAGCTGAAGAGAAATGGGCTCTGTGCTTCAGTCTGAGGACATCCA 1417
QY 401 ArgGlnIleMetValGluValIleLysValAlaLeuGlnGluLeuAsnValArgTrpLys 420
DB 1418 CGAAGAAATTAATAGTGAAGTGTAAAGCTCTGCAAGAACTGAATGTTTACTGGAAAG 1477
QY 421 AsnGlyHisTyrAsnValLysCysArgTrpCysProGlyPheProGluValAsnAspThr 440
DB 1478 ATTGCACTACACAAATGAGAAATGAGATGAGATCTGCTGCTGCTGAG-----AGTATG 1531
QY 441 LeuAspAlaSerAsnSerPheLeuGlyAspSerThrIleMetAspAsnAspAlaAsn 460
DB 1532 ATGCATTAACAGTGTATACCTTCAGTGGAGAGTCTCTTAATTTGAACCTGATTTTCATG 1591
QY 461 GlyArgLeuProThrValIleLysPheGluPheGlnLeuTyrLysThrLysAspAspLys 480
DB 1592 GAGAAATCAACCCCGACAGTGAAGTGTGAAGTTGAGTTTCAACAAAGAGGAGAGAAAG 1651
QY 481 TyrLeuLeuAspMetGlnArgValThrGlyProGlnLeuLeuPheLeuAspPheCysAla 500
DB 1652 TACTTTTTCACCTGCAAGAGGATCAGTGAATCATATCTTCTTTCGACTTGTCTCC 1711
QY 501 AlaPheLeuThrLysLeuArgValLeu 509
DB 1712 GCTTTCTAATCTGAGTGAAGTCTT 1738
RESULT 13
AA047789
ID AA047789 standard; DNA; 1536 BP.
XX
AC AA047789;

DT 27-AUG-2003 (revised)
XX 02-MAR-1994 (first entry)
DE SHP gene.
XX Yeast; SNF1; homologous protein; SHP; Nicotinia tabacum; invertase; ss.
XX Saccharomyces cerevisiae.
XX JPO5199884-A.
XX 10-AUG-1993.
XX 13-DEC-1991; 91JP-00330417.
XX 13-DEC-1991; 91JP-00330417.
XX (SUMO) SUMITOMO CHEM CO LTD.
XX WPI; 1993-284682/36.
XX P-PSDB; AAR40842.
XX Yeast SNF1 homologous protein phosphorylase gene of SOLANACEAE plants -
PT useful for controlling expression of invertase for the increase of crop
PT yield.
XX Claim 1; Page 6; 7pp: Japanese.
XX This sequence represents the yeast SNF1 homologous protein gene (SHP).
CC The yeast SHP gene may be obtained from Nicotinia tabacum and may be
CC used to control expression of invertase for the increase of crop yield.
CC (Updated on 27-AUG-2003 to correct OS field.)
XX Sequence 1536 BP; 437 A; 291 C; 382 G; 426 T; 0 U; 0 Other;
SQ
Alignment Scores:
Pred. No.: 4.09e-186 Length: 1536
Score: 1923.00 Matches: 372
Percent Similarity: 83.72% Conservative: 60
Best Local Similarity: 72.09% Mismatches: 72
Query Match: 71.41% Indels: 12
DB: 2 Gaps: 7
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QY 1 MetAspGlySerSer-----LysGlySerGlyHisSerGluAlaLeuArgAsnTyrAsn 18
DB 1 ATGGATGATCAACAGTCCAAAGTGGAGACAGCTGAGTCAATTTTACGAACTATAG 60
QY 19 LeuGlyATGThrLeuGlyIleGlyThrPheGlyLysValIleAlaGluHisLysLeu 38
DB 61 CTGGGAAACCTCTGGCATTGGATTCGGAATAAATGCTGAACATACCTTA 120
QY 39 ThrGlyHisArgValAlaIleLysIleLeuAsnCyAsArgGlnMetArgAsnMetGlnMet 58
DB 121 ACAGGCGATTAAGTGTCTGCTCAAGATCTCAATCTCGAAAAATCAAAACATGGAATG 180
QY 59 GlnGlyLysAlaLysArgGluLysPheLysIleLeuLysLeuPheIleHisProHisIleLe 78
DB 181 GAAGAAAAAGTGAAGGAAATTAATAATGAGATTGTCATGCACTCCACATCACTT 240
QY 79 ArgLeuTyrGluValIleLysThrProThrAspIleTyrValIleMetGluTyrCysLys 98
DB 241 CGGCGTATAGGTTGTAGAGACACCATCATATATATGTTGATGAGATGAGTAAA 300
QY 99 TyrGlyLysLeuPheAspTyrIleValGluLysGlyArgLeuGlnGluAspGluAlaArg 118
DB 301 TCTGCTGAGCTGTTGATTACATTCGTGAGAAAGGACACATCAAGAGATGAAGCTGCT 360
QY 119 ArgIlePheGlnGlnIleLysSerGlyValGluTyrCysHisArgAsnMetValValHis 138
DB 361 AAATCTTCACGACATATCTCTGCTGAGTACTCCACAGGAACATGCTGCTCAT 420

QY 139 ArgAspLeuLysProGluAsnLeuLeuAspSerLysTyrAsnValIleLysLeuAlaAsp 158
DB 421 AGAGATCTAAAGCCTGGAACCTCTTTTGATTCCAATGAAATGGAATGACATG 480
QY 159 PheGlyLeuSerAsnValMetHisAspGlyHisPheLeuLysThrSerCysGlySerPro 178
DB 481 TTTGGTTGAGTATATCATGCGGTGATGTCACCTTCTCAAGACAACTTGTGAGCCCA 540
QY 179 AsnTyrAlaAlaProGluValIleSerGlyLysLeuTyrAlaGlyProGluValAspVal 198
DB 541 AATTATCTCGCGCGAGGATGATTCAGAAAGTATATCTGACCTGACCTGAGTANGTGA 600
QY 199 TrpSerCysGlyValIleLeuTyrAlaLeuLeuCysGlyThrLeuProPheAspArgGlu 218
DB 601 TGAGCTGTGCTGTTATATATGCTCTCTGCTGAGCACCTTCATTTGATGATGAA 660
QY 219 AsnIleProAsnLeuPheLysLysIleLysGlyGlyIleTyrThrLeuProSerHisLeu 238
DB 661 AACATTCCAAACCTTTTAAAGAAATTAAGGCTGATATATCTCGCCACGCACTTTA 720
QY 239 SerAlaLeuAlaArgAspLeuIleProArgMetLeuValIleGluProMetLysArgIle 258
DB 721 TCAGCTGTGCGAAGGATCTGATCCCAAGATGCTTATAGTTGACCTTATGAAGCGAATG 780
QY 259 ThrIleArgGluIleArgGluHisGlnTyrPheGlnIleArgLeuProArgTyrLeuAla 278
DB 781 ACTATTCCTGAGATTCTGATGACCTTGGTTCCAAGCTCATGACCACTATTTAGCT 840
QY 279 ValProProProAspThrThrGlnGlnAlaLysMetIleAspGlyLysAspThrLeuAsp 298
DB 841 GTACCTCCACAGTATGATGATGCAACAGCGAAAGTTATGAAATATTTCTCAAGAG 900
QY 299 ValValAsnMetGlyPheAsnLysAsnHisValCysGlnSerLeuCysSerArgLeuGln 318
DB 901 GTGGTCAAAGGGATTTGACAGGAACAGCTTGTCCCTCTCTGCAATAGATTCAG 960
QY 319 AsnGluAlaThrValAlaIleTyrLeuLeuLeuAspAsnArgPheArgAlaThrSerGly 338
DB 961 AATGAGGGTACTGGGCTATATTTCTGCTGGAAGAACAGTTTCTGCTTCCAGTGGC 1020
QY 339 TyrLeuGlyValAspTyrGlnGlnLysMetAspArgAsnLeuAsnGlnLeuAlaSerSer 358
DB 1021 TACATGGAGCTGAATTCAGAGACATGAAATACGGTTATCTCAAAATTAATTCAGT 1080
QY 359 GluSerSerSerSerGlyThrArgAsnTyrValProGlySerSerAspProHisSerSer 378
DB 1081 GAAGTGTCTCTCCC---TGTGGCAACACTGTGCTGGAATATGATTTTCAACAGTT 1137
QY 379 GlyLeuArgProTyrTyrProValGluArgLysTrpAlaLeuGlyLeuGlnSerArgAla 398
DB 1138 GGTGCGAGG---CAGTTCCCGTCGAAGAAATGGGCTCTTGGACTCCAGTCTCGAGCG 1194
QY 399 HisProArgGlnIleMetValGluValLeuLysAlaLeuGlnGluLeuAsnValArgTrp 418
DB 1195 CATCACGTGATGAATTAAGACAGAGGTTCTGAAGCTTGGACAGACATGAAATGACGTGG 1254
QY 419 LysLysAsnGlnHisTyrAsnValLysCysArgTrpCysProGlyPheProGluValAsn 438
DB 1255 AAGAAATCGGACCTTCAACATGAATGCAATGGTCTCTGCGCACTCGGCATCAT 1314
QY 439 AspThrLeuAspAlaSerAsnSer-----PheLeuGly---AspSerThrIle 453
DB 1315 GAAAGCATG---AGTATTAATTTCCATACATCCAAATCTTGTGAGATTCACACCGCT 1371
QY 454 MetAspAsnAspAspAlaAsnGlyArgLeuProThrValIleLysPheGlnPheGlnLeu 473
DB 1372 ATTAGAACCGTGTGTCACCT---ATACCTTAATCAGAGAAAGTTGAAAGTTCAAGCTT 1425
QY 474 TyrIleThrLysAspAspLysTyrLeuLeuAspMetGlnArgValThrGlyProGlnLeu 493
DB 1426 TATTAACCTCGGAGAGAAATACCTCTTACAGAGATACAGAGGTCACAGTTTC 1485
QY 494 LeuPheLeuAspPheCysAlaAlaPheLeuThrLysLeuArgValLeu 509

Db 1486 CTTTCTTGATCTCTGCTGCTTCTCTGCTCAGCTCGGTTCTC 1533
RESULT 14
AB212357
ID AB212357 standard; DNA; 1539 BP.
XX
AC AB212357;
XX
DT 21-JAN-2003 (first entry)
XX
DE Arabidopsis thaliana stress regulated gene SEQ ID NO 162.
XX
KW Arabidopsis thaliana; plant; gene; stress; transgenic; ds.
XX
OS Arabidopsis thaliana.
XX
PN W0200216655-A2.
XX
PD 28-FEB-2002.
XX
PE 24-AUG-2001; 2001WO-US026685.
XX
PR 24-AUG-2000; 2000US-0227866P.
PR 26-JAN-2001; 2001US-0264647P.
PR 22-JUN-2001; 2001US-0300111P.
XX
PA (SCRI) SCRIPPS RES INST.
PA (SYGN) STINGENTA PARTICIPATIONS AG.
PI Harper JF, Kreps J, Wang X, Zhu T;
XX
DR WPI; 2002-304127/34.
XX
PT Identifying a stress condition to which a plant cell has been exposed and
XX producing plants with increased tolerance to these abiotic stresses.
XX
PS Claim 144; SEQ ID NO 162; 577bp + Sequence Listing; English.
XX
CC The invention relates to identifying a stress condition to which a plant
CC cell has been exposed, comprising: (a) contacting nucleic acid
CC representative of expressed polynucleotides in the plant cell with an
CC array or probes representative of the plant cell genome; and (b)
CC detecting a profile of expressed polynucleotides in the plant cell
CC characteristic of a stress response. The method is useful in the
CC production of transgenic plants, cells and seeds and in producing plants
CC with increased tolerance to abiotic stress. The present sequence is that
CC of an Arabidopsis thaliana stress regulated gene (AB212196-AB217574) used
CC in methods of the invention. Note: The sequence data for this patent is
CC not represented in the printed specification but is based on sequence
CC information supplied to Derwent by the European Patent Office
XX
XX
SQ Sequence 1539 BP; 439 A; 291 C; 369 G; 440 T; 0 U; 0 Other;
Alignment Scores:
Pred. No.: 4.02e-184 Length: 1539
Score: 1903.50 Matches: 362
Percent Similarity: 82.03% Conservative: 58
Best Local Similarity: 70.70% Mismatches: 89
Query Match: 70.68% Indels: 3
DB: Gaps: 1
US-09-857-522B-4 (1-509) x AB212357 (1-1539)
QY 1 MetAspGlySerSerLys-----GlySerGlyHisSerGluAlaLeuArgAsnTyr 17
Db 1 ATGATCATTCATCAATAAGATTGGCAATATAGAGTGAATGCAATTCATCCGAATTAC 60
QY 18 AsnLeuGlyArgThrLeuGlyIleGlyThrPheGlyLysValLysIleAlaGluHisLys 37
Db 61 AAGCTTGTAAGAACTCTTGGAATGGGCTTTTGGAGAGGTGAATAATGACGAGCATGTT 120
QY 38 LeuThrGlyHisArgValAlaIleLysIleLeuAsnCysArgGlnMetArgAsnMetGlu 57

Db 121 GTCAAGAGGCAATAAGTTGCTATCAAAATCCTTAATGCTGTAAAGATCAACATGAG 180
QY 58 MetGluGlyValAlaLysArgGluPheLysIleLeuLysLeuPheIleHisProHisIle 77
Db 181 ATGGAAGAGAAAGAGAGAGGAGGAGATTAAAGTTCTACCGTTGTTATGCAATCCATATT 240
QY 78 IleArgLeuTyrGluValIleTyrThrProThrAspIleTyrValIleMetGluTyrCys 97
Db 241 ATTGGCAGTATGAGTNATAGAGACGAGTACATTATGTTGATGATGATGATGTC 300
QY 98 LysTyrGlyGluLeuPheAspTyrIleValGluLysArgLeuGluGluAspGluAla 117
Db 301 AAGCTGAGAGACCTTTGATTATATTGTTAGAAAGACAAATTACAGAAAGATGAGGCT 360
QY 118 ArgArgIlePheGluGluIleIleSerGlyValGluTyrCysHisArgAsnMetValVal 137
Db 361 CGTAACCTTTTCCAGCAGATTAATCTGGTGTAGAGTACCTCCATCGTAATATGTTGTC 420
QY 138 HisArgAspLeuLysProGluAsnLeuLeuAsnLysSerLysTyrAsnValLysLeuAla 157
Db 421 CATAGAGACCTGAAGCCTGAGAAATTACTATGTGATTCGAGTGTAAATTAATTAAGATTGCA 480
QY 158 AspPheGlyLeuSerAsnValMetHisAspGlyHisPheLeuLysThrSerCysGlySer 177
Db 481 GACTTGGGTTGAGTAATGTTATCGGGATGCTCATTTCTAAAGACAGATGTGGAAGC 540
QY 178 ProAsnTyrAlaAlaProGluValIleSerGlyLysLeuTyrAlaGlyProGluValAsp 197
Db 541 CCCAACTAGCGCTGCCGAGGATTATACAGGTAAATTATGTGTGAGCCTGGAAGTGAT 600
QY 198 ValTrpSerCysGlyValIleLeuTyrAlaLeuLeuLysGlyThrLeuProPheAspAsp 217
Db 601 GTATGAGATTGCGAGTTATATTGTATGCTTATTAATGCGGTACTCTTCCTTTGATGAT 660
QY 218 GluAsnIleProAsnLeuPheLysIleLysGlyGlyIleTyrThrLeuProSerHis 237
Db 661 GAATAACATTCGCCAACCTTTTCAGAAATTAAGGTGGGATTTACATCTTCCAAAGTCAT 720
QY 238 LeuSerAlaLeuAlaArgAspLeuIleProArgMetLeuValValGluProMetLysArg 257
Db 721 TTATCATCTGAGGTAGTAAAGACCTGATCCAAAGATGCTTATTAATGACCCGGTGAAACGA 780
QY 258 IleThrIleArgGluIleArgGluHisGlnThrPheGluIleArgLeuProArgTyrLeu 277
Db 781 ATCAACATTCCTGAGATCCGTCACACCGTTGTTCCAGATCATCTCCCTGTTATCTT 840
QY 278 AlaValProProAspThrThrGlnGluAlaLysMetIleAspGluAspThrLeuArg 297
Db 841 GCTGTCTCTCCACCGGATCACAGTACAGTACAGCAAGCTTAAGATCAATGAGAGATAGTTCA 900
QY 298 AspValValAsnMetGlyPheAsnLysAsnHisValCysGluSerLeuCysSerArgLeu 317
Db 901 GAAGTGTTAACATGGGATTTGATTAAGAACAGAGTTTGGATCTTACACCAACAGAACCA 960
QY 318 GlnAsnGluAlaThrValAlaTyrTyrLeuLeuLeuAspAsnArgPheAlaThrSer 337
Db 961 CAAACCATCTACTCTGTATACACTACTCTGTATGATTAACCGGTTCCGTTGCCAAGT 1020
QY 338 GlyTyrLeuGluAlaAspTyrGlnGluSerMetAspArgAsnLeuAsnGlnLeuAlaSer 357
Db 1021 GGCTATTTAGAAATCCGAGTTTCAGAGAACCAACAGACAGTGGTCCAAATCCTATGCGACA 1080
QY 358 SerGluSerSerSerSerGlyThrArgAsnTyrValProGlySerSerAspProHisSer 377
Db 1081 CCTGAAGCGGAGGCTTCACTGATAGGCACTGATTCCTCACAATGAGTACATCACTACGGG 1140
QY 378 SerGlyLeuArgProTyrTyrProValGluArgLysIleAlaLeuGlyLeuGlnSerArg 397
Db 1141 TTGGAGCAACAGATCAACAGTCCCTGTTGATGAGAAATGGGCTCTTGACATTCAGTTCAT 1200
QY 398 AlaHisProArgGluIleMetValGluValLeuLysAlaLeuGlnGluLeuAsnValArg 417

Db 1201 GCGCATCTCGTGAATCATGATGATTTGGAAGCTCTTCAAGACTCATCATGTGNGT 1260
Qy 418 TTrlyslsYsengNlYHlStYrAsnValIysCyArgrTpyCysProglYpneProgluVal 437
Db 1261 TGGAGAGAGATTGGTCTACATCAACATGAAATGATGAGGTTCCTGGTTTACGTATGCT 1320
Qy 438 AsnAspThrIeuAspAlaSerAsnSerPheIeuGlYAspSerThrIleMetAspAsnAsp 457
Db 1321 CAGAAATCTATGCTGCACAAATCAGCTGCAGCTTCAGAGATGAAATCAGCATCATTTAGAGAT 1380
Qy 458 AspAlaAsnGlYArGleuProThrValIlelYsPheGlYpneGlYleuThrIYsThlYs 477
Db 1381 GACTGTGCATGACTTCACCACTGTCATCAAAATTTGAATTCAGCTATACAAAGCCCGG 1440
Qy 478 AspAspIYsTrYrIleuIeuAspMetGlYArGValThrGlYpProGlYleuIeuPheIeuAsp 497
Db 1441 GAAAGAGAGTACTGCTGATATACAGAGATTAACGATCCGCGATTTCTCTCTTGAT 1500
Qy 498 PheCysAlaAlaPheIeuThrIYsIeuArGValIeu 509
Db 1501 CTATGCGCGCTTCTTCTTACAGAGCTTGTGTGATC 1536
RESULT 15
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ID AAC44825 standard; DNA; 1792 BP.
XX AAC44825;
AC
XX 18-OCT-2000 (first entry)
DT
XX
DE Arabidopsis thaliana DNA fragment SEQ ID NO: 44271.
XX
KW Hybridisation assay; genetic mapping; gene expression control;
KW protein identification; signal transduction pathway; metabolic pathway;
KW promoter; termination sequence; ss.
XX
XX Arabidopsis thaliana.
OS
XX EPI033405-A2.
PN
XX 06-SEP-2000.
PD
XX
XX 25-FEB-2000; 2000EP-00301439.
PF
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XX 25-FEB-1999; 99US-0121825P.
PR 05-MAR-1999; 99US-012180P.
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PR 04-OCT-1999; 99US-0157117P.
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PR 26-OCT-1999; 99US-0161361P.
PR 28-OCT-1999; 99US-0161920P.
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PR 29-OCT-1999; 99US-0162142P.

Alignment Scores:

Pred. No.:	5e-184	Length:	1792
Score:	1903.50	Matches:	362
Percent Similarity:	82.03%	Conservative:	58
Best Local Similarity:	70.70%	Mismatches:	89
Query Match:	70.68%	Indels:	3
		Gaps:	1

US-09-857-522b-4 (1-509) x AAC44825 (1-1792)

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QY 18 AsnLeuGlyArgThrLeuGlyIleGlyThrPheGlyLysValLysIleAlaGluHisLys 37
DB 314 AAGCTTGATAAACCCTTGGAAATGGGCTTTTGGGAAAGGAAATAGCAGACAGATGTT 373
QY 38 LeuThrGlyHisArgValAlaIleLysIleLeuAsnCyArgGluMetCysAsnMetGlu 57
DB 374 GTCACAGGCGCTAAGGCTGCTATCAAAATCCTTAATGCTGTAAGATCAAGAACATGAG 433
QY 58 MetGluGlySalArgGluPheLysIleLeuLysLeuPheIleHisProHisIle 77
DB 434 ATGAAAGAAAGAGAGAGAGAGAGATTAGATTCTAGCGTTGTTATGATCCCTCATATT 493
QY 78 IleArgLeuTyrGluValIleIleTyrThrProThrAspIleTyrValValMetGluTyrCys 97
DB 494 ATTGGGAGATATGAGTAATAGACACGACGATCACTTAATGTGTGATGAGATATGTC 553
QY 98 LysTyrGlyGluLeuPheAspTyrIleValGluLysGlyArgLeuGlnLysAspGluAla 117
DB 554 AAGCTGAGAGCTCTTGATTATATGTTGAGAAAGCGCATTAACAAGAAATGAGGCT 613
QY 118 ArgArgIlePheGlnGlnIleIleSerGlyValGluTyrCysHisArgAsnMetValVal 137
DB 614 CGTAACCTTTCCAGCAGATATATCTGCTAGTAGACAGCCATCGTAATATGTTGTC 673
QY 138 HisArgAspLeuLysProGluAsnLeuLeuAspSerLysTyrAsnValLysLeuAla 157
DB 674 CATAGAGCCTGAGCCTGGAATTACTATGATTCGAGGTGTAATATTAAGATTGCA 733
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DB 854 GTATGAGATTGCGGAGTTAATGTTAGCGCTTAATGACGTAATCTTCCTTTGATGAT 913
QY 218 GluAsnIleProAsnLeuPheLysIleLysGlyGlyIleTyrThrLeuProSerHis 237
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QY 278 AlaValProProPheAsnThrThrGlnGlnAlaLysMetIleAspGluAspThrLeuArg 297

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Search completed: July 9, 2004, 15:39:12
Job time : 662 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: July 9, 2004, 13:46:15 ; Search time 3777 Seconds

(without alignments)
4024.318 Million cell updates/sec

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Perfect score: 2693
Sequence: 1 MDSSSKSGSGSEALRNVLG.....GPOLLFDGCAFLTKLRVL 509

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Xgapop 10.0, Xgapext 0.5
Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
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-Q=/cgn2_1/USPTO.spool/US09857522/runat_07072004_161357_1882/app_query.fasta_1.647
-DB=EST -QFMT=fastap -SUFFIX=g2n.rst -MINMATCH=0.1 -LOOFC=0 -LOOEXT=0
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2: em_esthum :
3: em_estin :
4: em_estmu :
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7: em_estro :
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11: gb_hc :
12: gb_est3 :
13: gb_est4 :
14: gb_est5 :
15: em_estfun :
16: em_estom :
17: em_gss_hum :
18: em_gss_inv :
19: em_gss_p1n :
20: em_gss_vrt :
21: em_gss_fun :
22: em_gss_mam :
23: em_gss_mus :
24: em_gss_pro :
25: em_gss_rtd :
26: em_gss_phg :
27: em_gss_vrt :
28: gb_gss1 :

29: gb_gss2 :*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	1356	50.4	1391	11	AY112453
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19	1110	41.2	674	13	CA077133
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21	1104	41.0	706	14	CA999071
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ALIGNMENTS

RESULT 1	LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM	REFERENCE
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							Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.	

AUTHORS

Hainey, C. F., Dolan, M., Miao, G. H., Vogel, J. M., Whitesitt, M. S.,
Arthur, L. W., Hainey, M., Morgante, M., and Tingey, S. V.

TITLE

Maize Mapping Project/Dupont Consensus Sequences for Design of
Overgo Probes

JOURNAL

Unpublished (2002)
2 (bases 1 to 1948)

REFERENCE

Direct Submission

TITLE

Submitted (25-APR-2002) Maize Mapping Project, University of
Missouri, Columbia, MO 65211, USA

COMMENT

If you are interested in getting corresponding physical clones,
these are publicly available from ZmDB and may be found by BLAST
searching at MSU, maizemap.org; ZmDB, www.zmdb.iastate.edu; TIGR,
www.tigr.org; or NCBI, www.ncbi.nlm.nih.gov. When the source of the
maize cDNA sequences is either Virginia Malbot, Stanford or Pat
Schnable, Iowa State, then clones may be requested from ZmDB:
www.zmdb.iastate.edu.

FEATURES

source

1..1948
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overgo addressing of BACs in conjunction with the Maize
Mapping Project"

ORIGIN

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Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
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US-09-857-522B-4 (1-509) x AY107942 (1-1948)

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ORGANISM
Oryza sativa (indica cultivar-group)
Eukaryota, Viridiplantae, Streptophyta, Tracheophyta, Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, Ehrhartoideae, Oryzae, Oryza.

REFERENCE
1 (bases 1 to 784)
Jantasuriyarat,C., Lu,G., Gowda,M., Hatfield,J., Zhou,B., Mazur,E., Kudrna,D., Dean,R., Soderlund,C., Wing,R. and Wang,G.
Large-scale identification of ESTs involved in the interaction between rice and Magnaporthe oryzae
Unpublished (2003)

JOURNAL
COMMENT
Contact: Rod Wing
Arizona Genomics Institute
University of Arizona
Biological Sciences West, 448A, P.O. Box 210088, Tucson, AZ 85721-0088, USA
Tel: 520 626 3967
Fax: 520 621 9288
Email: <http://genome.arizona.edu>
PCR primers
FORWARD: gta aaa cga cgg cca gtc
BACKWARD: gga aac agc tat gac cat g
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ORIGIN

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US-09-857-522B-4 (1-509) x CB620008 (1-784)

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AUTHORS	Clade; Panicoideae; Andropogoneae; Saccharum.							
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JOURNAL	Vettore,A.L., da Silva,F.R., Kemper,E.L. and Arruda,P.							
COMMENT	The libraries that made SUCESP Genet. Mol. Biol. 24 (1-4), 1-7 (2001)							
	Contact: Arruda P							
	Centro de Biologia Molecular e Engenharia Genetica							
	Universidade Estadual de Campinas							
	Caixa Postal 6010, 13083-970, Campinas SP, Brazil							
	Tel: 55 19 3788 1137							
	Fax: 55 19 3788 1089							
	Email: parudu@unicamp.br							
	Clone distribution: clone distribution information can be found							
	through the Brazilian Clone Collection Center (BCCC) at							
	http://www.bcccenter.fcav.unesp.br							
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	/note="Organ: Lateral buds from plants adult plants							
	growing in greenhouse; Vector: pSport1; Site_1: Salt;							
	Site_2: NotI; An unidirectional cDNA library generated							
	from [lateral buds from plants adult plants growing in							
	greenhouse]. cDNA was prepared from polyA+ mRNA using							
	Superscript Plasmid System Kit (Invitrogen). The							
	double-strand cDNAs were fractionated in a sepharose							
	Cl-2B 40cm-columns and fragments sitting between 0.8 and							
	1.5 Kb were directionally cloned into the vector							

ORIGIN

of each source of RNA and library construction can be obtained at <http://sucess.lad.ic.unicaamp.br/public>

Alignment Scores:
 Pred. No.: 2,06e-137 Length: 904
 Score: 1293.50 Matches: 257
 Percent Similarity: 91.28% Conservative: 15
 Best Local Similarity: 86.24% Mismatches: 25
 Query Match: 48.03% Indels: 4
 Gaps: 0

US-09-857-522B-4 (1-509) x CA272308 (1-904)

Qy 74 HisProHsIleIleArgLeuTyrgluValIleTyrrThProThAspIleTyrrValVal 93
 Db 4 CACCCCAATATCATCCGGCTTATAGAGTCAATACACCAACCAAGATATATGTTG 63
 Qy 94 MetgluTyrcyslytyrglygluleupheaspyrilevalglulysglyargleugln 113
 Db 64 ATGGATATTGGAGGTATGGCGAGTGTGTTGATTACATTGTTGAGAAAGCAGATTACTA 123
 Qy 114 GluaspGluAlaargargilepheglnIleIleSerglyvalgluTyrcysHisarg 133
 Db 124 GAAGATGAGGCTCGCCGATCTCCAGCAGATCATATCTGGTGCAGAACTGCGCATAGA 183
 Qy 134 AsnmetValIleHisargAspLeuTyrrProgluLeuLeuLeuAspSerytyrIle 153
 Db 184 AACATGGTTGTCCACCGGACCTTAAGCAGAAACCTGTACTGATTCAAGATATAT 243
 Qy 154 VallyleuAlaaspPheglyleuSerasnValMethiaspGlyHisPheleuTyrr 173
 Db 244 GTAAACTTGTGACTTTGGTTTGAAGCATGTCATGATGCGCATTTTGAAGACC 303
 Qy 174 SerCysglySerProAsnTyrrAlaAlaProgluValIleSerglylyleuTyrrAla 193
 Db 304 AGCTGTGGAGTCCGAACTATGCTGCTCCAGAGGATATATCTGTAATATATGCTGA 363
 Qy 194 ProgluValaspValIleTyrSerCysglyValIleleuTyrrAlaLeuLeuCysgly 213
 Db 364 CCTAGGTCAGATGATGAGTGTGAGATGATCCCTTAATGCTCTTGTGGAACTCTT 423
 Qy 214 ProPheaspAspGluAsnIleProAsnLeuPheIlelysglylyIleTyrrThr 233
 Db 424 CCATTGATGATGAGAAATATCCCACTGTTCAAAAAATTAAAGGAGGATCTACACA 483
 Qy 234 LeuProSerHisleuSeralaleuAlaargAspleuIleProargMetLeuValglu 253
 Db 484 CTTCCAAGTCAATTTATCTGCTTGGCTTAGGATTTGATCCACGAATGCTTGTGCGAG 543
 Qy 254 PrometlysarglyIleThrIleargGluIleargGluHisglnTTPPheglnIleargleu 273
 Db 544 CCAATGAGAAATACCAATTCGGAAATTCGGAGCATTCATGCTTCCAACTCGCCTT 603
 Qy 274 ProargTyrrleuAlaValProProAspThrThrglnGlnAlaIleSmetIleaspGlu 293
 Db 604 TCTGTTACTTGGCAGTGCCTTCACACGACGACACACAAACAAATATATTGATGAA 663
 Qy 294 AspThrleuArgaspValValAsnMetClyPheAsnlysaAsnHisvalCysgluSeryleu 313
 Db 664 GATTCACCTTCAGATGTCGT- AATATGGGATTAACAG- AACCATGTGTG- GAATGCTTG 720
 Qy 314 CysSerArgleuGlnanGluAlaThrValAlaTyrrTyrrleuLeuLeuAspAsnArgPhe 333
 Db 721 TGCAACCAACTTAATAAATGAGGCACTGTGCAATATTAATTAATTAATGGAATTTGTTA 780
 Qy 334 ArgAlaThrSerglyTyrrleuGlyAlaAspTyrrGlnIleSermetAspArgAsnleuAsn 353
 Db 781 AAGCACTAGTGTCTTTTGGGGCGGAATTTCAAAATCAAGGGCCCAAGATTTTAA 840
 Qy 354 GlnleuAlaSerSerglyu-SerSerSerglyThrArgAsnTyrrValPro 370
 Db 841 TTAATCGCGGGGCGCAATATTAATTAATTTTGGGCCCAAGAAATTTTTCACA 892

RESULT 5

CB659701

LOCUS

CB659701 782 bp mRNA linear EST 09-APR-2003

DEFINITION

OSJNEC16012.f OSJNEC Oryza sativa (japonica cultivar-group) cDNA

ACCESSION

CB659701

VERSION

CB659701.1 GI:29663426

KEYWORDS

EST.

SOURCE

Oryza sativa (japonica cultivar-group)

ORGANISM

Oryza sativa (japonica cultivar-group)

REFERENCE

1 (bases 1 to 782)
 Jantaseur,Yarat,C., Lu,G., Gowda,M., Hatfield,J., Zhou,B., Mazur,E.,
 Kudrna,D., Dean,R., Soderlund,C., Wang,R. and Wang,G.
 Large-scale identification of ESTs involved in the interaction
 between rice and Magnaporthe grisea
 Unpublished (2003)

AUTHORS

Contact: Rod Wing

TITLE

Arizona Genomics Institute

JOURNAL

University of Arizona
 Biological Sciences West, 448A, P.O. Box 210088, Tucson, AZ
 85721-0088, USA
 Tel: 520 626 3967
 Fax: 520 621 9288
 Email: <http://genome.arizona.edu>

COMMENT

PCR Primers
 FORWARD: gta aaa cga cgg cca gtc
 BACKWARD: gga aac agc tat gac cat g
 Plate: 16 row: 0 column: 12
 Seq primer: gta aaa cga cgg cca gtc.

FEATURES

Location/Qualifiers

SOURCE

1..782
 /organism="Oryza sativa (japonica cultivar-group)"
 /mol_type="mRNA"
 /culivar="Nipponbare"
 /db_xref="taxon:39947"
 /clone="OSJNEC16012"
 /tissue_type="leaf"
 /dev_stage="3 week"
 /lab_host="DH10B"
 /clone_lib="OSJNEC"
 /note="Vector: pBluescript II KS +; Site 1: EcoRI, Site 2:
 XhoI; 6 hrs after inoculation with Rice Blast (C9240-1)"

ORIGIN

Alignment Scores:
 Pred. No.: 1.9e-130 Length: 782
 Score: 1232.00 Matches: 231
 Percent Similarity: 98.76% Conservative: 7
 Best Local Similarity: 95.85% Mismatches: 3
 Query Match: 45.75% Indels: 0
 Gaps: 0

US-09-857-522B-4 (1-509) x CB659701 (1-782)

Qy 1 MetaspGlySerSeryIleSerglyHisSerglyAlaLeuArgAsnTyrrAsnleugly 20
 Db 59 ATGGATGGAATGATTAAGCGCGGCGGATTTGAGGACCTGAAGAACTCAATCTTGA 118
 Qy 21 ArgThrleuglyIleeglyThrPheglylyvallyleleleagluHisIleSlyleuThgly 40
 Db 119 AGAATTTAGATTTGCTCAATTTGAAAGTGAAGATTGACAGGCTTAAGCTTAACGA 178
 Qy 41 HisargValAlaIleIlelysiIleleAsnCysargGlnMecArgAsnMetGlnMetGluGlu 60
 Db 179 CACGAGATTCTTAATTAAGATCTCGAACCGCCCAATGGAATATGAAATGAGAGAG 238
 Qy 61 LysAlaLysArgGlnPheIleleuTyrrleuPheIleHisProHsIleIleargleu 80
 Db 239 AAGCAAGAGAGAAATCAAGATATGAGATTTGTTGATTCATCCCATATCATTCGCTT 298

Oy		81	TyGIGVallieTyThProThAspIleTyValValmetGIuTyCyseLyTyxIY	100
Db		299	TATAGGTATTATACCTCCTCAACGATATATTTGGTAGTGAGTACTCGAAgTTTGA	358
Oy		101	GluDeuPheapTYrIIeValGlulysGIlyargLeugInguaspGluValargArgIlle	120
Db		359	GAACGTGTTGATTACATTCATTGAGAAGGACAGGTGCAGAAAGATGAGGCTGCCGATTC	418
Oy		121	PheGInGuInIIeIleserGIyValGIulTyrcyshsAargamecValIHIsargasp	140
Db		419	TTCCAGCACGATTATATCTGGGGGTGAATACTGCCACAGAAACAAGTGTTCATCTGAT	478
Oy		141	LeuIysPProGIuaSnIleuLeuaspSerIysTYraSnaValIysLeualaspPheGIY	160
Db		479	CTGAAGCCAGAAAACCTTCCTACTGATTCGAATTCAAAGTATATGTAAGCTTCGTCGACTTGGT	538
Oy		161	LeuSerAenValMethIAspGIyHIsPheLeuIysThrserCYseGIyseProAsnTYr	180
Db		539	TTGAGTAACTCATGCATGATGCGCATTTTTTGAAGAAGCTGTGGAGTCCAAACTAT	598
Oy		181	AlalaPProGIuValIIeserGIyIysTyseuTyraagIyrProGIuValaspValTrhsr	200
Db		599	GCTGCTCCAGAGGTGATCTGTGINAATTATATGCTGACCTGAGAGTGAATGAGAGC	658
Oy		201	CysGIyValIIleuTyraIaleuDeuCysGIyThrluProPhaspAspGIuasnIle	220
Db		659	TGTGAGAGTACCTTATGCTCTCTTTGTGTGTACTCTTCATTTGATGATGAGAAATATC	718
Oy		221	ProAsnIeuPheIysIleIysGIyGIyIleTyThrluProSerHisIeuSerAla	240
Db		719	CCCCAACCTATTCAAAAAGATTAAGGGTGGTATATATACTCTCCCAAGTCATTTATCTGCT	778
Oy		241	Leu 241	
Db		779	CTG 781	
RESULT 6				
CB677208		779 bp	mRNA	linear EST 09-APR-2003
DEFINITION	OSUNEel3013.f OSJNee Oryza sativa (japonica cultivar-group) cDNA			
LOCUS	clone OSUNEel3013 5', mRNA sequence.			
ACCESSION	CB677208			
VERSION	CB677208.1			
KEYWORDS	EST.			
SOURCE	Oryza sativa (japonica cultivar-group)			
ORGANISM	Oryza sativa (japonica cultivar-group) Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophytes; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehharitoidae; Oryzaceae; Oryza. 1 (bases 1 to 779)			
REFERENCE	Jantaauriyarat,C., Lu,G., Gowda,M., Hatfield,J., Zhou,B., Mazur,E., AUTHORS Kudrna,D., Dean,R., Soderlund C., Wing,R. and Wang,G. TITLE Large-scale identification of ESTs involved in the interaction between rice and Magnaporthe grisea COMMENT unpublished (2003) CONTACT: Rod Wing ARIZONA GENOMICS INSTITUTE UNIVERSITY OF ARIZONA BIOLOGICAL SCIENCES WEST, 448A, P.O. Box 210088, Tucson, AZ 85721-0088, USA TEL: 520 626 3967 FAX: 520 621 9288 EMAIL: http://genome.arizona.edu PCR PRIMERS FORWARD: gta aaa cga cgg cca gtcg BACKWARD: gga aac agc tat gac cat g PLATE: 13 row: 0 column: 13 SEQ PRIMER: gta aaa cga cgg cca gtcg. LOCATION/QUALIFIERS 1..779 /organism="Oryza sativa (japonica cultivar-group)" /mol_type="mRNA"			
FEATURES				
SOURCE				

	/cultivar="Niponbare"				
	/db_xref="taxon:39947"				
	/clone="OSJNBel3013"				
	/tissue_type="Leaf"				
	/dev_stage="3 week"				
	/lab_host="DH10B"				
	/clone_id="OSJNB"				
	/note="Vector: pInuescript II KS + Site 1; Ecore1; Site 2				
	XhoI; 24 hrs after inoculation with Rice Blast (70-15)"				
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ORIGIN					
Alignment Scores:					
Pred. No.:	8.36e-128	Length:	779		
Score:	1209.00	Matches:	227		
Percent Similarity:	93.44%	Conservative:	15		
Best Local Similarity:	87.64%	Mismatches:	17		
Query Match:	44.89%	Indels:	0		
DB:	14	Gaps:	0		
<hr/>					
US-09-857-522B-4 (1-509) x CB677208 (1-779)					
OY	44	AAlallelslllelleAsnCyaArglImetArGaAnMetGlumetGluGluysAlayS	63		
Db	2	GCATTCAGAACTCCCAATCGCCGTGAATCAAGACCATGAGATGAAAGAAGTTAA	61		
OY	64	ArggluPheylsileLeuleysPheHleHisProHsilleAargyeutyrgluva	83		
Db	62	AGAGAAATCAAGATRATTAGATTATTATGCCACCACATATCATTGGCTTATAGAGTG	121		
OY	84	IleTythrProthraspileTyValvalmetGluTyCyseLysTyrglyGluLeuphe	103		
Db	122	ATAAGACACCCAGACTGATATTATTATGTGTATGAGATATGTCAAATCTGSAAGTGT	181		
OY	104	AspyrtilleVslGluLyseGlyAArgenGlnGluaspGluAlaArgArgllepheGlnGln	123		
Db	182	GATTACATCGTTGAGAAAGAAAGACTGCAAGAGAAAGCTGACGCTTTTCCAGCAC	241		
OY	124	IlelleSerGlyValGluTyrcyshiSaArgAmetValAlHIsARgaSPleulySpro	143		
Db	242	ATCMTATCTGGTGTGATATTGCCATAGAAACATGGTGTTCAATCGTATCTTAAGCCA	301		
OY	144	GlubentleuleLeuasPserLysTyrsbnVallysleualasPhleglyleusEan	163		
Db	302	GAGAACCTTCCTTTGGACTCCAAAAGCAATGTAAAGATTGCAAGCTTTGGCTGAATAT	361		
OY	164	ValmethIsaAPGLyHIsPheleunysThrSerCysGlySeProAsnTyraAlaPro	183		
Db	362	GTTATCGGTGATGGTCACTTCTTGAAAGACAAGTGTGGTAGCCCCAATTTATGACAGACT	421		
OY	184	GluValIlleserGlyLysleuTyraaglProGluValaspValtyrSerCysglyal	203		
Db	422	GAGGTGATATCTGGTAAACTATATGCTGGCCCTGAAGTTGATGTGTGGAGTGGTGTT	481		
OY	204	IleleutyrylalaleuleucyeglyThrirleupProHeapPaargGluasnleProkntleu	223		
Db	482	ATTCTTTATGCTCTTCCTTGGTGNACCTTCATTGTGANAGAGAAATATTCACCACTT	541		
OY	224	PheylslysilleyeglyGlyIyleTyThrleuProSerHIsleuSerAlaleuaLaarg	243		
Db	542	TTTTAGAAAAATRAAGGTGCGCATATRAATCCCTTCCAGCATTTTGCACTTTGGCAAG	601		
OY	244	AspleulleProArgMetleuValValGluProMetLysArgIlethrIleaargIulle	263		
Db	602	GATTTGATTCACGAATGCTTGTTGTGTATCCCATGAAGAGGATCAACCATAGCTGAATC	661		
OY	264	ArggluhIsGlnTrppheGlnIleargleupProArgTyrrleuAlaValProPropoPaBP	283		
Db	662	CGTGAACATCGATGGTGTACAGATTGGTCTTCGCGTATTATTAAGCTGTGCACCTCTGAC	721		
OY	284	ThrThrGlnGlnAlalyMeMetlleaspgluasPTnrleuArgAspValAlasnmec	302		
Db	722	ACTGCACAAACAGTTAAAAAGTGCACATGAATCACTCGAATGATGTTATCAATATAG	778		

RESULT 7
CB632244
LOCUS CB632244 850 bp mRNA linear EST 08-APR-2003
DEFINITION OSIIEB10F22.f OSIIEB Oryza sativa (indica cultivar-group) cDNA
ACCESSION CB632244
VERSION CB632244.1 GI:29627233
KEYWORDS EST.
SOURCE Oryza sativa (indica cultivar-group)
ORGANISM Oryza sativa (indica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Erbartoideae; Oryzaceae; Oryza.
REFERENCE 1 (bases 1 to 850)
Jantaauriyarat,C., Lu,G., Gowda,M., Hatfield,J., Zhou,B., Mazur,E.,
Kudrna,D., Dean,R., Soderlund,C., Wing,R. and Wang,G.
Large-scale identification of ESTs involved in the interaction
between rice and Magnaporthe grisea
Unpublished (2003)
JOURNAL Contact: Rod Wing
COMMENT Arizona Genomics Institute
University of Arizona
Biological Sciences West, 448A, P.O. Box 210088, Tucson, AZ
85721-0088, USA
Tel: 520 626 3967
Fax: 520 621 9288
Email: http://genome.arizona.edu
PCR Primers
FORWARD: gta aac cga cgg cca gtc
BACKWARD: gga aac agc tat gac cat g
Plate: 10 row: F column: 22
Seq primer: gta aac cga cgg cca gtc.
Location/Qualifiers
1..850
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/mol_type="mRNA"
/cultivar="IR36"
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/clone="OSIIEB10F22"
/tissue_type="leaf"
/dev_stage="3 week"
/lab_host="DH10B"
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/note="Vector: pBlueScript II KS +; Site 1: EcoRI; Site 2:
XhoI; 24 hrs after inoculation with Rice Blast (P06-6-3)"
ORIGIN
Alignment Scores:
Pred. No.: 1..376-126 Length: 850
Score: 1199.00 Matches: 226
Percent Similarity: 97.50% Conservative: 8
Best Local Similarity: 94.17% Mismatches: 6
Query Match: 44.52% Indels: 0
Gaps: 0
DB: 14
US-09-857-522B-4 (1-509) x CB632244 (1-850)
QY 1 MetAapGlySerSerLySgLySerGlyYhiSerGluAlaLeuArgAsnTyrAsnLeuGly 20
Db 130 ATGATGGAATGCTAAAGCGGTGGCATTCGTGAGCAGTGAAGAACTTACATCTTGA 189
QY 21 ArgThrLeuGlyYllEgLyThrPheGlyLySerValysIleAlaGluHisLeuThrGly 40
Db 190 AGAAGCTTAAAGTATGCTCAATTGGAGAAAGGAAAGATTGACAGACATTAACCTTACAGGA 249
QY 41 HisArgValAlaIleLeuIleLeuAsnCySArgGlnMetArgAsnMetGluMetGluGlu 60
Db 250 CACAGAGTTGCTATTAATCAATCTCTGAACCGCCCAATGAAGAAATATGGAATGAGAG 309
QY 61 LysAlaLysArgGluPheLysIleLeuLysLeuPheIleHisProHisIleIleArgLeu 80
Db 310 AAAGCAAGAGAGAAATCAAGATCACTGAGATTGTCATTCATCCCATATCATTCGCTT 369

QY 81 TyrGluValIleTyrThrProThrAspIleTyrValAlaMetGluTyrCysLysTyrGly 100
Db 370 TATAGGTTATATACATCTCTACCGATATATATTTGTGATGAGATCTGCAACTTGGGA 429
QY 101 GluLeuPheAspTyrIleValGluLysGlyArgLeuGlnGluAapGluAlaArgArgIle 120
Db 430 GAACGTTGATTAATCATTTGTAAGAAAGCGGTTGACGAAATGAGAGCTCCGCAATC 489
QY 121 PheGlnGlnIleIleSerGlyValGluTyrCysHisArgAsnMetValAlaHisArgAsp 140
Db 490 TTCCAGAGATTATATCTGGGGGTGAATACGCCACGAAACATGGGTTCATCTGAT 549
QY 141 LeuLysProGluAanLeuLeuLeuAspSerLyTyrAsnValLysLeuAlaAspPheGly 160
Db 550 CTGAAGCCAGAAACCTTGCTCTGATTCGATTCANAGTATATGTAAGCTTGCTGACTTGGT 609
QY 161 LeuSerAsnValMetHisAspGlyHisPheLeuLysThrSerCysGlySerProAsnTyr 180
Db 610 TTGAGTAAAGTCATGATGATGCGCATTTTGTGAAGCAAGCTGTGGAGTCCAAACTAT 669
QY 181 AlaAlaProGluValIleSerGlyLysLeuTyrAlaGlyProGluValAspValTyrSer 200
Db 670 GCTCTCCAGAGGTGATCTGTGATATATATCTGACCTGAGCTTGATGATGAGC 729
QY 201 CysGlyValIleLeuTyrAlaLeuLeuCysGlyThrLeuProPheAspAspGluAsnIle 220
Db 730 TGAGAGTATCTTTATGCTCTCTCTTTGTGGACTCTTCATATGATGAGAAATATC 789
QY 221 ProAsnLeuPheLysLysIleLysGlyGlyIleTyrThrLeuProSerHisLeuSerAla 240
Db 790 CCCAAGCTATTCAAAGATTAAGGTGGTATATATCTCCCGAGTCATTAATCTGCT 849
RESULT 8
CB621531 829 bp mRNA linear EST 08-APR-2003
LOCUS CB621531
DEFINITION OSIIEB07H13.f OSIIEB Oryza sativa (indica cultivar-group) cDNA
clone OSIIEB07H13 5', mRNA sequence.
ACCESSION CB621531
VERSION CB621531.1 GI:29616519
KEYWORDS EST.
SOURCE Oryza sativa (indica cultivar-group)
ORGANISM Oryza sativa (indica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Erbartoideae; Oryzaceae; Oryza.
REFERENCE 1 (bases 1 to 829)
Jantaauriyarat,C., Lu,G., Gowda,M., Hatfield,J., Zhou,B., Mazur,E.,
Kudrna,D., Dean,R., Soderlund,C., Wing,R. and Wang,G.
Large-scale identification of ESTs involved in the interaction
between rice and Magnaporthe grisea
Unpublished (2003)
JOURNAL Contact: Rod Wing
COMMENT Arizona Genomics Institute
University of Arizona
Biological Sciences West, 448A, P.O. Box 210088, Tucson, AZ
85721-0088, USA
Tel: 520 626 3967
Fax: 520 621 9288
Email: http://genome.arizona.edu
PCR Primers
FORWARD: gta aac cga cgg cca gtc
BACKWARD: gga aac agc tat gac cat g
Plate: 07 row: H column: 13
Seq primer: gta aac cga cgg cca gtc.
Location/Qualifiers
1..829
/organism="Oryza sativa (indica cultivar-group)"
/mol_type="mRNA"
/cultivar="IR36"
/db_xref="taxon:39946"
/clone="OSIIEB07H13"
/tissue_type="leaf"
/dev_stage="3 week"

ORIGIN

/lab host="DH10B"
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/note="vector: pBluescript II KS +; Site_1: EcoRI; Site_2:
XhoI; Lesion Mimic SPL 11"

Alignment Scores:

Pred. No.:	6,44e-126	Length:	829
Score:	1193.00	Matches:	223
Percent Similarity:	98.71%	Conservative:	7
Best Local Similarity:	95.71%	Mismatches:	3
Query Match:	44.30%	Indels:	0
DB:	14	Gaps:	0

US-09-857-522b-4 (1-509) x CB621531 (1-829)

Qy 1 MetAapGlySerSeryGlySerGlyYHISerGlyAlaLeuAArganTYrAsnLeuGly 20
Db 130 ATGATGGAAATGCTAAAGCGCGTGGCATTCGAGCACTGAATCAATCTTGGA 189
Qy 21 ArgThrLeuGlyIleGlyThrPheGlyYlyValYlyIleAlaGlyIleHisIleLeuThrGly 40
Db 190 AGAAGCTTAGGATTTGGCTCATTTGAAAGTGAAGATTGAGAGCATTAACCTTACAGA 249
Qy 41 HisArgValAlaIleIleYlyIleIleAsnCYsarGlyInMetArgAsnMetGlyMetGly 60
Db 250 CACAGAGTTGCTATTAAGATCTCGAACCGCCCAATGAGAAATATGAAATGAGAGAG 309
Qy 61 LysAlaIleYlyValGlyPheIleLeuYlyLeuPheIleHisIleProHisIleIleArgLeu 80
Db 310 AAACCAAGAGAGAAATCAAGATCTGAGATGTTTCATTCATCCCAATCATTCGCGCTT 369
Qy 81 TyrGlyValIleIleYlyThrProThrAspIleTyrValIleMetGlyIleYlySerGly 100
Db 370 TATGAGTTTATATACCTCTCAAGATATATATGTTGAGAGAGACTCTCAAGTTTGA 429
Qy 101 GluLeuPheAspTYrIleValGlyIleGlyValArgLeuGlyAspGlyAlaArgArgIle 120
Db 430 GACGTTTATGATTCATTCATTTGAGAAAGCGAGTTGACGAAATGAGAGCTCGCGAATC 489
Qy 121 PheGlyIleIleIleSerGlyValGlyIleYlyCysHisArgAsnMetValIleHisArgAsp 140
Db 490 TTCAGAGATTAATATCTGGGGTAGAATACGCCACAGAAACATGGTGTTCACTCGTAT 549
Qy 141 LeuYlyProGlyAsnLeuLeuLeuAspSerIlyTYrAsnValYlyLeuAlaAspPheGly 160
Db 550 CTGAAGCCAGAAACTTCTCTACTGATTCAAAGTATATATGTAACCTTGCGACTTTGCT 609
Qy 161 LeuSerAsnValMetHisAspGlyHisIleLeuYlyThrSerCysGlySerProAsnTYr 180
Db 610 TTGAGTAACTCATCATCATGATGCGCATTTTGAAGACAACTGCGGAGTCAAACTAT 669
Qy 181 AlaAlaProGlyValIleSerGlyYlyLeuTYrAlaGlyProGlyValAspValTyrSer 200
Db 670 GCTGCTCAAGAGGTATCTGTGTAATATATATGCTGACCTGAGGTGATGAGGC 729
Qy 201 CysGlyValIleLeuTYrAlaLeuLeuCysGlyTYrLeuProPheAspAspGlyAsnIle 220
Db 730 TGTGAGAGATCCCTTATGCTCTCTTTGTGTGACTCTTCCATTTGATGATGAGAAATTC 789
Qy 221 ProAsnLeuPheYlyValIleYlyGlyIleYlyTYr 233
Db 790 CCCAACCTATTCAAAGATTAAGGGTGTATATATCT 828

RESULT 9
BI950083
LOCUS
DEFINITION
HVSME10018H14f Hordeum vulgare spike EST library HVCNDA0012
(Fusarium infected) Hordeum vulgare subsp. vulgare cDNA clone
HVSME10018H14f, mRNA sequence.
ACCESSION
BI950083
VERSION
BI950083.1
KEYWORDS
EST.

SOURCE

ORGANISM
Hordeum vulgare subsp. vulgare
Hordeum vulgare subsp. vulgare
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Poideae; Triticeae; Hordeum.
1 (bases 1 to 863)

REFERENCE

Wing, R., Muehlbauer, G.J., Close, T.J., Kleinbols, A., Wise, R.,
Heinen, S., Begum, D., Fritsch, D., Yu, Y., Henry, D., Palmer, M.,
Rambo, T., Simmons, J., Fenton, R.D., Malatrasi, M., Choi, D.W.,
Oates, R. and Main, D.
Development of a genetically and physically anchored EST resource
for barley genomics: Fusarium infected Morex spike cDNA library
Unpublished (2001)

TITLE

JOURNAL

COMMENT

Contact: Wing RA
Clemson University Genomics Institute
100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 7288
Fax: 864 656 4293
Email: twing@clemson.edu
Total hg bases = 601
Seq primer: AATTACCTCAGTAAGG
High quality sequence stop: 729.
Location/Qualifiers

FEATURES

source

1. 863
/organism="Hordeum vulgare subsp. vulgare"
/mol_type="mRNA"
/cultivar="Morex"
/sub_species="vulgare"
/db_xref="taxon:112509"
/clone="HVSME10018H14f"
/tissue_type="Spike"
/lab_host="TUC121"
/clone_lib="Hordeum vulgare spike EST library HVCNDA0012
(Fusarium infected)"
/note="vector: pBluescript SK(-); Site_1: EcoRI; Site_2:
XhoI; Plants were grown at the University of Minnesota in
the GJ Muehlbauer lab; spikes were harvested and snap
frozen at 0, 1, 2, 3, 4, 5, 6, and 8 days after Fusarium
graminearum inoculation (Heinen). In the TJ Close lab at
the University of California, Riverside, total RNA was
prepared from each sample pool, equal quantities of all
eight RNA pools were combined, poly(A) RNA was purified
from the mixture, one primary unamplified cDNA library was
made, and 1 million pfu were in vivo excised to give
pBluescript SK(-) cDNA phagemids (Choi, Fenton,
Malatrasi). Phagemids were plated and picked at the
Clemson University Genomics Institute (CUGI) (Begum,
Palmer, Fritsch, Atkins and Wing). Plasmid DNA
preparations, DNA sequencing and sequence analysis were
performed at CUGI (Wing, Yu, Fritsch, Henry, Simmons,
Oates, Rambo, Main). The sequence has been trimmed to
remove vector sequence and contains a minimum of 100 bases
of phred value 20 or above. For more details on library
preparation and sequence analysis see
http://www.genome.clemson.edu/projects/barley. To order
this clone see http://www.genome.clemson.edu/orders Also
see Close TJ, Wing R, Kleinbols A, Wise R (2001)
Genetically and physically anchored EST resources for
barley genomics. Barley Genetics Newsletter 31:29-30
(http://wheat.pw.usda.gov/g9pages/bgn/31/cover.html)"

ORIGIN

Alignment Scores:

Pred. No.:	1.74e-125	Length:	863
Score:	1189.50	Matches:	240
Percent Similarity:	90.65%	Conservative:	12
Best Local Similarity:	86.33%	Mismatches:	25
Query Match:	44.17%	Indels:	4
DB:	12	Gaps:	1

US-09-857-522b-4 (1-509) x BI950083 (1-863)

QY 4 SerSerLysGlySerGlyHisSerGluAlaLeuArgAsnLysGlyArgThrLeu 23
 Db 2 AACCTAGAGAGAGGGGCAATTCGTAAGCGTTAAAGAACTCAATCTGGGAGAACATTA 61
 QY 24 GlyIleGlyThrPheGlyLysValLysIleAgluHisLysLeuThrGlyHisArgVal 43
 Db 62 GGTATAGGACATTTGGAAAGTGGATGGATGGAAACATTAAGCATACAGGGGACAAAGTT 121
 QY 44 AlaIleLysIleIleAsnGlyArgGluMetLysArgAsnMetGluMetGluLysLys 63
 Db 122 GCTTAAAGATTCGTAACCGTGTGCAATGAACTAATGAACATGAAAGAGAAACAAAG 181
 QY 64 ArgGluPheLysIleLeuLysLeuPheIleHisProHisIleIleArgLeuTyrGluVal 83
 Db 182 AGAGAGATCAAGATTAATGAGGTGTTCAATCCCTCATATCATCCGGCTTATAGAGTTC 241
 QY 84 IleTyrThrProThrAspIleTyrValValMetGluTyrCysLysTyrGlyGluLeuPhe 103
 Db 242 ATTATACACACCTACAGATATATTTGTGTGATGAAATATGCAAGTATGGGAGCTATTC 301
 QY 104 AspTyrIleValGluLysGlyArgLeuGluGluAspGluAlaArgArgIlePheGluGln 123
 Db 302 GACTGCATTTGTTGAAAGAGGGCGGTTCACAGAAATGAGGCTCGTCAATCTTCACAGAG 361
 QY 124 IleIleSerGlyValGluTyrCysHisArgAsnMetValValHisArgAspLeuLysPro 143
 Db 362 ATTATATTTGGTGTGTTGAATCTGCGACAGAAACATGTTGTTCAATCGATCTTAAGCCA 421
 QY 144 GluAsnLeuLeuLeuAspSerLysTyrAsnValLysLeuAlaAspPheGlyLeuSerAsn 163
 Db 422 GAAACCTGTTACTGATTCGAAATATATGATGAAATCTGGCGACTTTGGATTAAGTAT 481
 QY 164 ValMetHisArgGlyHisPheLeuLysThrSerCysGlySerProAsnTyrAlaAlaPro 183
 Db 482 GTCATGATGATGATGCGCATTTCTGAAAGCTAGCTCGGAGATCCAACTATGCTGCACCG 541
 QY 184 GluValIleSerGlyLysLeuTyrAlaGlyProGluValAspValTyrSerCysGlyVal 203
 Db 542 GAGGTATCTCAGTAAATTTGTAACCTGAGCTGAGTTGATGTTTGAAGCTGTGGGATG 601
 QY 204 IleLeuTyrAlaLeuLeuCysGlyThrLeuProPheAspAspGluAsnIleProAsnLeu 223
 Db 602 ATACTTATGCTCTCTTTGGGGGCACTCTTCCATTTGATGATGACAAATATCCAACTGG 661
 QY 224 PheLysLysIleLysGlyGlyIleTyrThrLeuProSerHisLeuSerAlaLeuAlaArg 243
 Db 662 TTCAAAGAGATTAAGGGGAGCATCTATCTTCCAGATCTTATCTGCTCTTGCACAGG 721
 QY 244 AspLeuIleProArgMetLeuValValGluProMetLysArgIleThrIleArgGluIle 263
 Db 722 GATTGATCCCAAG-ATGCTTGTGTTGATCTATGAAAGAGTAA-CCAAATCTGGAATTT 779
 QY 264 ArgLysHisGlnTyrPheGlnIleArgLeuProArgTyrLeuAlaValProPro 281
 Db 780 CGAAA-CACCTCGGGTTAAGATGCGCTCCCGG---TACCTGCAAGGCGTCCCA 829

RESULT 10
 BM084571 951 bp mRNA linear EST 07-JAN-2003
 LOCUS pPAP 08 G08 Apomictic pistil cDNA library Pennisetum ciliare cDNA
 DEFINITION 5', mRNA sequence.
 ACCESSION BM084571 GI:27532480
 VERSION BM084571.1
 SOURCE EST.
 ORGANISM Pennisetum ciliare (buffelgrass)
 SOURCE Pennisetum ciliare
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
 clade; Panicoideae; Paniceae; Pennisetum.
 REFERENCE 1 (bases 1 to 951)
 AUTHORS Schulte,S.R., Bowers,J.B., Burrow,G.B., Husey,M.A., Burson,B. and
 Paterson,A.H.
 TITLE Cloning and characterization of genes from an apomictic pistil cDNA

JOURNAL
 COMMENT Unpublished (2001)
 Contact: Schulte SR
 Plant Genome Mapping Lab
 University of Georgia, Center for Applied Genetic Technologies
 Riverbend Research Building, Room 162, 110 Riverbend Rd., Athens,
 GA 30602, USA
 Tel: 706 583 0166
 Fax: 706 583 0160
 Email: sechulz@arches.uga.edu

FEATURES
 source
 1..951
 /organism="Pennisetum ciliare"
 /mol_type="mRNA"
 /culivar="PI409164"
 /db_xref="taxon:35520"
 /clone_id="Apomictic pistil cDNA library"

ORIGIN
 Alignment Scores:
 Pred. No.: 1.09e-123 Length: 951
 Score: 1174.50 Matches: 237
 Percent Similarity: 86.05% Conservative: 16
 Best Local Similarity: 80.61% Mismatches: 36
 Query Match: 43.61% Indels: 5
 DB: 12 Gaps: 1

US-09-857-522B-4 (1-509) x BM084571 (1-951)

QY 61 LysAlaLysArgGluPheLysIleLeuLysLeuPheIleHisProHisIleIleArgLeu 80
 Db 1 AAAGTGAAGAGAGAAATCAATCAATCTCAGATTAATTTATGCACTTCATATCATGCGCTT 60
 QY 81 TyrGluValIleTyrThrProThrAspIleTyrValValMetGluTyrCysLysTyrGly 100
 Db 61 TATAGGATGATGATATACACCTGCTGATATTTATGTTATGAGTATGTTAAATCTGGA 120
 QY 101 GluLeuPheAspTyrIleValGluLysGlyArgLeuGluGluAspGluAlaArgArgIle 120
 Db 121 GAACCTTTTGATTCATTTGTTGAGAGAGGAGACTACATGAAGAAAGAGCTGCGCGTTT 180
 QY 121 PheGlnGlnIleIleSerGlyValGluTyrCysHisArgAsnMetValValHisArgAsp 140
 Db 181 TTCAGAGAGATCAATCTCGGTGTTGATTTGCCATGAACATGATGCTTCACTGAT 240
 QY 141 LeuLysProGluAsnLeuLeuLeuAspSerLysTyrAsnValLysLeuAlaAspPheGly 160
 Db 241 CTTAAAGCCAGAGAACTCTTTTGGATTCAAAATGTAATGTTAAGATTGCTGATTTGGC 300
 QY 161 LeuSerAsnValMetHisAspGlyHisPheLeuLysThrSerCysGlySerProAsnTyr 180
 Db 301 TTAAGTAAATGTTATGCGTATGATGTCATCTTCTTAAAGACAGCTGTGTAGCCCAAATAT 360
 QY 181 AlaIleProGluValIleSerGlyLysLeuTyrAlaGlyProGluValAspValTyrSer 200
 Db 361 GCAGCACTGAGGTCATATCTCGTAACTATATCTGCTCTTAAGTTGAGCTTCGAGC 420
 QY 201 CysGlyValIleLeuTyrAlaLeuLeuCysGlyThrLeuProPheAspAspGluAsnIle 220
 Db 421 TGTGTGTTATTTCTTATGCTCTCTTTGTGTGTCCTTCCATTTGATGAGAGAAATAT 480
 QY 221 ProAsnLeuPheLysLysIleLysGlyGlyIleTyrThrLeuProSerHisLeuSerAla 240
 Db 481 CCAAACTTTTAAAGAAATTAAGGGGTGGAATATATACCTTCCATGTCATTTGTCACT 540
 QY 241 LeuAlaArgAspLeuIleProArgMetLeuValValGluProMetLysArgIleThrIle 260
 Db 541 TCAGCAAGGAGATTTAATTCACAGATGCTGTTTATATCCAAAGAAAGATTAACATC 600
 QY 261 ArgGluIleArgGluHisGlnTyrPheGlnIleArgLeuProArgTyrLeuAlaValPro 280
 Db 601 CGTGAATCCGTGAACATGTGTGTGTTCAAGATTCAGCTTCACGCTATTTGGCTGTGCG 660

Qy 281 ProProaspThrThrGlnGlnAla-LysMetIleAspGluAsp-ThrLeuArgAspValV 300
 Db 661 NCTTCAGACACTGCACAAACAGTAAACCTTGACAGAGAAACCTTAAATGATGGA 720
 Qy 300 aAaenMetGlyPheasnLysasnHsValCysGluSerLeuCysSerArgLeuGlnAsn 320
 Db 721 TTAAGATGGCTTTTGACAAAGATCTGCTAATGATCTGTGCAACAGGNTGACAGATG 780
 Qy 320 lu-AlaThrValAlaIleThrLeuLeuLeuAspAsnArg-PheArgAlaThrSerGlyTy 339
 Db 781 AGGCGCAACAGTTGCTTATTTACTCTGACAAATAGAGCTTGTACACCAAGTGGTT 840
 Qy 339 rLeuGly---AlaAspTyGlnGlnIleSerMetAsp 349
 Db 841 TATCTCCAGACCAAGATTTCANAGATCTATGAC 874

RESULT 11
 BQ805778 794 bp mRNA linear EST 31-JUL-2002
 LOCUS MHB3570_H07_P14S Wheat developing grains cDNA library Triticum
 DEFINITION aestivum cDNA clone MHB3570_H07_P14, mRNA sequence.
 ACCESSION BQ805778
 VERSION BQ805778.1 GI:22029987
 KEYWORDS EST.
 SOURCE Triticum aestivum (bread wheat)
 ORGANISM Triticum aestivum
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Poideae; Triticeae; Triticum.
 1 (bases 1 to 794)
 Alenbach,S., Anderson,O.D., Chao,S., Chin,A., Close,T.J.,
 Cronin,K., Crossman,C., Fenton,R.D., Lazo,G.R., Pham,J.,
 Rausch,C.J., Wilson,C. and Woo,J.
 The structure and function of the expressed portion of the wheat
 genomes - Developing grains cDNA library
 Unpublished (2002)
 JOURNAL Contact: Olin Anderson
 US Department of Agriculture, Agriculture Research Service, Pacific
 West Area, Western Regional Research Center
 800 Buchanan Street, Albany, CA 94710, USA
 Tel: 5105595773
 Fax: 5105595818
 Email: oanderson@pw.usda.gov
 Sequences have been trimmed to remove vector sequence and low
 quality sequence with phred score less than 20
 Seq primer: SK primer
 Location/Qualifiers
 1..794
 /organism="Triticum aestivum"
 /mol_type="mRNA"
 /cultivar="Butte 86"
 /db_xref="taxon:4565"
 /clone="MHB3570_H07_P14"
 /tissue_type="whole grains"
 /dev_stage="3-44 days post anthesis seed"
 /lab_host="E. coli SOLR"
 /clone_idb="Wheat developing grains cDNA library"
 /note="Vector: lambda ZAP II, excised phagemid, Site 1:
 EcoRI; Plants were grown under six following different
 environmental regimes in greenhouse, Environment 1)
 240C/170C day/night, well-watered, with post-anthesis
 fertilizer, Environment 2) 240C/170C day/night,
 well-watered, without post-anthesis fertilizer,
 Environment 3) 370C/170C day/night, well-watered, with
 post-anthesis fertilizer, Environment 4) 370C/170C
 day/night, well-watered, without post-anthesis fertilizer,
 Environment 5) 370C/170C day/night plus drought, with
 post-anthesis fertilizer, Environment 6) 370C/170C
 day/night plus drought, without post-anthesis fertilizer,
 developing wheat grains from the following were excised
 and frozen in liquid nitrogen, Environment 1 at 3, 5, 7,
 8, 10, 12, 16, 20, 24, 28, 32, 36, 40, 44 DPA Environment
 2 at 3, 5, 7, 8, 10, 12, 16, 20, 24, 28, 32, 36, 40, 44

ORIGIN
 Alignment Scores:
 Pred. No.: 2,86e-122 Length: 794
 Score: 1161.00 Matches: 216
 Percent Similarity: 92.58% Conservative: 21
 Best Local Similarity: 84.38% Mismatches: 19
 Query Match: 43.11% Indels: 0
 DB: 13 Gaps: 0

US-09-857-522B-4 (1-509) x BQ805778 (1-794)
 Qy 73 lIehisProhisIleIleArgLeuTyGluValIleTyThrProthAspIleTyVal 92
 Db 25 ATTCACTCATATATCATCCGGCTTATGAGTCAATGAGACACTTAAGATATTTGTT 84
 Qy 93 ValMetGluTyCysLysTyGlyGluLeuPheAspTyIleValGluTyGlyArgLeu 112
 Db 85 GTGATGAAATTAATCCAGAAATGGAGATTATGATTAATGATTTGTTGAAAGGGGGTTA 144
 Qy 113 GlnGluAspGluAlaArgArgIlePheGlnGlnIleIleSerGlyValGluTyCysHis 132
 Db 145 CAGAAATGAAAGCTCGTCAATCTTCCACAGATTAATCTGTTGAAATATGCGCAC 204
 Qy 133 ArgAsnMetValValHisArgAspLeuTyProGluAsnLeuLeuAspSerLeTy 152
 Db 205 AGAAACATGTTGTTCACTCGATCTAAAGCCAAAGAACTGTTAATCTTAATATAT 264
 Qy 153 AsnValLysLeuAlaAspPheGlyLeuSerAsnValMetHisAspGlyHisPheLeuLys 172
 Db 265 AATGTGAAACTGTTGACTTGAGTTGATTAATGATGATGATGATGATGATGATGATG 324
 Qy 173 ThrSerCysGlySerProAsnTyAlaAlaProGluValIleSerGlyLysLeuTyAla 192
 Db 325 ACTAGCTCGGGAGACTCTAAACTATGCTGCACAGAGCTTATCTCAGGTAATCTGAGCT 384
 Qy 193 GlyProGluValaAspValTTPSerCysGlyValIleLeuTyAlaLeuLeuCysGlyThr 212
 Db 385 GGACTGAGGTTGATGCTGAGAGCTGAGAGTGAATCTTATAGCTCTTCTTGTGGCAGA 444
 Qy 213 LeuProPheAspArgGluAsnIleProAsnLeuPheLysLysIleTyGlyIleTy 232
 Db 445 GTTCCATTTGAGATGACAAATATCCCAACTGATCAAAAAGATTAAGAGGAGGTTCTAT 504
 Qy 233 ThrLeuProSerHisIleSerAlaLeuAlaArgAspLeuIleProAsnMetLeuValVal 252
 Db 505 ATCTTCCAACTTATTTATCTGATCTTGCATGATGATGATGATGATGATGATGATG 564
 Qy 253 GluProMetLysArgIleThrIleArgGluIleArgLysIleGlnTyPheGlnIleArg 272
 Db 565 GATCCCATGAAGAGAAATCACATATCTGGAATTCGGAGACCAACCATGTTTCAANAATCGC 624
 Qy 273 LeuProArgTyLeuAlaValaProProProAspThrThrGlnGlnAlaLysMetIleAsp 292
 Db 625 CTTCCTCGCTACCTGGAGAGGCTCCGCCAAACACGACACGACGACGACGACGACGAC 684
 Qy 293 GluAspThrLeuArgAspValaValaAsnMetGlyPheAsnLysAsnHisValCysGluSer 312
 Db 685 AAATATACATCTCAAGACATTTGATCTGGAATATATGATATATGATGATGATGATCA 744
 Qy 313 LeuCysSerArgLeuGlnAsnGluAlaThrValaIleTyTyLeuLeu 328

|||||:::|||||

Db 745 CTGCGCATAGGCTGCAAAATGAGCAACTGTGCATTTACTTGGCTC 792

RESULT 12
CK195998 862 bp mRNA linear EST 08-DEC-2003
FGAS004444 Triticum aestivum FGAS: Library 3 Gate 6 Triticum
aestivum cDNA, mRNA sequence.

DEFINITION
CK195998
CK195998.1 GI:39558388

ACCESSION
EST.

VERSION
Triticum aestivum (bread wheat)

KEYWORDS
Triticum aestivum

SOURCE
Bakeryota: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Poideae; Triticeae; Triticum.

REFERENCE
1 (bases 1 to 862)
Allard, F., Crosby, W.L., Danyluk, J., Eudes, F., Frick, M., Gaudet, D.,
Genswein, B., Graf, R., Gulick, P., Hrycan, L.D., Laroche, A.,
Links, M.G., McCarthy, E.L., Monroy, A., Muzak, I., Nilsson, D.,
Penniket, C., Roach, J.L. and Sarhan, F.
Functional Genomics of Abiotic Stress in Wheat and Canola Crops
Unpublished (2003)

AUTHORS
Contact: Mm L Crosby
Bioinformatics

TITLE
University of Saskatchewan, Department of Computer Science
1C101 Engineering Building, S7 Campus Drive, Saskatoon,
Saskatchewan, S7N 5A9, Canada
Tel: 306 966 1769
Fax: 306 966 2033

JOURNAL
Email: fgas.est@cs.usask.ca
This sequence is the direct result of the Base calling software
phred (default parameters). It is the raw base calls. To aid in the
identification of the high quality insert the software Lucy
(default parameters) has been run on this sequence. Lucy identified
the region [102,683].
Plate: L3C105 row: H column: 15.

COMMENT

FEATURES
source
1..862
location/Qualifiers
/organism="Triticum aestivum"
/mol_type="mRNA"
/db_xref="taxon:4565"
/clone_lib="Triticum aestivum FGAS: Library 3 Gate 6"
/notes="Organ: Root; Vector: pCMV.SPORT6; Root tissue from
control, cold-acclimated and salt stressed wheat cultivar
Norstar. 7 mRNA populations were combined before
constructing the library; 7 day non-acclimated roots, 1,
23, and 53 days cold-acclimated at 4C, and 30 minutes, 3
hours and 6 hours treated roots with 200mM NaCl.
Non-acclimated and cold-acclimated plants were grown in
vermiculite while salt stressed plant were grown
hydropionically. First strand synthesis in this library was
done in the presence of methylated dCTP thereby protecting
from internal cleavage with NciI."

ORIGIN

Alignment Scores:
Pred. No.: 4.3e-122 Length: 862
Score: 1160.00 Matches: 226
Percent Similarity: 93.28% Conservative: 10
Best Local Similarity: 89.33% Mismatches: 16
Query Match: 43.07% Indels: 2
DB: 14 Gaps: 0

US-09-857-522B-4 (1-509) x CK195998 (1-862)

Qy 51 ArgGlnMetArgAenMetGluMetGluGluValysArgGluPheLeuLys 70
Db 107 CGTCCGATGGAATATGGAATGGAAGACCAAGACAGATCAATATTAGG 166

Qy 71 LeupheIleHisProHisIleIleArgLeuTyGluValIleTyThrProThrAspIle 90
Db 167 TTGTC-ATTCACTCATATCATCCGGCTTATAGGTCAATTTACACACCTACGATATA 225

Qy 91 TyrValIalMetGluTyGlySerTyGlyGluLeuPheAspTyrIleValGluValGly 110
Db 226 TTGTGTGTGATGGAAATATTCAGATATGTGAGCTATTCACATGCTATTTGGACAAAGGG 285

Qy 111 ArgLeuGlnGluAspGluAlaArgArgIlePheGlnGlnIleIleSerGlyValGluTyr 130
Db 286 CGGTACAGGAAGAATAGAGGCTCGTCGATCTTCACAGCATTTATCTGGGTGGAAATAC 345

Qy 131 CysHisArgAsnMetValIleHisArgAspLeuLysProGluAsnLeuLeuAspSer 150
Db 346 TGCCACAGAAACAATGCTGTGCTCATCGCATCAAGCAAAAACCTGTTACTTGAATTC 405

Qy 151 TyGTrsnValIysLeuAlaAspPheGlyLeuSerAsnValMetHisAspGlyHisPhe 170
Db 406 AAATATATATGTAAGAACTTGGCCGACTTTGGGTATGATGATCATGATGATGGCCATTT 465

Qy 171 LeuLysThrSerCysGlySerProAsnTyrAlaAlaProGluValIleSerGlyValLeu 190
Db 466 CTGAAGACTAGCTGCGGAGATCCAACTATGCTGCACAGAGTTATCTCAGGTAAATTA 525

Qy 191 TyrAlaGlyProGluValAspValTyrSerCysGlyValIleLeuTyrAlaLeuLysCys 210
Db 526 TACCTGGAACCTGAGCTTGATGTTTGAGCTGTGGGTGATTAATCTTATGCTCTTTTGT 585

Qy 211 GLTyrLeuProPheAspAspGluAsnIleProAsnLeuPheLysIleValGlyGly 230
Db 586 GTGACTCTTCATTTGATGATGATGACAAATATTCACAAATGTTCCAAAAGATAAAGGGAGGC 645

Qy 231 IleTyrThrLeuProSerHisLeuSerAlaLeuAlaArgAspLeuIlePro-ArgMetLe 250
Db 646 ATCATATCTCTTCCAAATCATTTATATCGCTCTTGCAAGGACTTGATCCGAAGAATGCT 705

Qy 250 uValIalGluProMetLysArgIleThrIleArgGluIleArgGluHisGlnTyrPheG 270
Db 706 TGTGTTGATCATCATGAGAGAAATCAAGATTCGATTCGGGAAACCAATGCTTTCA 765

Qy 270 nIleArgLeuProArgTyrLeuAlaValProProProAspThrThGlnGlnIalysMe 290
Db 766 GAATCGCTTCCTCGCTTACTGCGAGTGGCTCCACAGACAGCGCATGACGCAAAAT 825

Qy 290 tIleAspGluAspThrLeuArgAspValValAsnMet 302
Db 826 GATTGCTGAAGATACCTTAAGAGATGTCAACTG 862

RESULT 13
CA076858 690 bp mRNA linear EST 23-SEP-2003
SCMCM1105D11.G AM1 Saccharum officinarum cDNA clone SCMCM1105D11
5', mRNA sequence.

DEFINITION
CA076858
CA076858.1 GI:34929119

ACCESSION
EST.

VERSION
Saccharum officinarum

KEYWORDS
Saccharum officinarum

SOURCE
Bakeryota: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Saccharum.

REFERENCE
1 (bases 1 to 690)
Vettore, A.L., da Silva, F.R., Kemper, E.L. and Arruda, P.
The libraries that made SUCSEST

AUTHORS
Genet. Mol. Biol. 24 (1-4), 1-7 (2001)

TITLE
Contact: Arruda, P

JOURNAL
Centro de Biologia Molecular e Engenharia Genetica
Universidade Estadual de Campinas
Caixa Postal 6010, 13083-970, Campinas SP, Brazil
Tel: 55 19 3788 1137
Fax: 55 19 3788 1089

COMMENT
Email: parruda@unicamp.br
Clone distribution: clone distribution information can be found
through the Brazilian Clone Collection Center (BCCC) at
<http://www.bcccenter.fcav.unesp.br>
Plate: 105 row: D column: 11

Seq primer: T7 Promoter Primer.
Location/Qualifiers
1. 690

/organism="Saccharum officinarum"
/mol_type="mRNA"
/db_xref="taxon:4547"
/clone="SCWCM1105D11"
/lab_host="DH10B"
/clone_lib="AM1"
/note="Organ: Apical meristem and tissues surrounding of mature plants; Vector: pSport1; Site_1: SalI; Site_2: NotI; An unidirectional cDNA library generated from [apical meristem and tissues surrounding of mature plants]. cDNA was prepared from polyA+ mRNA using Superscript Plasmid System Kit (Invitrogen). The double-strand cDNAs were fractionated in a sepharose CL-2B 40cm-columns and fragments sizing between 0.8 and 1.5 Kb were directionally cloned into the vector. Details of each source of RNA and library construction can be obtained at <http://sucest.lad.ic.uicamp.br/public>"

ORIGIN

Alignment Scores:
Pred. No.: 4,98e-122 Length: 690
Score: 1158.00 Matches: 218
Percent Similarity: 97.35% Conservative: 2
Best Local Similarity: 96.46% Mismatches: 6
Query Match: 43.00% Indels: 0
DB: 13 Gaps: 0

US-09-857-522B-4 (1-509) x CA076858 (1-690)

Qy 1 MetAspGlySerSerLysGlySerGlyHisSerGluAlaLeuArgAsnTyrAsnLeuGly 20
Db 11 ATGATGGAAGTACTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 70
Qy 21 ArgThrLeuGlyIleGlyThrPheGlyLysValLysIleAlaGluHisLysLeuThrGly 40
Db 71 AGAAGCTTTAGTATTTGGACATTTGGAAAGTGAAGATGGCGACATTAAGCTTACGGGA 130
Qy 41 HisArgValAlaIleLysIleIleAsnCysArgGlnMetArgAsnMetGluMetGluGlu 60
Db 131 CATGAGGTTGCTTAAAGATCATCAATGTCGCCAATGAAGAAATATGGAATGGAAGAG 190
Qy 61 LysAlaLysArgGluPheLysIleLeuLysLeuPheIleHisProHisIleIleArgLeu 80
Db 191 AAAGCAAGAGAAATCAAGATATGAAAGTTGTTCAATCCCAATATATCCGGCTT 250
Qy 81 TyrGluValIleTyrThrProThrAspIleTyrValValMetGluTyrCysLysTyrGly 100
Db 251 TATGAGGTCATATACACCAACAGATATATATGTTGATGGAATATATGTAAGTATGGC 310
Qy 101 GluLeuPheAspTyrIleValGluLysGlyValArgLeuGlnGluAspGluAlaArgArgIle 120
Db 311 GAGTGTGTTGATTCATTTGAGAAAGCAGATTAAGGAGGAGGAGGAGGAGGAGGAGGAGG 370
Qy 121 PheGlnGlnIleIleSerGlyValGluTyrCysHisArgAsnMetValIleHisArgAsp 140
Db 371 TTCAGGAGATCATATCTGTTGATGATCTGCCATTAACAACTGTTGTCACCGTAC 430
Qy 141 LeuLysProGluAsnLeuLeuAspSerLysTyrAsnValLysLeuAlaAspPheGly 160
Db 431 CTAAGCCAGAAACTTGTACTTCAATCAAGATATATGTAAGCTTGGACCTTGGT 490
Qy 161 LeuSerAsnValMetHisAspGlyHisPheLeuLysThrSerCysGlySerProAsnTyr 180
Db 491 TTGAGCATGTCATGATGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 550
Qy 181 AlaAlaProGluValIleSerGlyLysLeuTyrAlaGlyProGluValAspValTyrSer 200
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Qy 201 CysGlyValIleLeuTyrAlaLeuLeuCysGlyThrLeuProPheAspAspGluAsnIle 220

Db 611 TGTGAGTGAACCTTATGCTCTTTTGTGGACCTCTTCATTTGATGATGAGAAATATT 670
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Db 671 CCACACTGTTCAAAAAA 688

RESULT 14
CF307150
LOCUS
DEFINITION
704 bp mRNA linear EST 15-AUG-2003
HDA1--05-006.g1 OshDACL-overexpressing transgenic rice lambda phage
cDNA library I (HDA1) Oryza sativa cDNA clone HDA1--05-006, mRNA
sequence.

ACCESSION
CF307150
VERSION
CF307150.1 GI:33678911
KEYWORDS
EST.

SOURCE
ORGANISM
Oryza sativa

REFERENCE
AUTHORS
Kim, V.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
CONTACT
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Genomics and Genetics Institute, Greendene Biotech Inc., Division
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Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

COMMENT
JOURNAL
TITLE
Large-scale Sequencing Analysis of Rice ESTs

REFERENCE
AUTHORS
Kim, V.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
CONTACT
Contact: Nahm B.H.
Genomics and Genetics Institute, Greendene Biotech Inc., Division
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Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
source
Location/Qualifiers
1..704

/organism="Oryza sativa"
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phage cDNA library I (HDA1)"
/note="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2:
XhoI; Callus was treated with ABA(20um) for 1hour. cDNA
was inserted into lambda Uni-ZAP XR vector at 5' end with
EcoRI and 3' end with XhoI site. mRNA was derived from
rice Histone Deacetylase overexpression line."

ORIGIN

Alignment Scores:
Pred. No.: 8,75e-122 Length: 704
Score: 1156.00 Matches: 216
Percent Similarity: 98.67% Conservative: 7
Best Local Similarity: 95.58% Mismatches: 3
Query Match: 42.93% Indels: 0
DB: 14 Gaps: 0

US-09-857-522B-4 (1-509) x CF307150 (1-704)

Qy 1 MetAspGlySerSerLysGlySerGlyHisSerGluAlaLeuArgAsnTyrAsnLeuGly 20
Db 25 ATGATGGAAGTACTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 84
Qy 21 ArgThrLeuGlyIleGlyThrPheGlyLysValLysIleAlaGluHisLysLeuThrGly 40
Db 85 AGAAGCTTTAGTATTTGGACATTTGGAAAGTGAAGATTCAGAGCATTAAGCTTACAGGA 144
Qy 41 HisArgValAlaIleLysIleIleAsnCysArgGlnMetArgAsnMetGluMetGluGlu 60
Db 145 CACGAGTGTCTTAAAGATCTGAACCGCGCCCAATGAAGAAATATGGAATGGAAGAGGAG 204

Qy	61	lysaiatayaxggluPhelyslelleuuyseuPheillehProHillellekreyeu	80
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Qy	81	TyrgluValilleTyThrProThraspileTyValValMetgluTyCyelstyrgly	100
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Qy	101	GlueuPheapTyrlleValgluylsGlyArgleuGluGluaspGluAlaArgHArglle	120
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Qy	161	LeuSerAenValMetHIsaspGlyHIsPheLeuLysthSerCyGlyIseSProAsnTyR	180
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Qy	181	AlaAlaSProGluValIleSerGlyLyseuTyrrAlaGlyProGluValaSPValITPser	200
Db	565	GCTGCTCCAGAGATATCTCTGGTAAATTAATATATGCTGGACCTGAGAGTGAATATAGAGAC	624
Qy	201	CysGlyValIleLeuTyrrAlaLeuLeuCyGlyThrLeuProPheAspaspGluAsnIle	220
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Qy	221	ProAenLeuPheIyelys 226	
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						CF069225	CF069225	
						CF069225.1	CF069225.1	
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						Medicago truncatula	Medicago truncatula	
						744 bp	744 bp	
						sequence.	sequence.	
						GI:33105884	GI:33105884	
						EST.	EST	
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						(barrel medic)	(barrel medic)	
						Medicago truncatula	Medicago truncatula	
						Euxariotia; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;	Euxariotia; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;	
						Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;	
						rosids; eurosid1; Fabales; Fabaceae; Papilionoideae; Trifolieae;	rosids; eurosid1; Fabales; Fabaceae; Papilionoideae; Trifolieae;	
						Medicago.	Medicago.	
						1 (bases 1 to 744)	1 (bases 1 to 744)	
						Vandenbosch, K., Endre, G., Silverstein, K., Town, C.D., Van Aken, S.,	Vandenbosch, K., Endre, G., Silverstein, K., Town, C.D., Van Aken, S.,	
						Uterback, T., Cheung, F., and Fraser, C.M.	Uterback, T., Cheung, F., and Fraser, C.M.	
						The Medicago truncatula 6K unigene set: cDNA clones selected and	The Medicago truncatula 6K unigene set: cDNA clones selected and	
						re-arrayed from various libraries	re-arrayed from various libraries	
						Unpublished (2002)	Unpublished (2002)	
						Contact: Vandenbosch K	Contact: Vandenbosch K	
						Department of Plant Biology	Department of Plant Biology	
						University of Minnesota	University of Minnesota	
						220 Biosci Center, 1445 Gortner Ave, St. Paul, MN 55108, USA	220 Biosci Center, 1445 Gortner Ave, St. Paul, MN 55108, USA	
						Tel: 612 624 2755	Tel: 612 624 2755	
						Fax: 612 625 1738	Fax: 612 625 1738	
						Email: kvandenbosch@umn.edu	Email: kvandenbosch@umn.edu	
						TIGR sequence name: MTUS09JTK Alias clone name:pgVN-51G6 More	TIGR sequence name: MTUS09JTK Alias clone name:pgVN-51G6 More	
						information is available at: www.medicago.org	information is available at: www.medicago.org	
						Seq primer: SKmod (CTA gAA CTA gTg gAT CC).	Seq primer: SKmod (CTA gAA CTA gTg gAT CC).	
						Location/Qualifiers	Location/Qualifiers	

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XhoI; cDNA was prepared from polyA+ enriched RNA. The cDNA
was directionally ligated into the Unizap XR vector from
Stratagene and packaged using GigaPack III Gold packaging
extracts. Plasmids containing cDNA inserts were excised
from the recombinant lambda-Zap phage using Ex-assist
helper phage and propagated in XLOLR cells."

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Alignment Scores:	
Pred. No.: 7-83e-118	Length: 744
Score: 1122.00	Matches: 210
Percent Similarity: 94.24%	Conservative: 19
Best Local Similarity: 86.42%	Mismatches: 14
Query Match: 41.66%	Indels: 0
DB: 14	Gaps: 0

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Db	69	GCGGAGCATCTACTGACTGGGCAACAAAGTTGCCATTAAAGATTCTTCATCGCCGGAAATA	128
QY	54	ArgAsmMetGlUmetGlUglUubYsAlaySarGluPheLysIleLeuYsLeuPheIle	73
Db	129	AAAAATATGSAATGGAAGAAGAGGAGAAGAGAAATTAAGATTTAAGATTGTTCATG	188
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QY	94	MetGlUtyCYsLysTyrglYglUeupPheAspTyrlleValGlUubYsGIATrgLeuGln	113
Db	249	ATGGAGTATGTGAAATCCGGAGAGCTCTTGATTTCATTGTAGAAAGGGTAGGCTACAA	308
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QY	254	ProMetLys	256

Db |||||
 729 CCCATGAAA 737

Search completed: July 9, 2004, 18:19:36
Job time : 3789 secs

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: July 9, 2004, 15:12:45 ; Search time 694 Seconds

(without alignments)
3574.649 Million cell updates/sec

Title: US-09-857-522B-4

Perfect score: 2693

Sequence: 1 MDGSKSGCHSEALRNINIG.....GPQLFLDFCAFYTKLRVL 509

Scoring table:
BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 3183909 seqs, 2436941669 residues

Total number of hits satisfying chosen parameters: 6367818

Minimum DB seq length: 0
Maximum DB seq length: 200000000Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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-O=/cgn2_1/USPFO_spool/US09857552/runat_07072004_161357_1904/app_query.fasta_1.647
-DB=Published Applications NA -OFMT=fastap -SUFFIX=p2n.tmpb -MINMATCH=0.1
-LOOPCL=0 -LOOEXT=0 -UNITS=bites -START=1 -END=1 -MATRIX=blomsum62
-TRANS=human40.cdi -LIST=45 -DOCALLIGN=200 -THR SCORE=pcit -THR MAX=100
-THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pcit -NORM=ext -HEAPSIZE=500 -MNTLEN=0
-MAXLEN=200000000 -USER=US09857552@cgn2_1.511@runat_07072004_161357_1904
-NCPU=6 -ICPU=3 -NO MMAP -LANG=QUERY -NEG SCORES=0 -WAIT -DSPLOCK=100
-LONGLOG -DEV TIMOUT=120 -WARN TIMOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5
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Published Applications NA.*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

Result Query Match Length DB ID Description
SUMMARIES

1	2693	100.0	1926	13	US-10-425-114-5805	Sequence 5805, App
2	2693	100.0	1948	13	US-10-183-687-235	Sequence 235, App
3	2411.5	89.5	2119	13	US-10-425-114-22369	Sequence 22369, A
4	2411.5	89.5	2607	17	US-10-437-963-49666	Sequence 49666, A
5	2378	88.3	1899	13	US-10-183-687-255	Sequence 255, App
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8	1974.5	73.3	2123	13	US-10-183-687-247	Sequence 247, App
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11	1945	72.2	1991	13	US-10-425-114-35131	Sequence 35131, A
12	1942	72.1	2052	13	US-10-183-687-239	Sequence 239, App
13	1939	72.0	2543	13	US-10-183-687-251	Sequence 251, App
14	1937	71.9	1778	13	US-10-425-114-2148	Sequence 2148, App
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16	1922.5	71.4	1742	13	US-10-425-114-4365	Sequence 4365, App
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23	1448.5	53.8	1277	13	US-10-424-599-38233	Sequence 38233, A
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26	1013.5	37.6	1902	16	US-10-369-493-25383	Sequence 25383, A
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31	749	27.8	2352	9	US-09-815-915-3	Sequence 3, Appli
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36	746	27.7	2193	15	US-10-161-565-17	Sequence 17, Appli
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41	737.5	27.4	2085	15	US-10-161-565-20	Sequence 20, Appli
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43	737.5	27.4	2462	13	US-10-363-616-158	Sequence 158, App
44	737.5	27.4	3226	15	US-10-161-565-23	Sequence 23, Appli
45	737.5	27.4	3269	16	US-10-258-106-34	Sequence 34, Appli

ALIGNMENTS

RESULT 1
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; Sequence 5805, Application US/10425114
; Publication No. US20040034888A1
GENERAL INFORMATION:
APPLICANT: Liu, Jingdong
APPLICANT: Zhou, Yihua
APPLICANT: Kovalic, David K.
APPLICANT: Screen, Steven E
APPLICANT: Tabaska, Jack E
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
FILE REFERENCE: 38-21(5313)B
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 5805
LENGTH: 1926
TYPE: DNA
ORGANISM: Zea mays
FEATURE:
OTHER INFORMATION: Clone ID: 700473306_FLI

US-10-425-114-5805.

Alignment Scores:

Pred. No.:	1.53e-315	Length:	1926
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US-09-857-522b-4 (1-509) x US-10-425-114-5805 (1-1926)

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QY 81 TyrGluValIleIleYThrProThrAspIleTyrValIleMetGluTyrCysLysTyrGly 100
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QY 101 GluLeuPheAspTyrIleValGluLysGlyLeuGlnGlnIleAspGluAlaArgArgIle 120
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QY 201 CysGlyValIleLeuTyrAlaLeuLeuGlyThrLeuProPheAspAspGluAsnIle 220
Db 756 TGTGGGGTGATCTTATGCTCTCTTCTTGTGGAACTCTTCCATTTGATGAGTGAAGATTT 815
QY 221 ProAsnLeuPheLysIleLysGlyGlyIleTyrThrLeuProSerHisLysSerAla 240
Db 816 CCCAATCTGTTCAAAAATTAAGGAGATATCTACACATTTCCAGATCTTGTCTCT 875
QY 241 LeuAlaArgAspLeuIleProArgMetLeuValAlaGluProMetLysArgIleThrIle 260
Db 876 TTGGCCAGAGATTTGATCCAGATGCTGTTGTTGAGCTTATGAGATGAGATCAATCAAT 935
QY 261 ArgGluIleArgGluHisGlnTyrPheGlnIleAlaGluLeuProArgTyrLeuAlaValPro 280
Db 936 AGGGAATTCGGGACATCAATGATTCAGATTCCTCCCTTCCACGTTACTTGGCAGTGGCT 995
QY 281 ProProAspTyrThrGlnGlnAlaLysMetIleAspGluAspThrLeuArgAspValAla 300
Db 996 CCACCAATGATGACACCAACCAACCAAAATGATTTGATGAGATCACTTCCGAGATGTTGTT 1055
QY 301 AsnMetGlyPheAsnLysAsnHisValCysGluSerLeuCysSerArgLeuGlnAsnGlu 320
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```
Db 1056 AATATGGAATTTAAACAAGACCATGTGTGAAATCACTGTGCAGCAGACCTTCAAAATGAG 1115
QY 321 AlThrValAlaTyrTyrLeuLeuLeuAspAsnArgPheArgAlaThrSerGlyTyrLeu 340
Db 1116 GCAACTGTGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1175
QY 341 GlyAlaAspTyrGlnGlnLysMetAspArgAsnLeuAsnGlnLeuAlaSerSerGlySer 360
Db 1176 GGGGCATTTATCAAGATCATGATGACAGGAATTTAATCAGCTGGCGTATCTGATCA 1235
QY 361 SerSerSerGlyThrArgAsnTyrValProGlySerSerAspProHisSerSerGlyLeu 380
Db 1236 TCTAGTTCTGATCGAAGAAATTAATGTTCCAGAAAGCAGTATCTCTTACAGATGCTTGG 1295
QY 381 ArgProTyrTyrProValGluArgLysTyrAlaLeuGlyLeuGlnSerArgAlaHisPro 400
Db 1296 CGGCATATTAATCTGTTGAAAGAAATGGGCGCTTGAGCTTCACTTCCGGGCCACCT 1355
QY 401 ArgGluIleMetValGluValLeuLysAlaLeuGlnGlnLeuLysAsnValArgTyrLys 420
Db 1356 CGTGAATTAATGTTGAGGTCTTAAAGCACTTCAAGATTTAAACGTCAAGTGAAGAAG 1415
QY 421 AsnGlyHisTyrAsnValLysCysArgTyrCysProGlyPheProGluValAsnAspThr 440
Db 1416 AATGGGACATCAACAGTGAATGAGATGAGTGGCCAGGGTTCCTGAAGTTAATGACAG 1475
QY 441 LeuAspAlaSerAsnSerPheLeuGlyAspSerThrIleMetAspAsnAspAspAlaAsn 460
Db 1476 TTAGATCGCCAGCAACACCTTCTTGAGACTTACATCAATGATTAATGATGATGAT 1535
QY 461 GlyArgLeuProThrValIleLysPheGluPheGlnLeuTyrLysAspAspLys 480
Db 1536 GGGAGGCTACCTTAATGATCAAGTGAATTCAGCTTTACAGAGAGAGAGAGAGAG 1595
QY 481 TyrLeuLysAsnMetGlnArgValThrGlyProGlnLeuLeuPheLeuAspPheCysAla 500
Db 1596 TACCTTGAATAGCAGAGAGTACTGACCTCAGCTGCTCTTCTTGAATCTGTCGCG 1655
QY 501 AlaPheLeuThrLysLeuArgValLeu 509
Db 1656 GCTTCTTACCAAGCTTAAGGTTCTA 1682

RESULT 2
US-10-183-687-235
; Sequence 235, Application US/10183687
; Publication No. US20030204870A1
; GENERAL INFORMATION:
; APPLICANT: Allen, Steve
; APPLICANT: Allen, William B.
; APPLICANT: Cahoon, Rebecca
; APPLICANT: Epelbaum, Sabine
; APPLICANT: Hamodu, Omolayo O.
; APPLICANT: Harvell, Leslie T.
; APPLICANT: Jones, Todd
; APPLICANT: Kinney, Tony
; APPLICANT: Klein, Ted
; APPLICANT: Li, Changliang
; APPLICANT: Oliveira, Igor Cunha
; APPLICANT: Sakai, Hajime
; APPLICANT: Shen, Bo
; APPLICANT: Tarczyński, Mitchell C.
; TITLE OF INVENTION: Alteration Of Oil Traits In Plants
; FILE REFERENCE: B81458 US NA
; CURRENT FILING DATE: 2002-06-27
; PRIOR APPLICATION NUMBER: US/10/183,687
; NUMBER OF SEQ ID NOS: 532
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 235
; LENGTH: 1948
; TYPE: DNA
```


ORGANISM: Zea mays
US-10-183-687-235

Alignment Scores:

Pred. No.:	1,56e-315	Length:	1948
Score:	2693.00	Matches:	509
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	13	Indels:	0
		Gaps:	0

US-09-857-522b-4 (1-509) x US-10-183-687-235 (1-1948)

```
Qy 1 MetAspGlySerSerIysGlySerGlyVhiSerGluAlaLeuArgAsnTyrAsnLeuGly 20
Db 173 ATGATGAGAGATGAAAGAGAGTGGCATTCGTAAGCATTAAAGCACTTACACCTGGGA 232
Qy 21 ArgThrLeuGlyIleGlyThrPheGlyYysValIysIleAlaGluHisIleLeuThrGly 40
Db 233 AGAAGCTTAGGTATCCGTACATTTGGAAAGTGAAGATGGACAGCATMACTTACTGGA 292
Qy 41 HisArgValAlaIleIysIleIleAsnCyahArgGlnMetArgAsnMetGluMetGlu 60
Db 293 CATAGGGTTCCTAAAGATCATCACTGCCCAATGAGAAATATGAAATGGAAGAG 352
Qy 61 LysAlaIysArgGluPheIysIleLeuIysLeuPheIleHisProHisIleIleArgLeu 80
Db 353 AAACCAAGAGAGAAATTCAGATATGAAATGTTGTCATTCACCCCATATCATTCGGCTT 412
Qy 81 TyrGluValIleTyrThrProThrAspIleTyrValValMetGluTyrCysIysTyrGly 100
Db 413 TATAGGTCATATACACCTACAGATATATATGTGTGATGAGAAATATGTAAGTATGCG 472
Qy 101 GluLeuPheAspTyrIleValGluIysGlyArgLeuGlnIuAspGluAlaArgArgIle 120
Db 473 GAGTATTTGATTATCATTTGTGAGAAAGGAGATTAACAGAAATGAAAGCTCGTCGATC 532
Qy 121 PheGlnGlnIleIleSerGlyValGluTyrCysHisAspAsnMetValHisArgAsp 140
Db 533 TTCAGAGATCATATATCGCGGTGCAATACGCAATACAAACATGATGTCACCGGTAC 592
Qy 141 LeuIysProGluAsnLeuLeuLeuAspSerIysTyrAsnValIysLeuAlaAspPheGly 160
Db 593 CTAAGCCGGAAGAACTTGTATCTTGATTCAAAGTATATATGTAACCTTGGCGATTTTGGT 652
Qy 161 LeuSerAsnValMetHisAspGlyHisPheLeuIysThrSerCysGlySerProAsnTyr 180
Db 653 CTGAGCAATGATCATGATGATGACCATTTTCTGAAGACTAGCTGGGAGTCCGAACATAT 712
Qy 181 AlaAlaProGluValIleSerGlyIysLeuTyrAlaGlyProGluValAspValTyrSer 200
Db 713 GCTGCTCCAGAGGTAATATCTGTGTAACATAATATCTGACCTGAGGTGAGTATGAGGT 772
Qy 201 CysGlyValIleLeuTyrAlaLeuLeuCysGlyThrLeuProPheAspGluAsnIle 220
Db 773 TGTGGGGTGAATCTTATATGCTCTTCTTGTGGAACCTCTTCATTTGATGAGAAATAT 832
Qy 221 ProAsnLeuPheIysIleIysGlyGlyIleTyrThrLeuProSerHisLeuSerAla 240
Db 833 CCCAATCTGTTCAAAAAATTAAGGAGTATCTACACACTTCCAAAGCATTTGTCTGCT 892
Qy 241 LeuAlaArgAspLeuIleProArgMetLeuValAlaGluProMetIysArgIleThrIle 260
Db 893 TTGGCCAGGGATTGATCCAGAAATGCTGTGTGTGTGAGCTTAAGAAAGATACAAAT 952
Qy 261 ArgGluIleArgGluHisGlnTyrPheGlnIleArgLeuProArgTyrLeuAlaValPro 280
Db 953 AGGGAATTCGGGAGCATCATGATGCTTCAGATTTGGCTTCCACGTTACTTGGCAGTGGCT 1012
Qy 281 ProProAspThrThrGlnGlnAlaIysMetIleAspGluAspThrLeuArgAspValVal 300
Db 1013 CCACCAATATCGACACAAACAGCCAAATATGATGATGAAATACACTTCGAGATGTTGTT 1072
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Qy 301 AsnMetGlyPheAsnIysAsnHisValCysGluSerLeuCysSerArgLeuGlnAsnGlu 320
Db 1073 AATATGGGATTTTAAACAGAACCATGCTGTGATCATCTGTGACAGACACTTCAAAATGAG 1132
Qy 321 AlaThrValAlaTyrTyrLeuLeuLeuAspAsnArgPheArgAlaThrSerGlyTyrLeu 340
Db 1133 GCAACTGTGCATATTTATTTACTATTTGACAAATCGGTTAGAGCAACTAGAGCTATCTT 1192
Qy 341 GlyAlaAspTyrGlnGlnIysMetAspArgAsnLeuAsnGlnIleAlaSerSerGluSer 360
Db 1193 GGGGCAATTAATCAAGATCAATGAGACAGAAATTTAATCAGCTGGGTGCTATCTGAATCA 1252
Qy 361 SerSerSerGlyThrAspAsnTyrValProGlySerSerAspProHisSerSerGlyLeu 380
Db 1253 TCTAGTTCTGGTACAGAAATTTATGTTCCAGAAAGCATGATCTCTTACAGATGCTTTG 1312
Qy 381 ArgProTyrTyrProValGluArgIysTyrAlaLeuGlyLeuGlnSerArgAlaHisPro 400
Db 1313 CGGCATATTTATCTGTTGAAGAAATAGGGCGCTTGACTTGAGTCTCGGGCCACCT 1372
Qy 401 ArgGluIleMetValGluValLeuIysAlaLeuGlnIleLeuAsnValArgTyrIys 420
Db 1373 CGTGAAATTAATGTTGAGGTCTTAAAGCACTTCAAGAAATTAACGTCAAGATGGAAG 1432
Qy 421 AsnGlyHisTyrAsnValIysCysArgTyrCysProGlyPheProGluValAsnAspThr 440
Db 1433 AATGGCATTAACACGTAATATGCAAGTGTGCTCCAGGGTTTCTGAAAGTTAATGACAG 1492
Qy 441 LeuAspIleSerAsnSerPheLeuGlyAspSerThrIleMetAspAsnAspAlaAsn 460
Db 1493 TTAGATCCAGCAACACCTTCTTGGTACCTACATCATGATATGATGATGATGAT 1552
Qy 461 GlyArgLeuProThrValIleIysPheGluPheGlnLeuTyrIysThrIysAspAspIys 480
Db 1553 GGGAGGTACTCTACTGTGATCAAGTTGAATTCACAGCTTACAGAGAAAGAGACAG 1612
Qy 481 TyrLeuLeuAspMetGlnArgValThrGlyProGlnLeuLeuPheLeuAspPheCysAla 500
Db 1613 TACCTCTTAAGTATGCAAGAGATTTACTGACCTCAGCTGCTCTTCTTGACTTGTGCG 1672
Qy 501 AlaPheLeuThrIysLeuArgValLeu 509
Db 1673 GCCTTCCTTACCAAGCTTAGGTTCTTA 1699

RESULT 3
US-10-425-114-22369
: Sequence 22369, Application US/10425114
: Publication No. US20040034888A1
: GENERAL INFORMATION:
: APPLICANT: Liu, Jindong
: APPLICANT: Zhou, Yihua
: APPLICANT: Kovacic, David K.
: APPLICANT: Screen, Steven E.
: APPLICANT: Tabaska, Jack E.
: APPLICANT: Cao, Yongwei
: TITLE OR INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
: FILE REFERENCE: 38-21(5313)B
: CURRENT APPLICATION NUMBER: US/10/425,114
: CURRENT FILING DATE: 2003-04-28
: NUMBER OF SEQ ID NOS: 73128
: SEQ ID NO 22369
: LENGTH: 2119
: TYPE: DNA
: ORGANISM: Oryza sativa nipponbare
: FEATURE:
: OTHER INFORMATION: Clone ID: LIB3477-009-G7_FLI
US-10-425-114-22369

Alignment Scores:
Pred. No.: 2,45e-281 Length: 2119
Score: 2411.50 Matches: 453
Percent Similarity: 94.70% Conservative: 29
```

Best Local Similarity: 89.00% Mismatches: 26
 Query Match: 89.55% Indels: 1
 DB: 13 Gaps: 1

US-09-857-522B-4 (1-509) x US-10-425-114-22369 (1-2119)

```

Qy 1 MetAspGlySerLeuSerGlySerGlyYHISerGluLeuArgAsnTYRAsnLeuGly 20
Db 130 ATGATGAAATGCTAAAGCGGTGGCATTTCTAGAGCACTTAACATCTTGGA 189
Qy 21 ArgThrLeuGlyIleGlyThrPheGlyLysValLysIleAlaGluHISLysLeuThrGly 40
Db 190 AGAAGCTTAGGTAATGGCTCATTTGGAAGAGTGAAGATTGACAGCATTAAGCTTACAGA 249
Qy 41 HisArgValAlaIleLysIleLeuAsnCyArgGluMetArgAsnMetGluMetGlu 60
Db 250 CACGAGTGTCTAAAGATCTGAAACCGCCCAAAATGAGAAATATGAGAAATGAGAGAG 309
Qy 61 LysAlaLysArgGluPheLysIleLeuLysLeuPheIleHISProHISLleArgLeu 80
Db 310 AAAGCAAGAGAGAAATCAGATACAGATTGATTTCATTATCCCATATCATTTCCGCTT 369
Qy 81 TyrGluValIleTyrThrProThrAspIleTyrValValMetGluTyrCyLysTyrGly 100
Db 370 TATGAGGTTATATACCTCTACCGATATATATGTTGATGAGTACGTAAGTTTGA 429
Qy 101 GluLeuPheAspTyrIleValGluLysGlyValArgLeuGluLysAspGluAlaArgArgIle 120
Db 430 GAACTGTTGATTCATTTGTGAGAAAGGCGAGTTCGAGAAATGAGGCTCGCCGATC 489
Qy 121 PheGluGluIleIleSerGlyValGluTyrCysHISArgAsnMetValIleHISArgAsp 140
Db 490 TTCAGAGATTAATATCTGGGATTAATCTGCCACAGAAACATGAGTGTTCATCGAT 549
Qy 141 LeuLysProGluAsnLeuLeuLysAspSerLysTyrAsnValLysLeuAlaAspPheGly 160
Db 550 CTGAAGCCAGAAACCTTGCTACTGGAATTCAGATATATATGTAAGCTTGGAATCTTGAT 609
Qy 161 LeuSerAsnValMetHISAspGlyHISpHeLeuLysTyrSerCyGlySerProAsnTyr 180
Db 610 TTGAGTAACTCATGATGATGCGCATTTTGAAGACAACTGTGGAGTCCAAACTAT 669
Qy 181 AlaAlaProGluValIleSerGlyLysLeuTyrAlaGlyProGluValAspValTyrSer 200
Db 670 GCTGCTCCAGAGGATCTTGTGTAATTAATGCTGACCTGAGTGTATGATGAGC 729
Qy 201 CysGlyValIleLeuTyrAlaLeuLeuCyGlyThrLeuProPheAspGluAsnIle 220
Db 730 TGTGAGATGATCTTATGCTCTCTTGTGTAATCTTCCATTTGATGAGAAATATC 789
Qy 221 ProAsnLeuPheLysIleLysGlyIleTyrThrLeuProSerHISLeuSerAla 240
Db 790 CCCAACCTATTCAAAAGATAAAGGTGTATATATCTCTCCCAAGCATTTATCTGCT 849
Qy 241 LeuAlaAspLeuIleProArgMetLeuValValGluProMetLysArgIleThrIle 260
Db 850 CTGGCCAGAGATTTGATCCAGAGATGCTTGTGTGATCCAGATGAGATCAATC 909
Qy 261 ArgGluLeuArgGluHISGluTyrPheGluIleArgLeuProArgTyrLysLeuAlaValPro 280
Db 910 COTGAATTCAGAGCATCAGTGGTTTCAAGATTGCCCTTCTCGTTACTTGAAGTGGCT 969
Qy 281 ProProAspThrThrGluGluAlaLysMetIleAspGluAspThrLeuArgAspValVal 300
Db 970 CCACACAGACACAGCACAGCAAAATGATGTATGTAAGATACCTTCAAGATGTCGTA 1029
Qy 301 AsnMetGlyPheAsnLysAsnHISValCysGluSerLeuCySerArgLeuGluAsnGlu 320
Db 1030 AACTTGGATTATGCAAGAGCATATGTGTGATTTCTTCCGCAATAGCTCAGAAATAG 1069
Qy 321 AlaThrValAlaTyrTyrLeuLeuLeuAspAsnArgPheArgAlaThrSerGlyTyrLeu 340
Db 1090 GCAACTGTTGATATTTATTTACTTGTGACATCATTCGAGGTAACAGTGGCTATTTG 1149
  
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Qy 341 GlyAlaAspTyrGluGluSerMetAspAsnLeuAsnGluLeuAlaSerSerGluSer 360
Db 1150 GAGACACATATCAAGATCTTTGAGAGGAATTTTAATGCTTGTGCTTATGGAATCA 1209
Qy 361 SerSerSerGlyThrArgAsnTyrValProGlySerSerAspProHISerSerGlyLeu 380
Db 1210 GCAAGTTCAAAATCAAGCATTATCTTCCAGAAAGCATGATCTCATGCGCATGGTTTG 1269
Qy 381 ArgProTyrTyrProValGluArgLysTyrPheLysGlyLeuGluSerArgAlaHISPro 400
Db 1270 CGCCCATTTATCTGTGTAAAGAAATGGCTCTTGAGCTTCAAGTCACAGCTCAACCT 1329
Qy 401 ArgGluIleMetValGluValLysAlaLeuGluGluLeuLeuAsnValArgTyrLys 420
Db 1330 CGGAGATATATGATGAGGCTTAAAGCATTCAGACTTAATATGCTCTGGAAGAG 1389
Qy 421 AsnGlyHISThrAsnValLysCyArgTyrCyProGlyPheProGluValAsnAspThr 440
Db 1390 AATGACAGTACAAATCAAGAAATGACATGAGAGGCTTGGG---ACTCAGGCCACTGATATG 1446
Qy 441 LeuAspAlaSerAsnSerPheLeuGlyAspSerThrIleMetAspAsnAspAlaAsn 460
Db 1447 TTGATGTTAAACAACGCTTTGTGATGACTCAATCATTAATGATTAACGCTGATTAAT 1506
Qy 461 GlyArgLeuProThrValIleLysPheGluPheGluLeuTyrThrLysAspAspLys 480
Db 1507 GGGAGCTTACCTGCTGTGATCAAGTTGAAATCAGCTTTTCAAGACAGACAGAGAG 1566
Qy 481 TyrLeuLeuAspMetGluArgValThrGlyProGluLeuLeuPheLeuAspPheCysAla 500
Db 1567 TATCTGTGATATGACAGAGATTACGGGAGCTCAGCTCTTTTCCGACTTGTGCA 1626
Qy 501 AlaPheLeuThrLysLeuArgValLeu 509
Db 1627 GACTTCTTACCAAGCTGAGGCTTCTA 1653
  
```

RESULT 4
 US-10-437-963-49666/C
 Sequence 49666, Application US/10437963
 Publication No. US20040123343A1
 GENERAL INFORMATION:
 APPLICANT: La Rosa, Thomas J.
 APPLICANT: Kovalic, David K.
 APPLICANT: Zhou, Yihua
 APPLICANT: Cao, Yongwei
 APPLICANT: Wu, Wei
 APPLICANT: Boukharov, Andrey A.
 APPLICANT: Barbazuk, Brad
 APPLICANT: Li, Ping
 TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
 TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
 FILE REFERENCE: 38-21(53221)B
 CURRENT APPLICATION NUMBER: US/10/437,963
 CURRENT FILING DATE: 2003-05-14
 NUMBER OF SEQ ID NOS: 204966
 SEQ ID NO 49666
 LENGTH: 2607
 TYPE: DNA
 ORGANISM: Oryza sativa
 FEATURE:
 OTHER INFORMATION: Clone ID: PAT_MRT4530_52228C.1
 US-10-437-963-49666

Alignment Scores:
 Pred. No.: 3,43e-281 Length: 2607
 Score: 2411.50 Matches: 453
 Percent Similarity: 94.70% Conservative: 29
 Best Local Similarity: 89.00% Mismatches: 26
 Query Match: 89.55% Indels: 1
 DB: 17 Gaps: 1

US-09-857-522B-4 (1-509) x US-10-437-963-49666 (1-2607)

```

Qy 1 MetAspGlySerSerIysGlySerGlyYHISerGluAlaLeuArgAsnTyrAsnLeuGly 20
Db 2033 ATGGATGGAAATGCTGAAGGCGTGGCATTTCTGAGCAGTGAAGAACTTACAACTTGGGA 1974
Qy 21 ArgThrLeuGlyIleGlyThrPheGlyLysValIleAlaGluHisIleLeuThrGly 40
Db 1973 AGAAGCTTAGCTATTTGGCTATTGGAAAAGTGAAGATGGCAGAGCATTACCTTACAGGA 1914
Qy 41 HisArgValAlaIleLysIleIleAsnCysArgGlnMetArgAsnMetGluMetGlu 60
Db 1913 CACGAGAGTTGCTATTAAGATCCTGAAACCGCCCAATGAGAAATATGAAATGGAGAG 1854
Qy 61 LysAlaLysArgGlnPheLysIleLeuLysLeuPheIleHisProHisIleIleArgLeu 80
Db 1853 AAAGCAAGAGAAAGAAATCAAGATACAGATTTGTCATTATCCCATATACATTCGCTT 1794
Qy 81 TyrGluValIleTyrThrProThrAspIleTyrValIleMetGluTyrCysLeuTyrGly 100
Db 1793 TATGAGGTTATATACACTCTACGGAATATATGTTGATGAGATGACGCAAGTTTGGGA 1734
Qy 101 GluLeuPheAspTyrIleValGluLysGlyArgLeuGlnGluAspGluAlaArgArgIle 120
Db 1733 GAACGTTTGATTCATTGTTGAGAAAGCAGGTTGACAGAAAGATGAGGCTCGCCGATC 1674
Qy 121 PheGlnGlnIleIleSerGlyValGluTyrCysHisArgAsnMetValHisArgAsp 140
Db 1673 TTCCAGAGATTTATATCTGGGGGTTGAATACGCAACAAACATGAGTGTTCATCGTAT 1614
Qy 141 LeuLysProGluAsnLeuLeuLeuAspSerLysTyrAsnValIleLeuAlaAspPheGly 160
Db 1613 CTGAAGCAGAAACCTTGCTACTGGAATTCAAAGTATATATGTAAGCTTGCGACCTTGCT 1554
Qy 161 LeuSerAsnValMetHisAspGlyHisPheLeuLysThrSerCysGlySerProAsnTyr 180
Db 1553 TTGAGTAACTCATGATGATGCGCATTTTGAAGAACAGACTGGGAGTCCAAACTAT 1494
Qy 181 AlaAlaProGluValIleSerGlyLysLeuLysTyrAlaGlyProGluValAspValTyrSer 200
Db 1493 GCTCTCCAGAGGATCTCTGGTAAATATATATGCTGAGCTGAGTGTATGAGGC 1434
Qy 201 CysGlyValIleLeuTyrAlaLeuLeuCysGlyThrLeuProPheAspGluAsnIle 220
Db 1433 TGTGAGAGATCTTTATGCTCTCTCTTGTGTACTCTTCCATTGATGAGAAATATC 1374
Qy 221 ProAsnLeuPheLysIleLysGlyGlyIleTyrThrLeuProSerHisLeuSerAla 240
Db 1373 CCCAACCTATTCAAAAGATAAAGGTTGATATATATCTCCCAAGTCATTATCTGCT 1314
Qy 241 LeuAlaArgAspLeuIleProArgMetLeuValIleGluProMetLysArgIleThrIle 260
Db 1313 CTGGCCAGAGATTTGATCCCAAGATGCTGTGTGTGTATCCAAATGAAGAGATCACAAT 1254
Qy 261 ArgGluIleArgGluHisGlnTyrPheGlnIleArgLeuProArgTyrLeuAlaValPro 280
Db 1253 CGTGAATTCGAGAGCATCACTGTTTCAGATTCGCTCTCTGTTACTTACAGCTGCT 1194
Qy 281 ProProAspThrThrGlnGlnAlaLysMetIleAspGluAspThrLeuArgAspValIle 300
Db 1193 CCACACAGACACAGACAGCAAGCAAAATGATGATGAATACCTTCAAGATGCTGCTA 1134
Qy 301 AsnMetGlyPheAsnLysAsnHisValCysGluSerLeuCysSerArgLeuGluAsnGlu 320
Db 1133 AACTTGGTATGGAAGAGCAATGATGTGTGTAATCTCGCCCAATAGCTCAGAAATGAG 1074
Qy 321 AlaThrValAlaTyrTyrLeuLeuLysAspAsnArgPheArgAlaThrSerGlyTyrLeu 340
Db 1073 GCAACTGTTGCAATTTATTTACTCTTGGACAAATGATTCGAGGCTACAGTGGCTATTTG 1014
Qy 341 GlyAlaAspTyrGlnGluSerMetAspArgAsnLeuAsnGlnLeuAlaSerSerGluSer 360
Db 1013 GGAGCAGACTATCAAGAACTTTGGAGAGAAATTTTATTCCTTGTTCATTCGAAATCA 954

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Qy 361 SerSerSerGlyThrArgAsnTyrValProGlySerSerAspProHisSerSerGlyLeu 380
Db 953 GCAGATTCAATATACAGGCATTTATCTTCAGAGAGCATATCTTCACTGCAAGTGTG 894
Qy 381 ArgProTyrTyrProValGluArgLysTyrAlaLeuGlyLeuGlnSerArgAlaHisPro 400
Db 893 CGCCACATTTATCTGTTGAAAGAAATGGGCTCTTGACTTGAGTTCAGCAGGCTCAACT 834
Qy 401 ArgGluIleMetValGluValLeuLysValAlaLeuGlnGluLeuAsnValIleGlyLys 420
Db 833 CGCAGATTAATGATTTGAGGTCCTTAAAGCAGCTTCMAACTTAATGTCCTCTGGAAG 774
Qy 421 AsnGlyHisTyrAsnValLysCysArgTyrCysProGlyPheProGluValAsnAspThr 440
Db 773 AATGACAGTACATCAATGAATGCAATGAGAGCTTGG--ACTCAGGCCACTGATATG 717
Qy 441 LeuAspAlaSerAsnSerPheLeuGlyAspSerThrIleMetAspAsnAspAlaAsn 460
Db 716 TTAGATGTTTAAACAACACTTGTGATGACTCATATGATGATAACGGTATGTAAT 657
Qy 461 GlyArgLeuProThrValIleLysPheGluPheGlnLeuTyrTyrThrLysAspAspLys 480
Db 656 GGGAGGCTTACCTGCTGTGATCAAGTTTGAATCCAGCTTTCACAGACAGAGAGAG 597
Qy 481 TyrLeuLeuAspMetGlnArgValThrGlyProGlnLeuLeuPheLeuAspPheCysAla 500
Db 596 TATCTGCTGATATGCAAGAGATTTACGGGGCTTCACTCTTTCTGAGCTTGTGCA 537
Qy 501 AlaPheLeuThrLysLeuArgValLeu 509
Db 536 GACTTCTTACCAAGCTGAGGGTTCTA 510

```

RESULT 5

```

US-10-183-687-255
; Sequence 255, Application US/10183687
; Publication No. US20030204870A1
; GENERAL INFORMATION:

```

```

; APPLICANT: Allen, Steve
; APPLICANT: Allen, William B.
; APPLICANT: Cahoon, Rebecca
; APPLICANT: Epelbaum, Sabine
; APPLICANT: Famodu, Omolayo O.
; APPLICANT: Harvell, Leslie T.
; APPLICANT: Jones, Todd
; APPLICANT: Kinney, Tony
; APPLICANT: Klein, Ted
; APPLICANT: Li, Changliang
; APPLICANT: Oliveira, Igor Cunha
; APPLICANT: Sakai, Hajime
; APPLICANT: Shen, Bo
; APPLICANT: Tarczyński, Mitchell C.
; TITLE OF INVENTION: Alteration Of Oil Traits In Plants
; FILE REFERENCE: BBI458 US NA
; CURRENT APPLICATION NUMBER: US/10/183,687
; CURRENT FILING DATE: 2002-06-27
; PRIOR APPLICATION NUMBER: 60/301,913
; NUMBER OF SEQ ID NOS: 532
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 255
; LENGTH: 1899
; TYPE: DNA
; ORGANISM: Triticum aestivum
US-10-183-687-255

```

Alignment Scores:

```

Pred. No.: 2,37e-277 Length: 1899
Score: 2378.00 Matches: 442
Percent Similarity: 93.52% Conservative: 34
Best Local Similarity: 86.84% Mismatches: 33
Query Match: 88.30% Indels: 0
DB: 13 Gaps: 0

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US-09-857-522B-4 (1-509) x US-10-183-687-255 (1-1899)

```
OY 1 MetaspGlySerSerLySergLyHisSergLValLeuArganTyraenLeuGly 20
Db 67 ATGAAAGGAAACACTAGAGAGGTGGCATTTCTGACGATTAAGAATCAAGATGGGC 126
OY 21 ArgThrLeuGlyLleGlyThrPheGlyLysValLysLlealagLunHslySLeuThrGly 40
Db 127 AGAACATTAGGTATAGGCACATTTGGAAAGTGAAGGATTCGAGAGCATTAACATACAGGG 186
OY 41 HisArgValAlaLleLysLleLleasnCySarGlnMetArganMetGlnMetGlnGlu 60
Db 187 CATAAAGTTGCTATAAAGATTCTGAACCGTCGTAAGAGAACATATGGAATGAGAGAG 246
OY 61 LysAlaLysArgGluPheLysLleLeuLysLeuPheLleHisProHisLleLleArgLeu 80
Db 247 AAAGAAAGAGAGAGATCAAGATATTGAGGTTTTCATTCACCTCATATATCCGGCTT 306
OY 81 TyrGluValLleTyThrProThrAspLleTyraValMetGluTyrcysLysTyrcLy 100
Db 307 TATGAGGTCAATTCACACCTACAGATATATTGTTGATGGAATATTCGCAAGTATGCT 366
OY 101 GluLeuPheAspTyrcLysValGluLysGlyArgLeuGlnGluAspGluAlaArgArgLle 120
Db 367 GAGCTATTGCACTGCATTGTTGAGAAAGGCGGTTACAGAAAGATGAGGCTTCGCAATC 426
OY 121 PheGlnGlnLleLleSergLyValGluTyrcysHisArganMetValHisArgAsp 140
Db 427 TTCGACGATTTATATCTGGTGGTGAATATCTGCCAGAAACATGGTTGCTCATCGTAT 486
OY 141 LeuLysProGluAsnLeuLeuLysAspSerLyTyraenValLysLleLysLleAspPheGly 160
Db 487 CTTAAAGCCAGAGAACCTGTATCTTGATTCCAATATCAATATGAAACCTTGCCGACTTGGG 546
OY 161 LeuSeranValMetHisAspGlyHisSphLeuLysThrSergLySergLySerProasnTyrc 180
Db 547 TTAAGTATATGTCATGATGATGAGCCCATTTCTGAAGATCTAGCTGGGAGGCCAAACATAT 606
OY 181 AlaAlaProGluValLleSergLyLysLeuTyraLagLysProGluValAspValTyrSer 200
Db 607 GCTGACCAAGAGGTTATCTGAGTAATATTAACGCTGAGACCTGAGGTTGATTTGAGGC 666
OY 201 CysGlyValLleLeuTyraLleLeuLysCysGlyThrLeuProPheAspAspGluAsnLle 220
Db 667 TGGCGGGATACCTTATGCTCTTCTTTGGGACCTCTTCATTTGATGATGACAAATTT 726
OY 221 ProasnLeuPheLysLysLleLysGlyLleTyrcLysProSergHisLeuSerAla 240
Db 727 CCCAAACGTTCCAAAAGATAAAGGAGGACATCTATATCTTCCAAGTCATTTATCTGCT 786
OY 241 LeuAlaArgAspLeuLleProArgMetLeuValValGluProMetLysArgLleThrLle 260
Db 787 CTTGCAAGGATTTGATCCCAAGATGCTTGTGTATCTCTATGAGAGATACAAATTT 846
OY 261 ArgGluLleArgGluHisGlnTyrPheGlnLleArgLeuProArgTyrcLysLysAlaPro 280
Db 847 CGTGAATTCAGAAACACCCATGTTTCAGAAATCCCTCTCCGCTACCTGCGAGTGCT 906
OY 281 ProProAspPThrThrGlnGlnAlaLysMetLleAspGluAspPThrLeuAspValVal 300
Db 907 CCACCAAGCACGGCCGACCAAGCCAAATGATGTATGAAATACCTTAAGAGATTGTC 966
OY 301 AsnMetGlyPheAsnLysAsnHisValCysGluSerLysCysSerArgLeuGlnAsnGlu 320
Db 967 AACCTGGGATATGATTAAGACCATGTTGTGATATATTTGCAATAGGCTGCAAAATAG 1026
OY 321 AlaThrValAlaTyrcTyrcLeuLeuLysAspAsnArgPheArgAlaThrSergLyTyrcLeu 340
Db 1027 GCAACTGTTGATATATCTTACTCTTGACAAATGCTTCCGGGACCACTAGTGGCATTTTG 1086
OY 341 GlyAlaAspTyrcGlnGlnSerMetAspArganLeuAsnGlnLeuAlaSerSergLySer 360
Db 1087 GGGGCTGACTATCTTACAAATCAATGAGTGGTATTTAATCAAGTTTACTTCACTTGGAAATCA 1146
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OY 361 SerSerSergLyThrArganTyrcValProGlySerSerAspProHisSergLyLeu 380
Db 1147 GCAAGCCCAAGTACACAGGAGTATCTTCCAGCAGACATATCTCAAGGACATGGCTTG 1206
OY 381 ArgProTyrcTyrcProValGluArgLysTyrPAlaLeuGlyLeuGlnSerArgAlaHisPro 400
Db 1207 CGGCGCATATATACCCCGTTGAAAGAAATGAGGCTCTTGGGCTCCAGTCTCCAGCTCAACT 1266
OY 401 ArgGluLleMetValGluValLleLysAlaLeuGlnGluLeuAsnValaArgTyrLysLys 420
Db 1267 CGTAGATTAATGATCGAGGTTCTTAAGGCACTTCAMAAATTAATGTTCTGCTGAAAGAG 1326
OY 421 AsnGlyHisTyraenValLysCysArgTyrcPheProGlyPheProGluValaAsnAspThr 440
Db 1327 AATGACACATCAACATGAATGAGAGTGGTGCCTCGGTTTCTCAGTCAGTATATG 1386
OY 441 LeuAspAlaSeranSerPheLeuGlyAspSerThrLleMetAspAsnAspAlaAsn 460
Db 1387 TTAGATCCCAACACACACTTGTGTGATGACTTACATCAATGATTAACGGCGATGCTAAT 1446
OY 461 GlyArgLeuProThrValLleLysPheGluPheGlnLeuTyrcTyrcLysAspAspLys 480
Db 1447 GGGAGGCTTACCTGCCGTGATCAAGTTGAAATCCAGCTTTACAAAGCAGATGACAG 1506
OY 481 TyrcLeuAspMetGlnArgValThrGlyProGlnLeuLeuPheLeuAspPheCysAla 500
Db 1507 TACCTGTAGATATGACAGAGGTTACTGAGACCTCAGCTCTCTTCGATTTTGGCGG 1566
OY 501 AlaPheLeuThrLysLeuArgValLeu 509
Db 1567 GCCTTCCTTACCAACTTAGGGTTCTTA 1593
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RESULT 6

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US-10-437-963-49667
; Sequence 49667, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yinhua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OR INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 49667
; LENGTH: 2484
; TYPE: DNA
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_52229C.1
US-10-437-963-49667
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Alignment Scores:

Pred. No.:	2.6e-272	Length:	2484
Score:	2338.00	Matches:	451
Percent Similarity:	78.14%	Conservative:	35
Best Local Similarity:	72.51%	Mismatches:	23
Query Match:	86.82%	Indels:	113
DB:	17	Gaps:	1

US-09-857-522B-4 (1-509) x US-10-437-963-49667 (1-2484)

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OY 1 MetaspGlySerSerLySergLyHisSergLValLeuArganTyraenLeuGly 20
Db 162 ATGAAAGAAATGCTTAAGAGCGGTGGCATTTGAGGCACTAGAAATCAATCTAAGA 221
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Qy 21 ArgThrLeuGlyIleGlyThrPheGlyLysValIleAlaGluHisLeuThrGly 40
Db 222 AGAAGTTTGGATTTGGTTCATTGGAAAAGTGAAGATTGCGAGACATTAAGCTTACAGG 281
Qy 41 HisArgValAlaIleLysIleIleAsnGlySarGlnMetArgAsnMetGluMetGlu 60
Db 282 CACAGAGTTGCTATTAAGATCCTGAACCGTCCCAATGAGAAATATGAAATGAGAGAG 341
Qy 61 LysAlaLysArgGluPheLysIleLeuLysLeuPheIleHisProHisIleIleArgLeu 80
Db 342 AAAGCAAGAGAGAAATCAAGATATGAGGTTGTCATTCAATCCCAATATCAATCGCTT 401
Qy 81 TyrGluValIleIleIleThrProThrAspIleIleIleValIleMetGluTyrCysLeuTyrGly 100
Db 402 TATGAGTCATATACACTCTCTACGAAATATATATGTTGATGAGTACTGCAAGTTTGA 461
Qy 101 GluLeuPheAspTyrIleValGluLysGlyArgLeuGlnIleAspGluAlaArgArgIle 120
Db 462 GAAGCTTTGATTAATGATTGAGAAAGCAGGTTGCGAAGAAATGAGGCTCGCGAATC 521
Qy 121 PheGlnGlnIleIleSerGlyValGluTyrCysHisArgAsnMetValIleHisArgAsp 140
Db 522 TTCCAGCAGATTATATCTGGGGTTGAATATCTGCCACAGAAACATGCTGTTCACTGAT 581
Qy 141 LeuLysProGluAsnLeuLeuLeuAspSerLysTyrAsnValIleLysAlaAspPheGly 160
Db 582 CTGAAGCCAGAAACCTGCTACTGATTCGAATTAAGTAAAGTAAAGCTTGACCTTGTGT 641
Qy 161 LeuSerAsnValIleMetHisAspGlyHisPheLeuLysThrSerCysGlySerProAsnTyr 180
Db 642 TTGAGTATATGTCATGATGATGCGCAATTTTAAAGACAGCTGGGAGTCCGAATAT 701
Qy 181 AlaAlaProGluValIleSerGlyLysLeuTyrAlaGlyProGluValAspValTyrSer 200
Db 702 GCTGTCACAGAGTGATCTGTGTAAATATATATGCTGACCCGAGGTGATATGAGGC 761
Qy 201 CysGlyValIleLeuTyrAlaLeuLeuCysGlyThrLeuProPheAspAspGluAsnIle 220
Db 762 TGTGAGATGATCCTTATGCTCTCTTGTGTGATCTCTTCAATTTGATGAGAGAAATATC 821
Qy 221 ProAsnLeuPheLysIleLysGlyGlyIleTyrThrLeuProSerHisLeuSerAla 240
Db 822 CCCAACCTATTCAAAAGATTAAGGGTGATATATATCTCCCAAGCATTTATCTGCT 881
Qy 241 LeuAlaArgAspLeuIleProArgMetLeuValValGluProMetLysArgIleThrIle 260
Db 882 CTGGCAGGGATTTGATCCCAAGATGCTGTGTGTGATCCAAATGAAAGATCAATCAATT 941
Qy 261 ArgGluLeuArgGluHisGlnThrPheGlnIleArgLeuProArgTyrLeuAlaValPro 280
Db 942 CGTGAATTCGAGAGCATCAATAGTTTCAGATTCGCTTCCGTACTTACGAGTGCCT 1001
Qy 281 ProProAspThrThrGlnGlnAlaLysMet----- 290
Db 1002 CCACCAAGCAGACAGCAGCAAGCCAAATGGAATGTAATCTTGTCAATTCCTTAACAAGTTGT 1061
Qy 290 ----- 290
Db 1062 TCATTAATGATCAAACTTATATATATATATATTTCTTGAGATATATCTTATAGAGTA 1121
Qy 290 ----- 290
Db 1122 TGATTAATATATGTTTGGCAACATTAACCGTATTAAGACAGTGTGAAGGCAATTTGAA 1181
Qy 290 ----- 290
Db 1182 TAACATTTATGATATAGAGCTTGAGATATTTCTTGCTAGTAGTAGTTATCTTAC 1241
Qy 290 ----- 290
Db 1242 AGAATCCTTCATGATGATTAAGAAAGACAGATAGATTTCATCTGCAATATCACTTAT 1301

Qy 290 ----- 290
Db 1302 ACATGTTGATTTTATTAATATATCTTGCACCTTGTCTAATATCTGATATAGACCTTC 1361
Qy 291 ----- 1LeuAspGluAspThrLeuArgAspValIleAsnMetGlyPheAsnLysAsnHis 308
Db 1362 TTTGAATATGATGATGATATACCTTCAAGACGTTGTAACTGGGTATGATAAAGACCA 1421
Qy 308 ValCysGluSerLeuCysSerArgLeuGlnAsnGluAlaThrValAlaTyrTyrLeuIle 328
Db 1422 TGTGTGAATCTTGTGCAATAGACTGCAAAAGAGCAACTGTGCATATTAATTTGCT 1481
Qy 328 ULeuAspAsnArgPheArgAlaThrSerGlyTyrLeuGlyValAlaAspTyrGlnIleSerMet 348
Db 1482 ATTGCAATATGATTTCCGAGTACCAATGCTATCTGAGACAGACTATCAAGAAATCAT 1541
Qy 348 LAspArgAsnLeuAsnGlnIleuAlaSerSerGlyLysSerSerSerGlyThrArgAsnTyr 368
Db 1542 GGAGAGGAATCTTAATGCTTGTGCTTCATCAGATTCAGAAAGTTCAATATCAAGGCAATTA 1601
Qy 368 ValAlaProGlySerSerAspProHisSerSerGlyLysArgProTyrTyrProValGluArg 388
Db 1602 TCTCCAGGAAGCAGTATCTCATGCGCAGGTGTTGCGCCACATTAATCTGTGGAAG 1661
Qy 388 GlyThrAlaLeuGlyLeuGlnIleuAlaSerArgAlaHisProArgGluIleMetValGluValle 408
Db 1662 AAAATGGGCTTGTGACTTCAGTCTCAGCTCAGCTCGCAGATTAATGATGAGTCTCT 1721
Qy 408 ULeuAlaLeuGlnIleuLysAsnValArgTyrLysLysAsnGlyHisTyrAsnValLysCys 428
Db 1722 AAAGCACTTGAAGACTTAATGATCTGCTGGAAGAAATGGAACATTAACAGAAAGTG 1781
Qy 428 ArgTyrCysProGlyPheProGluValAsnAspThrLeuAspAlaSerAsnSerPheLe 448
Db 1782 CAGATGAGCGCTTGAGTATCTTCAAGCCACTGATATGTGAGTCAACCACTGCTGT 1841
Qy 448 UGlyAspSerThrIleMetAspAsnAspAlaAsnGlyArgLeuProThrValIleLys 468
Db 1842 TGATGACTCAATTAATGATATATGCGATGTAACGGAGGTTACTGCTGATCA 1901
Qy 468 sPheGluPheGlnIleuTyrLysThrLysAspAspLysTyrLeuLeuAspMetGlnArgVal 488
Db 1902 GTTTGAATCAGACTTAAAGACAGACAGACAGAAATATCTGCTGATATGACAGAGT 1961
Qy 488 1ThrGlyProGlnLeuLeuPheLeuAspPheCysAlaAlaPheLeuThrLysLeuArgVal 508
Db 1962 TACGGGCGCTCAGCTCTTTCCTGCGACTTCTGCGAGCCTTCTTCAAACTGAGGCT 2021
Qy 508 1Leu 509
Db 2022 TCTA 2025

RESULT 7
US-10-437-963-80980
; Sequence 80980, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated with
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437, 963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 80980
; LENGTH: 2224

TYPE: DNA
ORGANISM: Oryza sativa
FEATURE:
OTHER INFORMATION: Clone ID: PAT_MRT4530_80552C.1
US-10-437-963-80980

Alignment Scores:

Score:	1.3e-228	Length:	2224
Percent Similarity:	1977.00	Matches:	377
Best Local Similarity:	84.28%	Conservative:	52
Query Match:	74.07%	Mismatches:	76
	73.41%	Indels:	4
		Gaps:	2

US-09-857-522b-4 (1-509) x US-10-437-963-80980 (1-2224)

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Qy 1 MetApGlySerSerySerglySerglyHisSerglyAlaLeuArgAsnTyrAsnLeuGly 20
Db 199 ATGAGGAGGAGCTGGCAGAG-----GATGGAAACCTCTTGGCGGTTACCGGATTGGC 249
Qy 21 ArgThrLeuGlyIleGlyThrPheGlyIleValysIleAlaGlyHisIleLeuThrGly 40
Db 250 AAAACCCCTAGGAGATTGGGTCTTTGGCAAGTGAAGATCGCGAGCATAATATATGCTGGT 309
Qy 41 HisArgValAlaIleIleValIleIleAsnCySargGlnMetArgAsnMetGlnMetGlu 60
Db 310 CACAAAGGCGAATCAAGATCTCTCAATGCCCTTAAGATCAAGACATGAGATGGAAGAG 369
Qy 61 LysAlaIysArgGluPheIleIleValysIleLeuPheIleHisProHisIleIleArgLeu 80
Db 370 AAAGTTAAAGAAATCAAGATCAAGATCTTATGATTATATGACCAACCATATCATTCGCTT 429
Qy 81 TyrGluValIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIle 100
Db 430 TATAGAGTGAATGACACCCAGCTGATATATATATATATATATATATATATATATATATAT 489
Qy 101 GluLeuPheAspTyrIleValIleIleValysIleArgLeuGlnIleAspGluAlaArgArgIle 120
Db 490 GAGTTGTTTATATCATGCTTGAAGAGGAGAGCTGCAAGAGAGAGAGAGAGAGAGAGAGAG 549
Qy 121 PheGlnGlnIleIleIleSerglyValIleIleIleIleIleIleIleIleIleIleIleIle 140
Db 550 TTCAGCAGATCATATCTGCTGTTGAATATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 609
Qy 141 LeuIysProGluAsnLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 160
Db 610 CTTAAGCCAGAGAACCTTCTTTTGGATCTCCAAATGCAATGTTAAGATTGACGACTTGGC 669
Qy 161 LeuSerAsnValMetHisAspGlyHisPheLeuIleIleIleIleIleIleIleIleIleIle 180
Db 670 TTGAGTATATGTTATCCGATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 729
Qy 181 AlaAlaProGluValIleIleSerglyValysIleIleIleIleIleIleIleIleIleIle 200
Db 730 GCACAGCCTGAGGATGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 789
Qy 201 CysGlyValIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIle 220
Db 790 TGTGTGTATATCTTATGCTCTTCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 849
Qy 221 ProAsnLeuPheIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIle 240
Db 850 CCCAACCTTTTAAAGAAATTAAGAGGTGGCAATATATATATATATATATATATATATAT 909
Qy 241 LeuAlaArgAspLeuIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIle 260
Db 910 TTGGCAAGGAGATTGATCTCCAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 969
Qy 261 ArgGluIleArgGluHisIleIleIleIleIleIleIleIleIleIleIleIleIleIleIle 280
Db 970 CGTGAATATCCGGAACATCAAGGTTCACAGTGTCTTCCGCGATTATTAAGCTGTGCCA 1029
Qy 281 ProProAspThrThrGlnGlnAlaIleIleIleIleIleIleIleIleIleIleIleIleIle 300

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Db 1030 CCTCTGACACTGCACAAACAGTGTAAAGCTGCAGATGAACTCGAATGATGTATATC 1089
Qy 301 AsnMetGlyPheAsnIleValIleValIleIleIleIleIleIleIleIleIleIleIleIle 320
Db 1090 AATATGGGTTTAAAGAAATCAAGATCAAGATCAAGATCAAGATCAAGATCAAGATCAAG 1149
Qy 321 AlaThrValAlaIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIle 340
Db 1150 GCGAGATCTTCCATCTATTTATTTGAGCAATATAGGTGGCAACACATGCTGCTGCTGCT 1209
Qy 341 GlyAlaAspTyrGlnIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIle 360
Db 1210 GAGACTGATCTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1269
Qy 361 SerSerSerglyThrArgAsnTyrValProGlySerSerAspProHisSerSerglyLeu 380
Db 1270 CCAAACTCACCTGATCATCGGAGCATGAGCATGAGCATGAGCATGAGCATGAGCATGAG 1329
Qy 381 ArgProTyrTyrProValIleIleIleIleIleIleIleIleIleIleIleIleIleIleIle 400
Db 1330 AGGATCATTTTCCAGCTGACAGAAATGGGCTTGTCTTCACTGCTGAGCAGCATCCA 1389
Qy 401 ArgGluIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIle 420
Db 1390 CGAAGAAATATTAAGTAAAGTCTTAAAGCTCTGCAAGAGCTAAATGTTTCTGAGAGAG 1449
Qy 421 AsnGlyHisIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIle 440
Db 1450 ATTGAGCATTTATTAAGAAATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAG 1509
Qy 441 LeuAspAlaSerAsnSerPheLeuGlyAspSerThrIleMetAspAsnAspAlaAsn 460
Db 1510 ATGCATTAACAACATGCTTGGTGGCAGATCTGCTATATATGTAATGACATGACAGTAC 1569
Qy 461 GlyArgLeuProThrValIleIleIleIleIleIleIleIleIleIleIleIleIleIleIle 480
Db 1570 AAATCAACCAACCTGCG--AAATTTGAATTCAGCTTTACAAACACAGAGATGAAAAA 1626
Qy 481 TyrIleLeuAspMetGlnArgValIleIleIleIleIleIleIleIleIleIleIleIleIle 500
Db 1627 TACCTTTTGAATCTTGAAGAGGTGATGAGACCAAGCTTCTTCTTGGACCTGTGCTCT 1686
Qy 501 AlaPheLeuThrIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIle 520
Db 1687 GCCTTTCACTCAGCTGAGAGTCTCT 1713

RESULT 8
US-10-183-687-247
; Sequence 247, Application US/10183687
; Publication No. US20030204870A1
; GENERAL INFORMATION:
; APPLICANT: Allen, Steve
; APPLICANT: Allen, William B.
; APPLICANT: Cahoon, Rebecca
; APPLICANT: Epelbaum, Sabine
; APPLICANT: Famodu, Omolayo O.
; APPLICANT: Harvell, Leslie T.
; APPLICANT: Jones, Todd
; APPLICANT: Kliney, Tony
; APPLICANT: Klein, Ted
; APPLICANT: Li, Changjiang
; APPLICANT: Oliveira, Igor Cunha
; APPLICANT: Sakai, Hajime
; APPLICANT: Shen, Bo
; APPLICANT: Tarczyński, Mitchell C.
; TITLE OF INVENTION: Alteration Of Oil Traits In Plants
; FILE REFERENCE: B81458 US NA
; CURRENT APPLICATION NUMBER: US/10/183,687
; PRIOR FILING DATE: 2002-06-27
; PRIOR APPLICATION NUMBER: 60/301,913
; PRIOR FILING DATE: 2001-06-29
; NUMBER OF SEQ ID NOS: 532

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SOFTWARE: Microsoft Office 97
; SEQ ID NO 247
; LENGTH: 2123
; TYPE: DNA
; ORGANISM: Glycine max
; US-10-183-687-247

Alignment Scores:
Pred. No.: 2,426-228      Length: 2123
Score: 1974.50           Matches: 382
Percent Similarity: 83.53%      Conservative: 49
Best Local Similarity: 74.03%    Mismatches: 76
Query Match: 73.32%           Indels: 9
DB: 13                      Gaps: 3

US-09-857-522b-4 (1-509) x US-10-183-687-247 (1-2123)

Qy 1 MetAspGlySerSer-----LysGlySerGlyHisSerGluAlaLeuArgAsnTyrAsn 18
Db 123 ATGATGACCAAGCTGGCGAGCTGCTGCTGGACATGTTCTTACCAATTTATATAA 182
Qy 19 LeuGlyArgThrLeuGlyTlleglyThrPheGlyLysValLysIleAlaGluHisLysLeu 38
Db 183 TTGGGAAAAACACTCGGATTTGATCTTTGGCAAGTGAAAAATTGCAGAACATGTGTTG 242
Qy 39 ThrGlyHisArgValAlaIleLysIleLeuAsnGlySerGluMetArgAsnMetGluMet 58
Db 243 ACTGGCCATAAGGTTCATCAAGATCCTTAACGACCCAGATTAAGAAACATGGAAATG 302
Qy 59 GluGlyLysAlaLysArgGluPheLysIleLeuLysLeuPheIleHisProHisIleIle 78
Db 303 GAAAGAAAAGTGAAGAAAGAAATCAAAATTTTAAGATTGTTCAATCCATCCATTTATT 362
Qy 79 ArgLeuTyrGluValIleTyrThrProThrAspIleTyrValMetGluTyrCysLys 98
Db 363 CGACTTTATGAAGTCATGAACCTCAACATGATATGTTGATGAGATGTGAAG 422
Qy 99 TyrGlyLysLeuPheAspTyrIleValGluLysGlyArgLeuGlnGluAspGluAlaArg 118
Db 423 TCTGGAGCTTTTCATTAACATGATAGTGAAGAGGTGAGTGCAGAAAGATGAGCTGT 482
Qy 119 ArgIlePheGlnGlnIleIleSerGlyValGluTyrCysHisArgAsnMetValAlaHis 138
Db 483 AATTTTTTTCAGCAGATATATCTCTGGGGTGGAGTACTCTCACAGAAATATGTTGTTAT 542
Qy 139 ArgAspLeuLysProGluAsnLeuLeuLysSerLysTyrAsnValLysLeuAlaAsp 158
Db 543 AGAGATTGGAAGCCCTGAAGAAATTTACTTTTGACCTCAATGTAATGTCAAGATTGCTGAT 602
Qy 159 PheGlyLeuSerArgAsnValMetHisAspGlyHisPheLeuLysThrSerCysGlySerPro 178
Db 603 TTGGCTTGACCAACATGATGCTGATGCTGATCTTTCTTAACCAAGTTGGGAAGCCCT 662
Qy 179 AsnTyrAlaAlaProGluValIleSerGlyLysLeuTyrAlaGlyProGluValAlaSerVal 198
Db 663 AACTATGACGCTCTCGAGCTTATCTCTGGAAATTGTAATGCTGACCTGAAGTGAATGCTC 722
Qy 199 TrpSerCysGlyValIleLeuTyrAlaLeuLeuCysGlyThrLeuProPheAspAspGlu 218
Db 723 TGGAGCTGTGTGTAATTTTATATGCCCCCTTTCTTGACACCCCTTCCTTTGATGATATAA 782
Qy 219 AsnIleProAsnLeuPheLysValIleLysGlyIleTyrThrLeuProSerHisIleu 238
Db 783 AATATTCCAAAATCTCTCAAGAAATTAAGGATGATTAACATCTTCCCAAGTCATCTTA 842
Qy 239 SerAlaLeuAlaArgAspLeuIleProArgMetLeuValAlaGluProMetLysArgIle 258
Db 843 TCACCCCGGTGCTAGAGATTGATACCAAGAGATGCTGTGTGTAACCCATAGAGAGATG 902
Qy 259 ThrIleArgGluIleArgGluHisGlnTyrPheGlnIleArgLeuProArgTyrLeuAla 278
Db 903 ACCATACCTGATGATCCGTCAACACCCATGTTCCAGCTTCACCTTCAAGTTATTTAGCT 962
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Qy 279 ValProProAspThrThrGlnGlnAlaLysMetIleAspGluAspThrLeuArgAsp 298
Db 963 GTGCCACCAACAGATATACATGCAACAGGCCAAAAGATTGATGAGAGATCTTTCAGGAA 1022
Qy 299 ValValAsnMetGlyPheAsnLysAsnHisValCysGlySerLeuCysSerArgLeuGln 318
Db 1023 GTGGTGAATAATGGGATTTGACAGAAATCAATATGTTGATATCTTGGGAACAGATACAA 1082
Qy 319 AsnGluAlaThrValAlaIleTyrThrLeuLeuLeuAspAsnArgPheAlaGlnThrSerGly 338
Db 1083 AATGAGGTACTGTGGCAATACATATTTGTTATTTGACCAACCATTTTGGTTTCAAGTGC 1142
Qy 339 TyrLeuGlyAlaAspTyrGlnGluSerMetAspArgAsnLeuAsnGlnLeuAlaSerSer 358
Db 1143 TATCTTGAGCTTGAGTTTCAAGAGACATGATTCGGGTTTATATCAATATCATTCAGT 1202
Qy 359 GluSerSerSerSerGlyThrArgAsnTyrValProGlySerSerAspProHisSerSer 378
Db 1203 GAATCTGCTTCTTCAAGTTGTTGAAACCGCTTTCAGGCTTACATGAAATATCCAGAGTA 1262
Qy 379 GlyLeuArgProTyrTyrProValGluArgLysTrpAlaLeuGlyLysGlnSerArgAla 398
Db 1263 GGATCGAGGCAACGTTCCCTGTTGAAAGAAATGGGCCCTTGGGCTTCACTCGAGACC 1322
Qy 399 HisProArgGluIleMetValGluValLeuLysAlaLeuGlnGluLeuAsnValArgTrp 418
Db 1323 CATCTGTGAATAATTAAGTACTGAGGTTCTTAAACCTTTGCAAGAAATTAATGTTGTTGG 1382
Qy 419 LysLysAsnGlyHisTyrAsnValLysCysArgTrpCysProGlyPhePro----- 435
Db 1383 AAGAAGATTGGTCACTCAACATGAGTGAAGTGGGTTGCTGCAATTCCTGTCACACAC 1442
Qy 436 -----GluValAsnAspThrLeuAspAlaSerAsnSerPheLeuGlyAspSerThrIle 453
Db 1443 GAAAGAAATGTGTTAACAATATATGTCATATGATTAATTTGAGATGATTTCCAACTT 1502
Qy 454 MetAspAsnAspAspAlaAsnGlyArgLeuProThrValIleLysPheGluPheGlnLeu 473
Db 1503 ATTGAATGATGCTGTTCT-----ACTTCAATGTGTCAGATTTGAAGTGCAGCTT 1556
Qy 474 TyrLysThrLysAspLysTyrLeuLeuAspMetGlnArgValThrGlyProGlnLeu 493
Db 1557 TACAAACCCGGGAAAGAAAGTATCTGCTGATCTTCAAGGGTGAGGATCCACAGTTT 1616
Qy 494 LeuPheLeuAspPheCysAlaAlaPheLeuThrLysLeuArgValLeu 509
Db 1617 CTTTCTTGATCTATGCTGCTTCTTCTTGCACAGCTTGTGCTCTC 1664

RESULT 9
US-09-938-842A-2657
; Sequence 2657, Application US/09938842A
; Patent No. US20020160378A1
; GENERAL INFORMATION:
; APPLICANT: Harper, Jeff
; APPLICANT: Kreps, Joel
; APPLICANT: Wang, Xun
; APPLICANT: Zhu, Tong
; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
; FILE REFERENCE: SAME, AND METHODS OF USE
; CURRENT APPLICATION NUMBER: US/09/938,842A
; PRIOR FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: US 60/227,866
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: US 60/264,647
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/300,111
; PRIOR FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 5379
; SEQ ID NO 2657
; LENGTH: 1539
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
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US-09-938-842A-2657

Alignment Scores:

Pred. No.:	5.81e-228	Length:	1539
Score:	1969.50	Matches:	377
Percent Similarity:	82.82%	Conservative:	52
Best Local Similarity:	72.78%	Mismatches:	74
Query Match:	73.13%	Indels:	15
		Gaps:	4

US-09-857-522B-4 (1-509) x US-09-938-842A-2657 (1-1539)

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Qy      1 MetaspGlySerSerlySgLy-----SerGlyHisSerGluAlaLeuArgAsnTyrAsn 18
Db      1 ATGATGATCATGGACAGCAGCATGAGATGGGGGAGAAATCGATTCTACCAATTATCAAG 60

Qy     19 LeuGlyArgThrLeuGlyIleGlyThrPheGlyLysValLysIleAlaGlnHisLysLeu 38
Db     61 CTGGAGAACTCTTGATGTTGCTTCTTGAGGGTGAAGATAGCTGACCATGCAATG 120

Qy     39 ThrGlyHisArgValAlaIleLysIleLeuAsnGlySerGlyMetArgAsnMetGlyMet 58
Db    121 ACAGACATCAAGTGTGCTATCAAGATCCTCAATCGTCCAAATCAAGACATGGAGATG 180

Qy     59 GluGlyLysAlaLysArgGluPheLysIleLeuLysLeuPheIleHisProHisIleIle 78
Db    181 GAGAGAAAGTGAAGAGAGATCAAAATCTTGAGACTATTATGCAATCTCAGATCATC 240

Qy     79 ArgLeuTyrGluValIleTyrThrProThrAspIleTyrValValMetGlyTyrCysLys 98
Db    241 CGTCTCATGAGGTATGAGACTCCACAGATATTATCTTGTCATGAGTATGTGAAAC 300

Qy     99 TyrGlyLysLeuPheAspTyrIleValGlyLysGlyArgLeuGlnGluAspGluAlaArg 118
Db    301 TCTGTGAGCTATTGACTATATGTGTGAGAGGATGATGCGAGAGATGAGCGAGG 360

Qy    119 ArgIlePheGlnGlnIleIleSerGlyValGlyTyrCysHisArgAsnMetValValHis 138
Db    361 AACTTTTTCAGCAGATATATATCAGAGTGGATATCTGCCATCGAAATCATGTGGTTAC 420

Qy    139 ArgAspLeuLysProGluAsnLeuLeuLysAspSerLysTyrAsnValLysLeuAlaAsp 158
Db    421 AGAGACCTCAAGCCGAAACCTTGCTTTGAGACTCTTAATCAATGTAAACATTTGCTCAT 480

Qy    159 PheGlyLeuSerAsnValMetHisAspGlyHisPheLeuLysThrSerCysGlySerPro 178
Db    481 TTGGCTGAGCAACATATATGAGATGCTCATTTTGAAGACAAGTTGGAGAGTCCA 540

Qy    179 AsnTyrAlaAlaProGluValIleSerGlyLysLeuTyrAlaGlyProGluValAspVal 198
Db    541 AATTATGCGCGTCCGAGATATTTCCGGCAAGTTATATGCGGCCCTGAAGTATGATGTC 600

Qy    199 TrpSerCysGlyValIleLeuTyrAlaLeuLeuCysGlyThrLeuProPheAspArgGlu 218
Db    601 TGGAGCTGTGGTGCATCTCTACCCCTCTCTCTGTGGAGAGCTTCCATTGATGATGATA 660

Qy    219 AsnIleProAsnLeuPheLysLysIleLysGlyIleTyrThrLeuProSerHisLeu 238
Db    661 AACATTTCCCAACTTTTAAAGAAATTAAGAGAGATATACACTTACCTTACGACCATTTA 720

Qy    239 SerAlaLeuAlaArgAspLeuIleProArgMetLeuValAlaGluProMetLysArgIle 258
Db    721 TCTCTGCTGCTAGAGATTTGATCCCGGAGTGTCTTGAGTGAACCCATGAAGAGATA 780

Qy    259 ThrIleArgGluIleArgGlnHisGlnTyrPheGlnIleArgLeuProArgTyrIleuAla 278
Db    781 ACCATCCCTGAGATCCGGCAACACCCCTTGTTCCAGCTCATCTCCAGAGTATTTAGCT 840

Qy    279 ValProProProAspThrThrGlnGlnAlaLysMetIleAspGluAspThrLeuArgAsp 298
Db    841 GTTCTCTCTCCAGATACTGTGCAACAGGCAAAAAGATTTGACGAGAGATTTCTCCAGAA 900

Qy    299 ValValAsnMetGlyPheAsnLysAsnHisValCysGluSerLeuCysSerArgLeuGln 318

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Db     901 GTTATCAATATGGGATTTGACAGAAACCACTCATCGAATCGCTCCGCAACCAACCCAG 960

Qy    319 AsnGluAlaThrValAlaTyrTyrLeuLeuAspAsnArgPheArgAlaThrSerGly 338
Db     961 AATGATGGCACTGTGACGTACTATCTGATCTGACATGATGTTTCCGTGCTTCAATGGT 1020

Qy    339 TyrLeuGlyAlaAspTyrGlnGluSerMetAspArgAsnLeuAsnGlnLeuAlaSerSer 358
Db    1021 TATCTGGGGCTAGATTTCAGAGACCATGAA---GCTACTCCCGGTATGATCCAGCA 1077

Qy    359 GluSerSerSerSerGlyThrArgAsnTyrValProGlySerSerAspProHisSerSer 378
Db    1078 GAAAGCGTTCCTTCACTCGTTAGCCATCGGCTTCCAGGACTGATGTGAATTCAGAGATT 1137

Qy    379 GlyLeuArgProTyrTyrProValAlaArgLysTyrAlaLeuGlyLeuGlnSerArgAla 398
Db    1138 GGCTTGAGATCTCAATACCTGTTGAGAGAAATGGGCTCTTGACTTCAAGTCTCGGCT 1197

Qy    399 HisProArgGluIleMetValGluValLeuLysAlaLeuGlnGluLeuAsnValArgTyr 418
Db    1198 CATCCCGGTGAATTAATGAGCGAAAGTCTTGAAGCCCTGCAAGATTGATGTATGTGG 1257

Qy    419 LysLysAsnGlyHisTyrAsnValLysCysArgTyrCysProGlyPheProGluValAsn 438
Db    1258 AAGAAATATGGGCACTCAACATGAATGAATGAGATGGTCTCT-----AAC 1302

Qy    439 AspThrLeuAspAla-----SerAsnSerPheLeuGlyAspSer 451
Db    1303 AGCAGCCCAATGGTATGCTCAGTAACTGATGCAAGATCAACATTAACCTTTGAGAGAG 1362

Qy    452 ThrIleMetAspAsnAspAlaAsnGlyArgLeuProThrValIleLysPheGluPhe 471
Db    1363 TCCAGCATTAATAGAGAACGAAAGCAGCTTTAAGTCCGCAATGTTCAGATTGAAAT 1422

Qy    472 GlnLeuTyrLysThrLysAspAspLysTyrLeuLeuAspMetGlnArgValIleArgLysPro 491
Db    1423 CAGTTGTATTAACCTCGGAGACGACAGATATCTAGTATTTGGCAGAGATCAAGGTCCT 1482

Qy    492 GlnLeuLeuPheLeuAspPheCysAlaAlaPheLeuThrHisLeuArgValLeu 509
Db    1483 CAGTTCTTGTCTGGATCTGTGCTGTCTTCTTCTGCTCAGCTCCAGATCTC 1536

RESULT 10
US-09-938-842A-2657
; Sequence 2657, Application US/09938842A
; Publication No. US20040009476A9
; GENERAL INFORMATION:
; APPLICANT: Harper, Jeff
; APPLICANT: Kreps, Joel
; APPLICANT: Wang, Xun
; APPLICANT: Zhu, Tong
; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
; TITLE OF INVENTION: SAME, AND METHODS OF USE
; FILE REFERENCE: SCRIP1300-3
; CURRENT APPLICATION NUMBER: US/09/938,842A
; CURRENT FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: US 60/264,647
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/300,111
; PRIOR FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 5379
; SEQ ID NO 2657
; LENGTH: 1539
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-938-842A-2657

Alignment Scores:
Pred. No.: 5.81e-228 Length: 1539
Score: 1969.50 Matches: 377

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Qy 1 MetaspGlySerSerLyGlySerGlyHisSerGluAlaLeuArgAsnTyrAsnLeuGly 20
Db 216 ATGAGGGGGGCGAGGAGG-----GATGGCAACCCCGTTGAGGAATATTCGGATTGGC 266
Qy 21 ArgThrLeuGlyIleGlyThrPheGlyLysValIleAlaGluHisLeuThrGly 40
Db 267 AAGACTCTCGGAATGGCTCATTCGGGAAGGTGAAAATTCGGGAGCATATCAGCACTGGA 326
Qy 41 HisArgValAlaIleLysIleLeuAsnCySarGlnMetLysArgAsnMetGluMetGlu 60
Db 327 CACACAGGCGGCAATCAGATTCCTCAACCGCTAAATACAGAGGCGATGAGATGGAAAG 386
Qy 61 LysAlaLysArgGluPheLysIleLeuLysLeuPheIleHisProHisIleLeuArgLeu 80
Db 387 AAGCTTAAGAGAGATTAAGATTAAGCTTATTAATGATTCACATATTAATTCGGCTTC 446
Qy 81 TyrGluValIleTyrThrProThrAspIleTyrValIleMetGluTyrCysLysTyrGly 100
Db 447 TATGAGCTTATAGACACACCGGCTGATATTAATGTTATGAGATGATTAAGTGTGG 506
Qy 101 GluLeuPheAspTyrIleValGlyLysGlyArgLeuGlnGluAspGluAlaArgArgIle 120
Db 507 GAATTAATTTGATTCATTTGTTGAGAAAGGTAGGCTGCAAGAGAAAGAGCTCGCGTTTC 566
Qy 121 PheGlnGlnIleIleSerGlyValGluTyrCysHisArgAsnMetValHisArgAsp 140
Db 567 TTCACAGATTAATTCGGGTGTGATTAATTCCTCAAGAACATGTGTGTGATGTAT 626
Qy 141 LeuLysProGluAsnLeuLeuLeuAspSerLysTyrAsnValLysLeuAlaAspPheGly 160
Db 627 CTAAAGCCAGAAACCTCTCATTTGATTCAAAATGCATTAATGATTCAGATTGTCG 686
Qy 161 LeuSerAsnValMetHisAspGlyHisPheLeuLysThrSerCysGlySerProAsnTyr 180
Db 687 TTAAGTAATGTATTCGGGATGCTCATTTCTCGAAGAACAGTTGTGTAGGCCCAATAT 746
Qy 181 AlaAlaProGluValIleSerGlyLysLeuTyrAlaGlyProGluValAspValIlePhe 200
Db 747 GCTGCTCTGAGGGATATCTGGTAACTATTAATGCTGAGCCTGAAGTGAAGTGTGGAGC 806
Qy 201 CysGlyValIleLeuTyrAlaLeuLeuCysGlyThrLeuProPheAspAspGluAsnIle 220
Db 807 TGTGGGGTATTTCTTATGCTCTTTTATGTGGTACTGCGCATTTGATGAGAGAACTA 866
Qy 221 ProAsnLeuPheLysIleLysGlyGlyIleTyrThrLeuProSerHisLeuSerAla 240
Db 867 CCAAACTTTTAAAGAAATTAAGGGGTGAATATATACCTTCCAGCCATTTGTCTGCT 926
Qy 241 LeuAlaArgAspLeuIleProArgMetLeuValIleGluProMetLysArgIleThrIle 260
Db 927 GCAGAGAGGATTTGATTTCCAAAGATGCTAGTGTGCTATGAACTGAGATCCCACT 986
Qy 261 ArgGluLeuArgGluHisGlnTyrPheGlnIleArgLeuProArgTyrLeuAlaValPro 280
Db 987 CGTGAATTCGCGAAGATGATGTTGTTCAAAATCTTCTCCGCGGTATTTGACTGTGCT 1046
Qy 281 ProProAspThrThrGlnGlnAlaLysMetIleAspGluAspThrLeuArgAspValIle 300
Db 1047 CCTCCAGATAGTGGCAACAAGTCAAAAAGGTGATGAGAAACTCTCGTGAAGGTTTAA 1106
Qy 301 AsnMetGlyPheAsnLysAsnHisValCysGlyLysLeuLysCysSerArgLeuGluAsnGlu 320
Db 1107 GGTATGGATATAGCAAGAACCTGTGTGATGATTAATTCAAAAGGCTGCAAAATATAG 1166
Qy 321 AlaThrValAlaTyrTyrLeuLeuLeuAspAsnArgPheArgAlaThrSerGlyTyrLeu 340
Db 1167 GCAACTGTTGATATTAATTAATCTTGTGCAATAGGCTCCGTACACAGAGGCTATCTT 1226
Qy 341 GlyAlaAspTyrGlnGlnLysSerMetAspArgAsnLeuAsnGlnLeuAlaSerSerGlu 359
Db 1227 GGAGCTGAATGCTCAAGAACTATGATGCTCTCATTTCTCAAACTCGCATATATGAAACA 1286

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Qy 360 ---SerSerSerSerGlyThrArgAsnTyrValProGlySerSerAspProHisSerSer 378
Db 1287 CCAAGTTTCAGCAGCTGGGAATATGACAGCAAAATATTATTAAGAGTCT-----CAAGTT 1337
Qy 379 GlyLeuArgProTyrTyrProValGluArgLysTrpAlaLeuGlyLeuGlnSerArgAla 398
Db 1338 GCGTTGAGACCACTCTTCCAGCTGAGAGGAAATGGGCTCTGCTTCAGTCTCGAGCA 1397
Qy 399 HisProArgGluIleMetValGluValLeuLysAlaLeuGlnGluLeuAsnValArgTrp 418
Db 1398 CATCCAAAAGAAATTAATGTCTGAAGTCTGAAAGCTCTGCAAGAAATTAATTAATCTGG 1457
Qy 419 LysLysAsnGlyHisTyrAsnValLysCysArgTyrCysProGlyPheProGluValAsn 438
Db 1458 AAAAAGATAGTCTCATTAATGATGAAGTGCAGATGAGAGTCTGCTTCTTCCGCT----- 1511
Qy 439 AspThrLeuAspAlaSerAsnSerPheLeuGlyAspSerThrIleMetAspAsnAspAsp 458
Db 1512 ---CAAATTCATAACATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCA 1562
Qy 459 AlaAsnGlyArgLeuProThrValIleLysPheGluLeuPheGlnLeuTyrLysThrLysAsp 478
Db 1563 CTGAGTGAAGAGTTA---AGTTTAATTAAGTTTGAATTAATTAATTAATTAATTAATTA 1619
Qy 479 AspLysTyrLeuLeuAspMetGlnArgValThrGlyProGlnLeuLeuPheLeuAspPhe 498
Db 1620 GAGAAATTCCTCTCTCGATTTGCCAAAGAGTCAAGTGGCCACAGCTCTCTTCTTGACTTG 1679
Qy 499 CysAlaAlaPheLeuThrLysLeuArgValLeu 509
Db 1680 TGCGGGCGCTTTCTTAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCA 1712

RESULT 13
US-10-183-687-251
; Sequence 251, Application US/10183687
; Publication No. US20030204870A1
; GENERAL INFORMATION:
; APPLICANT: Allen, Steve
; APPLICANT: Allen, William B.
; APPLICANT: Canoon, Rebecca
; APPLICANT: Epelbaum, Sabine
; APPLICANT: Famodu, Omolayo O.
; APPLICANT: Harvell, Leslie T.
; APPLICANT: Jones, Todd
; APPLICANT: Kinney, Tony
; APPLICANT: Klein, Ted
; APPLICANT: Li, Changliang
; APPLICANT: Oliveira, Igor Cunha
; APPLICANT: Sakai, Hajime
; APPLICANT: Shen, Bo
; APPLICANT: Tarczyński, Mitchell C.
; TITLE OF INVENTION: Alteration Of Oil Traits In Plants
; FILE REFERENCE: B81458 US NA
; CURRENT APPLICATION NUMBER: US/10/183,687
; PRIOR FILING DATE: 2002-06-27
; PRIOR APPLICATION NUMBER: 60/301,913
; NUMBER OF SEQ ID NOS: 532
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 251
; LENGTH: 2543
; TYPE: DNA
; ORGANISM: Glycine max
; US-10-183-687-251

Alignment Scores:
Pred. No.: 6,55e-224 Length: 2543
Score: 1939.00 Matches: 373
Percent Similarity: 83.37% Conservative: 58
Best Local Similarity: 72.15% Mismatches: 76
Query Match: 72.00% Indels: 10
DB: 13 Gaps: 4

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US-09-857-522b-4 (1-509) x US-10-183-687-251 (1-2543)

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Qy 1 MetAspGlySerSer---LysGlySerGlyHisSer-----GluAlaLeuArgAsnTyr 17
Db 73 ATGACAGATCACTGCGCGTGTGTGGAGTGTGACATGTTCTCCGAAATATAT 132
Qy 18 AsnLeuGlyArgThrLeuGlyIleGlyThrPheGlyLysValLysIleAlaGluHisLys 37
Db 133 AAGTTGGGAAAAACCTCGCATGGCTGGCTTGGCAAGGGAAGAAATTCGACAGATGA 192
Qy 38 LeuThrGlyHisArgValAlaIleLysIleIleAsnCySarGlnMetArgAsnMetGlu 57
Db 193 CGGACTGGTCAATAAGTTGCTATAAGATCCTTAACGCCACAGATTTAAAAAATCATGGAA 252
Qy 58 MetGluGluLysAlaLysArgGluPheLysIleLeuLysLeuPheIleHisProHisIle 77
Db 253 ATGGAAGAAAAAGTTAGAGAGAAATCAAAATTTTAAAGATTGTTATGCAATCAACATT 312
Qy 78 IleArgLeuTyrGluValIleTyrThrProThrAspIleTyrValIleMetGluTyrCys 97
Db 313 ATAGACTATATGAGCTTGTGATTAAGAAACCCCAACACATATATGTTATGAGATATGTG 372
Qy 98 LysTyrGlyGluLeuPheAspTyrIleValGluLysGlyArgLeuGlnIleAspGluAla 117
Db 373 AAATCTGGAGAGCTCTTGTGATTAATAGTAGAAGAGGTCCGCTGCAAGAGATGAAGCC 432
Qy 118 ArgArgIlePheGlnGlnIleIleSerGlyValGluTyrCysHisArgAsnMetValVal 137
Db 433 CGTCAATTTTTCAGACATATATTCGTGTGTGAGATCTGTCAAGAAATATATGTTGTT 492
Qy 138 HisArgAspLeuLysProGluAsnLeuLeuAspSerLysTyrAsnValLysLeuAla 157
Db 493 CATGAGACCTGGAACCTCGAAGATTTACTCTTGACATCAAAATTTAATACATCAAGATTGCT 552
Qy 158 AspPheGlyLeuSerAsnValMetHisAspGlyHisPheLeuLysThrSerCysGlySer 177
Db 553 GATTTGGGTGACCAACATCATCATGCTGATGTCATCTTTCTTAAGACAAAGTTGTGAGAGC 612
Qy 178 ProAsnTyrAlaIleProGluValIleSerGlyLysLeuTyrAlaGluProGluValAsp 197
Db 613 CCTAATTATGCGGCTCCAGAGATTATCTCTGAAAATTTGATGCTGACCAAGAGTGAT 672
Qy 198 ValTyrSerCysGlyValIleLeuTyrAlaLeuLeuCysGlyThrLeuProPheAspAsp 217
Db 673 GTCGAGACTGTGGTGAATTTTATATCTCTCTCTGTGCACTCTTCTTTTGATGAT 732
Qy 218 GluAsnIleProAsnLeuPheLysLysIleLysGlyGlyIleTyrThrLeuProSerHis 237
Db 733 GAAAAACATTTCCCAATCTCTCAAAAAATTAAGGGTGGATATACACTCTTCTTAAGTCAT 792
Qy 238 LeuSerAlaLeuAlaArgAspLeuIleProArgMetLeuValGluProMetLysArg 257
Db 793 CTATCACTGTGTCTAGAGATTGTATACAAAGAGTGTGTGTGATCCCATGAAGAGG 852
Qy 258 IleThrIleAsnGluIleArgGluHisGlnIleTyrPheGlnIleArgLeuProArgTyrLeu 277
Db 853 ATGACCAATCTCGATACCGCAACACCCATGTTCCAAAGTCAATCTACCCGCTTATTTA 912
Qy 278 AlaValProProAspThrThrGlnGlnAlaLysMetIleAspGluAspThrLeuArg 297
Db 913 GCAGGCGCACCAACCGATACACTGCAACACCAAAAAAGATTTGATGAGAGAAATCTTTCAG 972
Qy 298 AspValValAsnMetGlyPheAsnLysAsnHisValCysGluSerLeuCysSerArgLeu 317
Db 973 GAAAGGTGTTAATATGAGATTGACAGAGATCAATTTGTTGATCTCTTAAGCAACAGGATA 1032
Qy 318 GlnAsnGluAlaThrValAlaIleTyrTyrLeuLeuLeuAspAsnArgPheArgAlaThrSer 337
Db 1033 CAATATGAGGATACGTAAACATACATATTTGTTATTTGACAAACCGGTTTCGATTTCTAGT 1092
Qy 338 GlyTyrLeuGlyAlaAspTyrGlnIleSerMetAspArgAsnLeuAsnGlnLeuAlaSer 357
Db 1093 GGTATCTTGGAGCTGAATTTTCAAGAGCAATGTGATCTGTGTTTAAACCGTATGATTC 1152
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Qy 358 SerGluSerSerSerSerGlyThrArgAsnTyrValProGlySerSerAspProHisSer 377
Db 1153 GCGGAATGCTCTCTCCAGTGTGTTGGACACACAGCAAGGATATGATTTTCAAGGG 1212
Qy 378 SerGlyLeuArgProTyrTyrProValGluArgLysTrpAlaLeuGlyLeuGlnSerArg 397
Db 1213 GTAGGAATGCGGCAACAGTTCCCTGTTGAGAGAAATAGGCGCCCTTGGGCTTCAGTCCGA 1272
Qy 398 AlaHisProArgGluIleMetValGluValLeuLysAlaLeuGlnGluLeuAsnValArg 417
Db 1273 GCCCAACACAGTGAATAATGACTGAGGCTCTTAAAGCTTCAAGATTAATATGTTGT 1332
Qy 418 TrpLysLysAsnGlyHisTyrAsnValLysCysArgTrpCysProGlyPhePro----- 435
Db 1333 TGGAGAGAGATTGGACACTTATACATGAACTGCAGATGGGTTGCTGCACTGCGTCAT 1392
Qy 436 -----GluValAsnAspThrLeuAspAlaSerAsnSerPheLeuGlyAspSerThr 452
Db 1393 CATGAAGAAATGATTAACAATCTCTGATATGATATCATATTGGAATGATTCGCGC 1452
Qy 453 IleMetAspAsnAspAspAlaAsnGlyArgLeuProThrValIleLysPheGluPheGln 472
Db 1453 ATTAATGAATAATGAAGCTGTTCT---AAGTCAATGTGTCAAGTTTGAAGTGCAG 1506
Qy 473 LeuTyrLysThrLysAspAspLysTyrLeuLeuAspMetGlnArgValThrGlyProGln 492
Db 1507 CTTTACAAAACCTCGTGAAGAAATATCTGCTTGTATTTCAAGGGTCCAGGGCCACAG 1566
Qy 493 LeuLeuPheLeuAspPheCysAlaAlaPheLeuThrLysLeuArgValLeu 509
Db 1567 TTTCTTTCTTGTGATCTGTGCGCTTCTTCTTCAACAGCTAGGTGTTCTTC 1617

RESULT 14
US-10-425-114-2148
; Sequence 2148, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jindong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovacic, David K.
; APPLICANT: Screen, Steven E.
; APPLICANT: Tabaska, Jack E.
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(5313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 2148
; LENGTH: 1778
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: 700204782_FU1
US-10-425-114-2148

Alignment Scores:
Pred. No.: 6,41e-224 Length: 1778
Score: 1937.00 Matches: 374
Percent Similarity: 83.66% Conservative: 56
Best Local Similarity: 72.76% Mismatches: 68
Query Match: 71.93% Indels: 16
DB: 13 Gaps: 5

US-09-857-522b-4 (1-509) x US-10-425-114-2148 (1-1778)
Qy 1 MetAspGlySerSerLysGlySerGlyHisSerGluAlaLeuArgAsnTyrAsnLeuGly 20
Db 128 ATGAGAGAGAGCTGGAAGA-----GATGCCAACCTTTGGCGGCTTACCGAATTTGCC 178
Qy 21 ArgThrLeuGlyIleGlyThrPheGlyLysValLysIleAlaGluHisLysLeuThrGly 40
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Db 179 AAAACCCAGGAATGGCTCGTTGCTAAAGTAAGATCGCGAACAATATATGCTGCG 238
Qy 41 HlsarGValAlaIleValIleIleasnCyBarGlnMeCArgAsnMeCglUmeCglUnl 60
Db 239 CATAGGGGGAATCAAGATCCTCAATGCCGTAAAGCAGAGATGAAATGGAAG 298
Qy 61 LysAlaIysArgGluPheIysIleUeuIysPheIleHisProHisIleIleArgHeu 80
Db 299 AAAAGGAAGAGAAATCAAGATCTGAGATTATTTATGATCTCTCAATATGAGCCTT 358
Qy 81 TyrGluValIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIle 100
Db 359 TATGAGGTAGATAGATACACCTGCTGATATTTATGTTATGAGATATGTTAAATCTGA 418
Qy 101 GlUeuPheAspTyrIleValIleUlysgIyArgLeuGlnIleUaspGluAlaArgArgIle 120
Db 419 GAGTGTGTGATTCATTTGTTGAGAGAGAGAGACTACATGAAGAAAGCCCGGCTTT 478
Qy 121 PheGlnGlnIleIleSerGlyValGluTyrCysHisArgAsnMetValHisArgAsp 140
Db 479 TTTGACGATCATATCTGGGTGTGATATGTCATAGAACATGCTGCTACCGTAT 538
Qy 141 LeuIysProGluAsnLeuLeuIleUeuAspSerIysTyrAsnValIysLeuAlaAspPheGly 160
Db 539 TTTAAAGCAGAGAACTCTTTTGATTCGAAATGCAACATTTAAGATTCGATTTTGGC 598
Qy 161 LeuSerAsnValMetHisAspGlyHisPheLeuIysTyrSerCysGlySerProAsnTyr 180
Db 599 TTAAGTATGTTATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGAT 658
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Qy 416 ValArgTyrIysIysAsnGlyHisIleTyrAsnValIysCysArgTyrCysProGlyPhePro 435
Db 1361 GTTACTGCAAAAAGATTGGACATCAACACATGAAGATGCAATGAGAGCTCGGCTGCTT 1420
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Db 1421 GAG-----AGTATGATGATCATACCTGATGCTGTTAGTGACAGATGCTGATATTAAGAA 1474
Qy 456 AsnAspAspAlaAsnGlyArgLeuProThrValIleIysPheGlnUeuPheGlnIleUeuTyrIys 475
Db 1475 ACTATATCTCATAGCAAGAAATCAACCCGTATATGATGAGATTGAGATTCACCTTTACAA 1534
Qy 476 ThrIysAspAspIysTyrIleUeuIleUeuAspMetGlnArgValThrGlyProGlnIleUeuPhe 495
Db 1535 ACGAGGATGAGAAATCACTCTTCTGACCTGCAAGAGGTCAAGTGAACCAACTCTCTT 1594
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RESULT 15

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US-10-183-687-237
; Sequence 237, Application US/10183687
; Publication No. US20030204870A1
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GENERAL INFORMATION:

```
; APPLICANT: Allen, Steve
; APPLICANT: Allen, William B.
; APPLICANT: Canoon, Rebecca
; APPLICANT: Epelbaum, Sabine
; APPLICANT: Farnoud, Omlayo O.
; APPLICANT: Harvell, Leslie T.
; APPLICANT: Jones, Todd
; APPLICANT: Kimey, Tony
; APPLICANT: Klein, Ted
; APPLICANT: Li, Changliang
; APPLICANT: Oliveira, Igor Cunha
; APPLICANT: Sakai, Hajime
; APPLICANT: Shen, Bo
; APPLICANT: Tarczyński, Mitchell C.
; TITLE OF INVENTION: Alteration Of Oil Traits In Plants
; FILE REFERENCE: B1458 US NA
; CURRENT APPLICATION NUMBER: US/10/183,687
; CURRENT FILING DATE: 2002-06-27
; PRIOR APPLICATION NUMBER: 60/301,913
; PRIOR FILING DATE: 2001-06-29
; NUMBER OF SEQ ID NOS: 532
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 237
; LENGTH: 2107
; TYPE: DNA
; ORGANISM: Zea mays
; US-10-183-687-237
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Alignment Scores:

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Best Local Similarity: 73.08% Mismatches: 77
Query Match: 71.70% Indels: 6
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US-09-857-522B-4 (1-509) x US-10-183-687-237 (1-2107)
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Qy 121 PheGlnGlnIleIleSerGlyValGluTyrCysHisArgAsnMetValHisArgAsp 140
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Qy 141 LeuLysProGluAsnLeuLeuLeuAspSerLysTyrAsnValLysLeuAlaAspPheGly 160
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Qy 241 LeuAlaArgAspLeuIleProArgMetLeuValIleGluProMetLysArgIleThrIle 260
Db 941 TCAGCGAGGAGCTGATTCGCAAGATGCTGTTGTTGATCCATGAAAAGATTAACATA 1000
Qy 261 ArgGluIleArgGluHisGlnTrpPheGlnIleArgLeuProArgTyrLeuAlaValPro 280
Db 1001 CGTGAATCCGTGAACATGTCGTGTTCAAGATCCGACTTCGCGCTATTTGGCTGTGCG 1060
Qy 281 ProProAspThrThrGlnGlnAlaLysMetIleAspGluAspThrLeuArgAspValVal 300
Db 1061 CCTCCAGACACTGCTCAACAAAGTTAAAGGTCGACGAGAAACTCTTAATGATGTAT 1120
Qy 301 AsnMetGlyPheAsnLysAsnHisValCysGluSerLeuCysSerArgLeuGlnAsnGlu 320
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Db 1418 CGAATAATTAATAGTGAAGTCTTAAGCTCTGCAAGAACTGAATGTTTACTGGAATAAG 1477
Qy 421 AsnGlyHisTyrAsnValLysCysArgTrpCysProGlyPheProGluValAsnAspThr 440
Db 1478 ATTGCACATCAACAACATGAATGAGATGAGTCTTGCGCTGAG-----AGTATG 1531
Qy 441 LeuAspAlaSerAsnSerPheLeuGlyAspSerThrIleMetCaspAsnAspAlaAsn 460
Db 1532 ATGCATTAACAGTGATACCTTCAGTGCAGAGCTGCTATTAATGAACATGATGTTTCATG 1591
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Qy 481 TyrLeuLeuAspMetGlnArgValThrGlyProGlnLeuLeuPheLeuAspPheCysAla 500
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Qy 501 AlaPheLeuThrLysLeuArgValLeu 509
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Search completed: July 9, 2004, 18:31:40
 Job time : 727 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: July 9, 2004, 11:38:20 ; Search time 5849 Seconds

(without alignments)
3771.859 Million cell updates/sec

Title: US-09-857-522B-4
Perfect score: 2693
Sequence: 1 MDSSKSGSHSEALRNYNIG.....GPOLLPDPFCAFLTKLRVL 509

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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-Q=/cgn2_1/USPTO.epool/US09857522/runat_07072004_161357_1874/app_query.fasta.1.647
-DB=GenBdb1 -QPM=faetap -SUFFIX=p2n.rge -MINMATCH=0.1 -LOOPEXT=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALLIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pct -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09857522.QCGN.1.1.3731.0runat_07072004_161357_1874 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEDBDRY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

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2: gb_hcg.*
3: gb_in.*
4: gb_cm.*
5: gb_ov.*
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13: gb_un.*
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15: em_da.*
16: em_fun.*
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19: em_mu.*
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27: em_sts.*
28: em_un.*

29: em_vi.*
30: em_htcg_hum.*
31: em_htcg_in.*
32: em_htcg_other.*
33: em_htcg_mus.*
34: em_htcg_pln.*
35: em_htcg_rod.*
36: em_htcg_man.*
37: em_htcg_vrc.*
38: em_sy.*
39: em_htgo_hum.*
40: em_htgo_mus.*
41: em_htgo_other.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	2422	89.9	1838 8	D82035
2	2422	89.9	2213 8	AK100591
3	2422	89.9	2245 8	AK072723
4	2411.5	89.5	1872 8	D82038
5	2411.5	89.5	2161 8	D82036
6	2384	88.5	2927 8	AK069206
7	2378	88.3	1899 8	BT009004
8	2356.5	87.5	1770 8	OSUS5768
9	2100	78.0	1542 8	HVU7990
10	2072	76.9	1533 8	HVBKIN12M
11	2052.5	76.6	1809 8	HYERKIN1
12	2056	76.3	2138 8	D82037
13	1977	73.4	2203 8	AK067158
14	1977	73.4	2209 8	D82039
15	1969.5	73.1	1539 6	AX507962
16	1969.5	73.1	1608 8	BT010386
17	1969.5	73.1	1869 8	ATSKIN2
18	1969.5	73.1	2209 8	AY093170
19	1968	73.1	1778 8	CSNMF1RPK
20	1960.5	72.8	1948 8	AF143743
21	1945	72.2	1453 8	HVBKIN2
22	1942	72.1	8146 8	AB101656
23	1942	72.1	94710 8	AP005918
24	1942	72.1	124835 2	AP004164
25	1937.5	71.9	1929 6	ARI84289
26	1923	71.4	1536 6	E05288
27	1923	71.4	2028 8	TOBNPK5
28	1909	70.9	2100 8	AF062479
29	1903.5	70.7	1539 6	AX505467
30	1903.5	70.7	1539 6	AY149927
31	1903.5	70.7	1809 8	AY070468
32	1903.5	70.7	1834 8	ATNPK
33	1903.5	70.7	1966 8	STU63797
34	1889.5	70.5	1825 6	AX497023
35	1889.5	70.5	1852 8	ATSKIN1
36	1889.5	70.4	127426 8	AC137075
37	1893.5	70.4	7074 8	AB101657
38	1893.5	70.3	1941 8	AF128443
39	1891.5	70.2	1825 6	AX497027
40	1880.5	70.2	2006 8	BT009349
41	1626.5	60.4	3416 8	ATHAKIN10A
42	1616	60.0	93735 8	ATAC008261
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45	1537	57.1	3550 6	AX497024

RESULT 1

ALIGNMENTS

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ACCESSION D82035
VERSION D82035.1 GI:4107000
KEYWORDS OSK4.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE
AUTHORS Takano,M., Kajiya-Kanegae,H., Funatsuhi,H. and Kikuchi,S.
TITLE 1 (sites)
1 (sites)
Rice has two distinct classes of protein kinase genes related to
SNP1 of Saccharomyces cerevisiae, which are differently regulated
in early seed development
Mol. Gen. Genet. 260 (4), 388-394 (1998)
MEDLINE 99086251
PubMed 9870704
REFERENCE
AUTHORS 2 (bases 1 to 1838)
TITLE Direct Submission
JOURNAL Submitted (15-DEC-1995) Nakoto Takano, National Institute of
Agrobiological Resources, Department of Molecular Genetics, 2-1-2
Kamondai, Tsukuba, Ibaraki 305-8602, Japan
(E-mail:mtakano@affrc.go.jp, Tel:81-298-38-7446,
Fax:81-298-38-7408)
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/gene="osk4"
ORIGIN
polya_site
Alignment Scores:
Pred. No.: 1.17e-211 Length: 1838
Score: 2422.00 Matches: 451
Percent Similarity: 95.48% Conservative: 35
Best Local Similarity: 88.61% Mismatches: 23
Query Match: 89.94% Indels: 0
Gaps: 0
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DB 92 ATGGAAGAATGCTAGAGCGCGGCGCATCTGAGGACATGGAAGAACTAATCTAGGA 151
QY 21 ArgThrLeuGlyIleGlyThrPheGlyLysValLysIleAlaGluHisLysLeuThrGly 40
DB 152 AGAAGCTTAAAGTATGTTCAATTGGAAAAGTGAAGATGTCAGAGCAATTAAGCGG 211

QY 41 HisArgValAlaIleLysIleIleAsnCyArgGlnMetArgAsnMetGluMetGluGln 60
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QY 61 LysAlaLysArgGluPheLysIleLeuLysLeuPheIleHisProHisIleIleArgLeu 80
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QY 121 PheGlnGlnIleIleSerGlyValGluTYrCysHisArgAsnMetValHisArgAsp 140
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QY 201 CysGlyValIleLeuTYrAlaLeuLeuCysGlyTYrLeuProPheAspAspGluAsnIle 220
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[illegible]

Osato, N., Ota, Y., Ootomo, Y., Ryu, R., Satoh, H., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Sato, K., Satoh, K., Shibata, K., Shingawa, A., Shiraki, T., Shishiki, T., Sogabe, Y., Sugano, S., Sugiyama, A., Suzuki, K., Suzuki, Y., Tagami, M., Tagami-Takeda, Y., Tagawa, A., Takahashi, F., Takaku-Akashira, S., Tanaka, T., Tomaru, A., Toya, T., Tsunoda, Y., Ueda, M., Waki, K., Xie, Q., Yabagi, W., Yamada, H., Yamamoto, M., Yasunishi, A., Yazaki, U., Yokomizo, S. and Yoshimura, A.

Direct Submissions
Submitted (27-AUG-2002) Shoshi Kikuchi, National Institute of Agricultural Sciences, Department of Molecular Genetics, Head of Laboratory of Gene Expression, 2-1-2 Kannondai, Tsukuba, Ibaraki 305-8602, Japan (E-mail:skikuchi@nias.affrc.go.jp,
Tel:81-29-838-7007, Fax:81-29-838-7007)
This clone is one of the 28K full-length cDNA clones from japonica rice.

URL: <http://cdna01.dna.affrc.go.jp/cDNA/NIGAS Rice Full-length cDNA Project Team: Kikuchi, S., Satoh, K., Nagata, T., Kawagashira, N., Doi, K., Kishimoto, N., Yazaki, J., Inikawa, M., Yamada, H., Ooka, H., Hotta, I., Kojima, K., Nemito, T., Ohneda, E., Yabagi, W., Suzuki, K., Li, C., Ohtsuki, K., Shishiki, T. and Yamamoto, M.>

PAIS Genome Sequencing & Analysis Group: Ootomo, Y., Iida, Y., Fujimura, T., Ikeda, R., Ishibiki, U., Kawamata, M., Kobayashi, M., Kodama, T., Kurosaki, T., Kusumegi, T., Lu, M., Masuda, H., Miura, J., Mizuno, K., Narikawa, R., Nikura, U., Oka, M., Ryu, R., Sugano, S., Sugiyama, A., Suzuki, Y., Tsunoda, Y., Ueda, M., Xie, Q., Yokomizo, S., Yoshimura, A., Matubara, K. and Murakami, K.

Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in Riken: Adachi, J., Aizawa, K., Akimura, T., Arikawa, T., Carninci, P., Fukuda, S., Hangaki, T., Harra, A., Hashinume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hirooka, T., Hoti, F., Iida, U., Imanura, K., Imocani, K., Ishii, Y., Itoh, M., Kagewa, I., Kanagawa, S., Katoh, H., Kawai, J., Kishikawa-Hirozane, T., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Nunaseki, R., Ohno, M., Osato, N., Ota, Y., Satoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Sato, K., Shibata, K., Shingawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagami-Takeda, Y., Tagawa, A., Takahashi, F., Takaku-Akashira, S., Tanaka, T., Tomaru, A., Toya, T., Waki, K., Yasunishi, A. and Hayashizaki, Y.

Location/Qualifiers

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/clone="U021106J08"

FEATURES

SOURCE

ORIGIN

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Best local Similarity:	88.61%	Mismatches:	23
Query Match:	89.94%	Indels:	0
DB:	8	Gaps:	0

US-09-857-522b-4 (1-509) x AK100591 (1-2213)

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Db 288 AGAACTTTGATTCGATTCATTCTGAAAGAAAGTGAAGATTGCAGAGCAATAAGCTTACAGCG 347
0Y 41 HlaRyValAlaIleLysIleLeuLysCysRArgGlnMetArganMetGlnMetGln 60
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QY 61 LysAlaIysArgGluPheLysIleLeuLysLeuPheIleHisProHisIleIleArgLeu 80
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 QY 461 GlyArgLeuProThrValIleLysPheGluPheGlnLeuTyrLysThrLysAspAspLys 480
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 DB 1728 GCCTTCTTACCAACTGAGGTTCTA 1754
 RESULT 3
 AK072723
 LOCUS
 DEFINITION
 Oryza sativa (japonica cultivar-group) cDNA clone:J023135H07, full insert sequence.
 ACCESSION
 AK072723
 VERSION
 AK072723.1 GI:32982746
 KEYWORDS
 FLI CDNA; CAP trapper.
 SOURCE
 Oryza sativa (japonica cultivar-group)
 ORGANISM
 Oryza sativa (japonica cultivar-group)
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Eriophoroideae; Oryzaceae; Oryza.
 REFERENCE
 1
 The Rice Full-length cDNA Consortium, National Institute of Agricultural Sciences Rice Full-length cDNA project Team, Kikuchi, S., Satoh, K., Nagata, T., Kawadashira, N., Doi, K., Kishimoto, N., Yazaki, J., Ishikawa, M., Yamada, H., Ooka, H., Hotta, I., Kojima, K., Namiki, T., Ohneda, E., Yahagi, W., Suzuki, K., Li, C., Ohtsuki, K., Shishiki, T., Foundation of Advancement of International Science Genome Sequencing & Analysis Group; Ohtsuki, K., Iida, Y., Sugano, S., Fujimura, T., Suzuki, Y., Tsunoda, Y., Kuroseki, T., Kodama, T., Masuda, H., Kobayashi, M., Xie, Q., Lu, M., Nariikawa, R., Sugiyama, A., Mizuno, K., Yokomizo, S., Nishikura, J., Ikeda, R., Ishibiki, J., Kawamata, M., Yoshimura, A., Mura, J., Kusumegi, T., Oka, M., Ryu, R., Ueda, M., Matsubara, K., RIKEN; Kawai, J., Carninci, P., Adachi, J., Aizawa, K., Arakawa, T., Fukuda, S., Hara, A., Hashidume, W., Hayatsu, N., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kondo, S., Komori, H., Miyazaki, A., Osato, N., Oka, Y., Saito, R., Sasaki, D., Sato, K., Shibata, K., Shinagawa, A., Shiraki, T., Yoshino, M., and Hayashizaki, Y.
 Collection, mapping, and annotation of over 28,000 cDNA clones from japonica rice
 Science 301 (5631), 376-379 (2003)
 JOURNAL
 MEDLINE
 PUBMED
 22752273
 12869764
 2 (bases 1 to 2245)
 REFERENCE
 AUTHORS
 Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Carninci, P., Doi, K., Fujimura, T., Fukuda, S., Hanagaki, T., Hara, A., Hashidume, W., Hayashida, K., Hayashizaki, Y., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hori, F., Hotta, I., Iida, J., Iida, Y., Ikeda, R., Imamura, K., Imotani, K., Ishibiki, J., Ishii, Y., Ishikawa, M., Itoh, M., Kagawa, I., Kanagawa, S., Katoh, H., Kawagashira, N., Kawai, J., Kawamata, M., Kikuchi, S., Kishikawa-Hirozane, T., Kishimoto, N., Kobayashi, M., Kodama, T., Kojima, K., Kojima, Y., Kondo, S., Konno, H., Koda, M., Koya, S., Kurihara, C., Kuroseki, T., Kusumegi, T., Li, C., Lu, M., Masuda, H., Matsubara, K., Matsuyama, T., Mura, J., Miyazaki, A., Mizuno, K., Murekami, K., Mura, T., Nagata, T., Nakamura, M., Namiki, T., Nariikawa, R., Nishikura, J., Nishi, K., Nomura, K., Numaaki, R., Ohneda, E., Ohno, M., Ohtsuki, K., Oka, M., Ooka, H., Osato, N., Oka, Y., Ohtsuki, R., Ryu, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Sato, K., Satoh, K., Shibata, K., Shinagawa, A., Shiraki, T., Shishiki, T., Sogabe, Y., Sugano, S., Sugiyama, A., Suzuki, K., Suzuki, Y., Tagami, M., Tagami-Takeda, Y.,

TITLE
JOURNAL

Tsugawa, A., Takahashi, F., Takaku-Akahira, S., Tanaka, T., Tomaru, A.,
Toya, T., Tsunoda, Y., Ueda, M., Waki, K., Xie, Q., Yahagi, W.,
Yamada, H., Yamamoto, M., Yasunishi, A., Yazaki, J., Yokomizo, S. and
Yoshimura, A.

Direct Submission
Submitted (05-DEC-2001) Shoshi Kikuchi, National Institute of
Agricultural Sciences, Department of Molecular Genetics, Head of
Laboratory of Gene Expression, 2-1-2 Kannondai, Tsukuba, Ibaraki
305-8602, Japan (E-mail: kikuchi@nias.affrc.go.jp,
Tel: 81-29-838-7007, Fax: 81-29-838-7007)

COMMENT
This clone is one of the 28K full-length cDNA clones from japonica
rice.

URL: <http://cdna01.dna.affrc.go.jp/cDNA/>

NIAS Rice Full-length cDNA Project Team: Kikuchi, S., Satoh, K.,
Nagata, T., Kawagashira, N., Doi, K., Kishimoto, N., Yazaki, J.,
Ishikawa, M., Yamada, H., Ooka, H., Hotta, I., Kojima, K., Nemiki, T.,
Ohneda, E., Yahagi, W., Suzuki, K., Li, C., Ohtsuki, K., Shishiki, T. and
Yamamoto, M.

FAIS Genome Sequencing & Analysis Group: Okono, Y., Iida, Y.,
Fujimura, T., Ikeda, R., Ishibiki, J., Kawamata, M., Kobayashi, M.,
Kodama, T., Kurosaki, T., Kusumegi, T., Lu, M., Masuda, H., Miura, J.,
Mizuno, K., Naitaka, R., Naitaka, J., Oka, M., Ryu, R., Sugano, S.,
Sugiyama, A., Suzuki, Y., Tsunoda, Y., Ueda, M., Xie, Q., Yokomizo, S.,
Yoshimura, A., Matsubara, K. and Murakami, K.

Genome Exploration Research Group in Riken Genomic Sciences Center
and Genome Science Laboratory in Riken: Adachi, J., Aizawa, K.,
Akimura, T., Arikawa, T., Carninci, P., Fukuda, S., Hanagaki, T.,
Hara, A., Hoshizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K.,
Hirooka, T., Hori, F., Iida, J., Imamura, K., Imocani, K., Ishii, Y.,
Itoh, M., Kagawa, I., Kanagawa, S., Katoh, H., Kawai, J.,
Kishikawa-Hirozane, T., Kojima, Y., Kondo, S., Konno, H., Kouda, M.,
Koya, S., Kurihara, C., Maruyama, T., Miyazaki, A., Murata, M.,
Nakamura, M., Nishi, K., Nomura, K., Numasaki, R., Ono, M., Otsu, N.,
Oka, Y., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H.,
Sasaki, D., Sato, K., Shibata, K., Shinagawa, A., Shiraki, T.,
Sogabe, Y., Tagami, M., Tagami, T., Tanaka, Y., Tagawa, A., Takahashi, F.,
Takaku-Akahira, S., Tanaka, T., Tomaru, A., Toya, T., Waki, K.,
Yasunishi, A. and Hayashizaki, Y.

FEATURES
Source

Location/Qualifiers
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ORIGIN

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Pred. No.: 1.53e-211 Length: 2245
Score: 2422.00 Matches: 451
Percent Similarity: 95.48% Conservative: 35
Best Local Similarity: 88.61% Mismatches: 23
Query Match: 89.94% Indels: 0
Gaps: 0

US-09-857-522B-4 (1-509) x AK072723 (1-2245)

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LOCUS	D82038	1872 bp	mRNA	linear
DEFINITION	Oryza sativa mRNA for OSK3, complete cds.			PLN 06-FEB-1999
ACCESSION	D82038			
VERSION	D82038.1			
KEYWORDS	OSK3.			
SOURCE	Oryza sativa			
ORGANISM	Oryza sativa			
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.			
AUTHORS	1 (sites)			
TITLE	Takano, M., Kajiya-Kangae, H., Funatsuki, H. and Kikuchi, S.			
JOURNAL	Rice has two distinct classes of protein kinase genes related to SNI of Saccharomyces cerevisiae, which are differentially regulated in early seed development			
MEDLINE	Mol. Gen. Genet. 260 (4), 388-394 (1998)			
PUBMED	9807074			
REFERENCE	2 (bases 1 to 1872)			
AUTHORS	Takano, M.			
TITLE	Direct Submission			
JOURNAL	Submitted (15-DEC-1995) Makoto Takano, National Institute of Agricultural Resources, Department of Molecular Genetics, 2-1-2 Kannondai, Tsukuba, Ibaraki 305-8602, Japan			
FEATURES	(E-mail:mtakano@abr.affrc.go.jp, Tel:81-298-38-7446, Fax:81-298-38-7408)			
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Best Local Similarity:	89.00%	Mismatches:	26
Query Match:	89.55%	Indels:	1
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Oy		501	A A P h e u T h r Y s L e u A r Y V a l e u	509
Dd		1624	G A C T T C T T A C C A G C T G A G G T T C T A	1650

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D82036
LOCUS D82036 2161 bp mRNA linear PLN 06-FEB-1999

DEFINITION	Oryza sativa mRNA for OSK5, complete cds.
ACCESSION	D82036
VERSION	D82036.1 GI:4107002
KEYWORDS	OSK5.
SOURCE	Oryza sativa
ORGANISM	Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophytes; Magnoliophyta; Liliopsida; Poales; Poaceae; Erbartoideae; Oryzaceae; Oryza. 1 (sites) Takano,M., Kajiya-Kanegae,H., Funatsuiki,H. and Kikuchi,S. Rice has two distinct classes of protein kinase genes related to SN1 of Saccharomyces cerevisiae, which are differentially regulated in early seed development Mol. Gen. Genet. 260 (4), 388-394 (1998)	
JOURNAL MEDLINE	99086251
PUBMED	9870704
REFERENCE	2 (bases 1 to 2161)
AUTHORS	Takano,M.
JOURNAL TITLE	Direct Submission Submitted (15-Dec-1995) Makoto Takano, National Institute of Agrobiological Resources, Department of Molecular Genetics, 2-1-2 Kanondai, Tsukuba, Ibaraki 305-8602, Japan (E-mail:mekano@agr.affrc.go.jp, Tel:81-298-38-7446, Fax:81-298-38-7408)

FEATURES
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Dd	667 GCTGCTCCAGAGGTATCTCTGCTAAATTTATATGCTGACACTGAGTTGATGATGAGC 726
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Dd	727 TGTCGAGTGAATCTTTATGCTCTCTCTTGTGGATACCTTTTCATTTGATGATGAGAAATATC 786
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RESULT 6      AK069206      2927 bp      mRNA      linear      PLN 24-JUL-2003
LOCUS        AK069206
DEFINITION   Oryza sativa (japonica cultivar-group) cDNA clone:J023008117, full
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ACCESSION    AK069206
VERSION      AK069206.1 GI:32979230
KEYWORDS     FLI CDNA; CAP trapper.
SOURCE       Oryza sativa (japonica cultivar-group)
ORGANISM     Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
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```

AUTHORS

The Rice Full-length cDNA Consortium, National Institute of
 Agrobiological Sciences Rice Full-length cDNA Project Team:
 Kikuchi, S., Satoh, K., Nagata, T., Kawagashira, N., Doi, K.,
 Kishimoto, N., Yazaki, J., Ishikawa, M., Yamada, H., Ooka, H., Hotta, I.,
 Kojima, K., Namiki, T., Ohneda, E., Yahagi, W., Suzuki, K., Li, C.,
 Ohtsuki, K., Shishiki, T., Foundation of Advancement of International
 Science Genome Sequencing & Analysis Group: Ootomo, Y., Murakami, K.,
 Iida, Y., Sugano, S., Fujimura, T., Suzuki, Y., Tsunoda, Y.,
 Kurosaki, T., Kodama, T., Masuda, H., Kobayashi, M., Xie, Q., Lu, M.,
 Nariakawa, R., Sugiyama, A., Mizuno, K., Yokomizo, S., Nishikura, J.,
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 Kusumegi, T., Oka, M., Ryu, R., Ueda, M., Matsubara, K., RIKEN,
 Kawai, Y., Carninci, P., Adachi, U., Aizawa, K., Arakawa, T., Fukuda, S.,
 Hara, A., Hashizume, W., Hayatsu, N., Imetani, K., Ishii, Y., Itoh, M.,
 Kagawa, I., Kondo, S., Kono, H., Miyazaki, A., Ootomo, Y., Ota, Y.,
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 Yoshino, M., and Hayashizaki, Y.

TITLE

Science 301 (5631), 376-379 (2003)

JOURNAL

MEDLINE

PUBMED

REFERENCE

2 (bases 1 to 2927)

AUTHORS

Adachi, U., Aizawa, K., Akimura, T., Arakawa, T., Carninci, P., Doi, K.,
 Fujimura, T., Fukuda, S., Hanagaki, T., Hara, A., Hashizume, W.,
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 Toya, T., Tsunoda, Y., Ueda, M., Waki, K., Xie, Q., Yahagi, W.,
 Yamada, H., Yamamoto, M., Yasunishi, A., Yazaki, J., Yokomizo, S., and
 Yoshimura, A.

TITLE

JOURNAL

MEDLINE

PUBMED

REFERENCE

AUTHORS

Submitted (05-DEC-2001) Shoshi Kikuchi, National Institute of
 Agrobiological Sciences, Department of Molecular Genetics, Head of
 Laboratory of Gene Expression; 2-1-2 Kamondai, Tsukuba, Ibaraki
 305-8602, Japan (E-mail: skikuchi@nias.affrc.go.jp,
 Tel: 81-29-838-7007, Fax: 81-29-838-7007)
 This clone is one of the 28k full-length cDNA clones from japonica
 rice.
 URL: <http://cdna01.dna.affrc.go.jp/cDNA/>
 NIAS Rice Full-length cDNA Project Team: Kikuchi, S., Satoh, K.,
 Nagata, T., Kawagashira, N., Doi, K., Kishimoto, N., Yazaki, J.,
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Yasunishi,A. and Hayashizaki,Y.

FEATURES

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Query Match: 88.53% Indels: 4
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US-09-857-522b-4 (1-509) x AK069206 (1-2927)

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Db 1492 GAACCTGTTTGAATTCATTGTTGAGAAAGGAGGTTGACGAAAGTGAAGGCTCGCCGATC 1551
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Qy 141 LeuLysProGluAsnLeuLeuLeuAspSerLysTyrAsnValLysLeuAlaAspPheGly 160
Db 1612 CTGAAGCCAGAAAACCTTGCTACTGGAATTCAAAGTATATAGTAAAGCTTGCGACTTTGGT 1671
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RESULT 7
BT009004
LOCUS
DEFINITION
Triticum aestivum clone wdk2c.pk018.c16.f15, full insert mRNA
sequence.
ACCESSION
BT009004
VERSION
BT009004.1
KEYWORDS
GI:32128555
SOURCE
FRL-CDNA.
ORGANISM
Triticum aestivum (bread wheat)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Poideae; Triticaceae; Triticum.
1 (bases 1 to 1899)
REFERENCE
Tingey,S.V., Wolters,P., Powell,W., Dolan,M., Miao,G.-H.,
Caraher,N.R., Hanafey,M.K. and Hailey,C.F.
AUTHORS
Direct Submission
TITLE
JOURNAL
Submitted (20-JUN-2003) Crop Genetics, B. I. Dupont de Nemours and

Company, 1 Innovation Way, P.O. Box 6104, Newark, DE 19714-6104,
USA

FEATURES

SOURCE

Location/Qualifiers

1. 1899
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Percent Similarity: 93.52% Conservative: 34
Best Local Similarity: 86.84% Mismatches: 33
Query Match: 88.30% Indels: 0
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US-09-857-522b-4 (1-509) x BT009004 (1-1899)

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DB 487 CTAAGCCAGAGAACTGTTACTTGATTCCAAATACATGTAAGAACTTGGCG 546
QY 161 LeuSerAsnValMetHisAspGlyHisPheLeuLysThrSerCyAsrGlySerProAsnTyr 180
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DEFINITION Oryza sativa SNF1-related protein kinase (RSK1) mRNA, complete cds.
VERSION U55768
KEYWORDS U55768.1 GI:1477683
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Rhizarioideae; Oryzaceae; Oryza.
REFERENCE 1 (bases 1 to 1770)
AUTHORS Tsai,T.-H. and Le,H.-T.
TITLE SNF1-related protein kinase of rice
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1770)
AUTHORS Tsai,T.-H.
TITLE Direct Submission
JOURNAL Submitted (19-APR-1996) Teh-Huei Tsai, Life Science, National
Tsing-Hua University, Hsinchu 30043, Republic of China
FEATURES Location/Qualifiers


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	Mismatches: 33
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QY	160 GlyLeuSerAsnValMetHisAspGlyHisPheLeuIeThrSerCyGlyIysEProAsn	178
Db	493 GGTTAGTAACTCATGATGATGATGGCAATTTTTTGAAGACAAAGCTGTGGAGATCTCAAC	552

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Dd		553	TATCTGTCTCCAGAGCGATCTCTGGTAATAATTATTCGTGAACCTGAGCTTGATGATATGC	612
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OY		360	SerSerSerSerGIYThrArgAntYrValProGlySerSerAspProHisSerSerGIy	379
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RESULT 9
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 DEFINITION
 ACCESSION F0007990

VERSION AU07990.1 GI:3341451
KEYWORDS kin2a gene; SnRK1-type protein kinase.
SOURCE Hordeum vulgare subsp. vulgare
ORGANISM Hordeum vulgare subsp. vulgare
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Poideae; Triticeae; Hordeum.
REFERENCE
1 Stoccombe S.P., Bertini, L., Beaudoin, F., Dickinson, J.R. and Halford, N.G. Molecular cloning of Bsnr1p, a novel putative SNF4-related protein identified in a two-hybrid screen with barley seed SnRK1 protein kinase
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1542)
Stoccombe, S.P.
AUTHORS Direct Submission
TITLE Submitted (21-JUL-1998) Stoccombe S.P., Salamini Department, Max
JOURNAL Planck Institut fuer Zuechtungsforschung, Carl-von-Linne Weg 10,
D-50829 Koeln, GERMANY
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ORIGIN
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DB: 8 Gaps: 2
US-09-857-522b-4 (1-509) x HVU7990 (1-1542)

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Qy 198 ValTYrSerCysGlyValIleLeuTYrAlaLeuLeuCysGlyTYrLeuProPheAsp 217
Db 601 GTTTGAGCTGTGGGGGTGACTTATGCTCTTCTTGTGGCTGTCTGCAATTTGATGAT 660
Qy 218 GluAsnIleProAsnLeuPheLysIleLysGlyGlyIleTYrThrLeuProSerHis 237
Db 661 GACATATTTCTTACCTGTTCAAGAAATTAAGAGGATCTTATATCTTCAAGCTAT 720
Qy 238 LeuSerAlaLeuAlaArgAspLeuIleProArgMetLeuValValGluProMetLysArg 257
Db 721 TTATCTGATCTTCAAGGATTTGATCCCAAAATGCTTATATGATCAATGAAGAGG 780
Qy 258 IleThrIleArgGluIleArgGluHisIleGlnTYrPheGlnIleArgLeuProArgTYrLeu 277
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Db 1021 GGCCTATTGGGGGCTGCACCAACATCTCATGATTAAGGATTTTAATGACTTACCTTA 1080
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Qy 398 AlaHisProArgGluIleMetValGluValLeuLysAlaLeuGlnGlnIleuAsnValArg 417
Db 1201 GCTCACCTCTGTATTAATGATTAAGGTTCTTAAAGCACTTAAAGCAATTAATGTCTGC 1260
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Qy 477 LysaspalyserlyrleuLeuaspmeGlnaryValThrglyProgluLeuLeuPheleu 496
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RESULT 10
HVBKIN12M 1539 bp mRNA linear PLN 05-MAY-1995
DEFINITION H.vulgaris BKTIN12 mRNA for protein kinase (partial).
ACCESSION X65604
VERSION X65604.1 GI:18933
KEYWORDS protein kinase.
SOURCE Hordeum vulgare subsp. vulgare
ORGANISM Hordeum vulgare subsp. vulgare
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Poideae; Triticeae; Hordeum.
1 (bases 1 to 1539)
Halford, N.G., Vicente-Carbalosa, J., Sabel, P.A., Shewry, P.R.,
Hammond, J.U. and Kreis, M.
Molecular analyses of a barley multigene family homologous to the
yeast protein kinase gene SNF1
Plant J. 2 (5), 791-797 (1992)
93258420
1302632

REFERENCE
AUTHORS
TITLE
JOURNAL
MEDLINE
PUBMED
2 (bases 1 to 1539)
Halford, N.G.
Direct Submission
Submitted (16-APR-1992) N.G. Halford, Long Ashton Research Station,
University of Bristol, Dept of Agricultural Sciences, Long Ashton,
Bristol BS18 9AF, UK
FEATURES
Source
Location/Qualifiers
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NLRYL"

ORIGIN

Alignment Scores:

Pred. No.:	9.6e-180	Length:	1539
Score:	2072.00	Matches:	383
Percent Similarity:	87.13%	Conservative:	64
Best Local Similarity:	74.66%	Mismatches:	62
Query Match:	76.94%	Indels:	4
DB:	8	Gaps:	2

US-09-857-522B-4 (1-509) x HVBKIN12M (1-1539)

Qy 1 MetaspalyserlyserlysglyserglyhissergluAlaLeuAryasnThrylser 20
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Qy 41 HisArgValAlaIleLysIleIleAsnCyAArgGluMetArgAsnMetGluGlu 60
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Qy 178 ProAsnThryAlaAlaProGluValIleSerGlyLysLeuThryAlaGlyProGluValAsp 197
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Db 841 GCGATACCTCCCATATTAAGAGCAAGCAACCAATATGATTAAGATATATCTCCGA 900
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 RESULT 12
 LOCUS D82037 2138 bp mRNA linear PLN 06-FEB-1999
 DEFINITION Oryza sativa mRNA for OSK2, partial cds.
 ACCESSION D82037.1 GI:4107004
 VERSION D82037.1
 KEYWORDS OSK2.
 SOURCE Oryza sativa
 ORGANISM Oryza sativa
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Ehrhartoideae; Oryzaceae; Oryza.
 REFERENCE
 AUTHORS Takano,M., Kajiya-Kanegae,H., Funatsuiki,H. and Kikuchi,S.
 1 (sites)
 TITLE Rice has two distinct classes of protein kinase genes related to

SNF1 of Saccharomyces cerevisiae, which are differently regulated
 in early seed development
 Mol. Gen. Genet. 260 (4), 388-394 (1998)
 JOURNAL 99086251
 MEDLINE 98070704
 PUBMED 2 (bases 1 to 2138)
 REFERENCE
 AUTHORS Takano,M.
 TITLE Direct Submission
 JOURNAL Submitted (15-DEC-1995) Makoto Takano, National Institute of
 Agrobiological Resources, Department of Molecular Genetics, 2-1-2
 Kannondai, Tsukuba, Ibaraki 305-8602, Japan
 (E-mail:mtakano@abr.affrc.go.jp, Tel:81-298-38-7446,
 Fax:81-298-38-7408)
 FEATURES
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 Best Local Similarity: 71.07% Mismatches: 21
 Query Match: 76.35% Indels: 113
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 Db 2 AAGAGAGAAATCAAGATATGAGGTTGTCATTCATCCCATATCATTCGCTTTATGAG 61
 Oy 83 ValIleTyrThrProThrAspIleTyrValAlaMetGluTyrCysLysTyrGlyGluLeu 102
 Db 62 GTCATATACACTCTTACGGAATATATATGTTGTATGAGATCTCAAGTTTGAGAACTG 121
 Oy 103 PheAspTyrIleValGluLysGlyArgLeuGlnGlnLysProGluAlaAspArgIlePheGln 122
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Db	422	GTGATCCCTTTATGTCTCTCTTGTGTGTCCTCTTCATTTGATGAGAAATATCCCCAAC	481
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Db	482	CTATTCAAAAAGATMAAGGTGGTATATATATCTCCCAAGCATTTATCTGCTCTGGCC	541
Qy	243	ArgAspLeuIleProArgMetLeuValGluProMetIysArgIleThrIleArgGlu	262
Db	542	AGGATTTTGATCCCAAGATGCTTGTGTGATCCAAAGAAAGAAATCACAATTCGTGA	601
Qy	263	IleArgGluHisGlnTrpPheGlnIleArgLeuProArgTyrrLeuAlaValProProPro	282
Db	602	ATTGAGAGCATCATATGGTTTCAGATTCGCTTCCTCGTTACTTACAGAGTGCCTCACCA	661
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Qy	370	ogIysSerSerAspProHisSerSerSerGlyIleuAsnArgProTyrrTyrrProValGluArgIysTr	390
Db	1262	AGGAAGCAGTATCTCCATGACGAGGTGGTGGCCCACTTATCTCGTTGAAAGGAAATATG	1321
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Db	1442	GAGCGTTGGGTATCTCCAGGCCACTGATATGTTTAATGTCAACCAACGCTTTGTGATGA	1501

Oy		450	pSetThlIleMeKaspsnshspaplaaenGIVargLeuProThrValIleLysPhegl	470
Db		1502	CTCAATTATATATGGATATATGCAGTGTAAACGGGAGGTTACTCGTCGTGATCAAGTTGA	1561
Oy		470	upHeglIleuTYrLYsThrLyAsApAlySYrLEuLeuAspMetGlInArValThrgl	490
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Oy		490	yPrOgLnLeuLeuPheLeuAspPheCySaLaAlaPheLeuThrLYsLeuArgValLeu	509
Db		1622	GCTCAGCTCCTTTCTTGAGACTTCTGTGACAGCTTCTTAACMAATGAGGGTTCTTA	1679
RESULT 13				
AK067158				
LOCUS				
DEFINITION	Oryza sativa (japonica cultivar-group) cDNA clone:J013094M6, full insert sequence.	2073 bp	mRNA	linear PLN 24-JUL-2003
ACCESSION	AK067158			
VERSION	AK067158.1	GI:32977176		
KEYWORDS	Fil_CDNA; CAP trapper.			
SOURCE	Oryza sativa (japonica cultivar-group)			
ORGANISM	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.			
REFERENCE				
AUTHORS	1 The Rice Full-Length cDNA Consortium, National Institute of Agricultural Sciences Rice Full-length cDNA Project Team, Kikuchi,S., Sato,K., Nagata,T., Kawagashira,N., Doi,K., Kishimoto,N., Yazaki,T., Ishikawa,M., Yamada,H., Ooka,H., Hotta,I., Kojima,K., Nemiki,T., Ohneda,E., Yahagi,W., Suzuki,K., Li,C., Ohtsuki,K., Shishiki,T., Foundation of Advancement of International Science Genome Sequencing & Analysis Group; Otono,Y., Murakami,K., Iida,Y., Sugano,S., Fujimura,T., Suzuki,Y., Tsunoda,Y., Kuratski,T., Kodama,T., Masuda,H., Kobayashi,M., Xie,Q., Lu,M., Naitaka,R., Sugiyama,A., Mizuno,K., Yokomizo,S., Nikura,J., Ikeda,R., Ishibiki,J., Kawamata,M., Yoshimura,A., Mura,J., Kusumegi,T., Oka,M., Ryu,R., Ueda,M., Matsubara,K., RIKEN; Kawai,J., Carninci,P., Adachi,J., Aizawa,K., Arakawa,T., Fukuda,S., Hara,A., Hashidume,W., Hayatsu,N., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kondo,S., Komori,H., Miyazaki,A., Oosato,N., Oga,Y., Saito,R., Sasaki,D., Sato,K., Shibata,K., Shinagawa,A., Shiraki,T., Yoshino,M., and Hayashizaki,Y.			
TITLE	Collection, mapping, and annotation of over 28,000 cDNA clones from japonica rice			
JOURNAL	Science	301 (5631), 376-379	(2003)	
MEDLINE	22752273			
PUBMED	12869764			
AUTHORS	2 (bases 1 to 2073) Adachi,J., Aizawa,K., Aktamura,T., Arakawa,T., Carninci,P., Doi,K., Fujimura,T., Fukuda,S., Hanagaki,T., Hara,A., Hashizume,M., Hayashida,K., Hayashizaki,Y., Hayatsu,N., Hiramoto,K., Hirooka,T., Hoti,F., Hotta,T., Iida,J., Iida,Y., Ikeda,R., Inamura,K., Imotoh,K., Ishibiki,T., Ishii,Y., Ishikawa,M., Itoh,M., Kagawa,I., Kawagawa,S., Katoh,H., Kawagashira,N., Kawai,J., Kawamata,M., Kikuchi,S., Kishikawa-Hirozane,T., Kishimoto,N., Kobayashi,M., Kodama,T., Kojima,K., Kojima,Y., Kondo,S., Komori,H., Kouda,M., Koya,S., Kurihara,C., Kuratski,T., Kusumegi,T., Li,C., Lu,M., Maeda,H., Matsubara,K., Matsuyama,T., Mura,J., Miyazaki,A., Mizuno,K., Murakami,K., Murata,M., Nagata,T., Nakamura,M., Namiki,T., Narikawa,R., Nikura,J., Nishi,K., Nomura,K., Nunakoshi,R., Ohneda,E., Oho,M., Ohtsuki,K., Oka,M., Ooka,H., Oosato,N., Oga,Y., Otono,Y., Ryu,R., Saitoh,H., Sakai,C., Sakai,K., Sakazume,N., Sano,H., Sasaki,D., Sato,K., Sato,K., Shibata,K., Shinagawa,A., Shiraki,T., Shishiki,T., Sogabe,Y., Sugano,S., Sugiyama,A., Suzuki,K., Suzuki,Y., Tagami,M., Tagami-Takeda,Y., Tagawa,A., Takahashi,F., Takuo-Akahita,S., Tanaka,T., Tomaru,A., Toyoda,T., Tsunoda,Y., Ueda,M., Waki,K., Xie,Q., Yahagi,W., Yamada,H., Yamamoto,M., Yasunishi,A., Yazaki,J., Yokomizo,S. and Yoshimura,A.			
TITLE	Direct Submission			
JOURNAL	Submitted (05-DEC-2001)			
	Shoichi Kikuchi, National Institute of			

Agrobiological Sciences, Department of Molecular Genetics, Head of Laboratory of Gene Expression, 2-1-2 Kamondai, Tsukuba, Ibaraki 305-8602, Japan (E-mail: skikuchi@nias.affrc.go.jp, Tel:81-29-838-7007, Fax:81-29-838-7007)
This clone is one of the 28k full-length cDNA clones from japonica rice.

URL : <http://cdna01.dna.affrc.go.jp/cDNA/>

NIAS Rice Full-length cDNA Project Team: Kikuchi, S., Satoh, K., Nagata, T., Kawagashira, N., Doi, K., Kishimoto, N., Yazaki, J., Ishikawa, M., Yamada, H., Ooka, H., Hotta, I., Kojima, K., Naito, T., Ohneda, E., Yanagi, W., Suzuki, K., Li, C., Ohtsuki, K., Shishiki, T. and Yamamoto, M.

FAIS Genome Sequencing & Analysis Group: Ootomo, Y., Iida, Y., Fujimura, T., Ikeda, R., Ishibiki, J., Kawamata, M., Kobayashi, M., Kodama, T., Kurotsaki, T., Kusumegi, T., Lu, M., Masuda, H., Mura, J., Mizuno, K., Naito, K., Naito, R., Naito, J., Oka, M., Ryo, R., Sugano, S., Suiyama, A., Suzuki, Y., Tsunoda, Y., Ueda, M., Xie, Q., Yokomizo, S., Yoshimura, A., Matsubara, K. and Murakami, K.
Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in Riken: Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Carninci, P., Fukuda, S., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hirooka, T., Hori, F., Iida, J., Imamura, K., Imoto, K., Ishii, Y., Itoh, M., Kagawa, I., Kanagawa, S., Katoh, H., Kawai, J., Kishikawa-Hirozane, T., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishii, K., Nomura, K., Numasaki, R., Ohno, M., Otsu, N., Ota, Y., Satoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Saeki, D., Sato, K., Shibata, K., Shingawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagami-Takeda, Y., Tagawa, A., Takahashi, F., Takaku-Akashira, S., Tanaka, T., Tomaru, A., Toyota, T., Waki, K., Yasunishi, A. and Hayashizaki, Y.

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Best Local Similarity: 74.07% Mismatches: 76
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Ehharitoidae; Oryzaceae; Oryza.
REFERENCE
AUTHORS Takano,M., Kajiya-Kanegae,H., Funatsuki,H. and Kikuchi,S.
TITLE 1 (sites)
1 Takano,M., Kajiya-Kanegae,H., Funatsuki,H. and Kikuchi,S.
Rice has two distinct classes of protein kinase genes related to
SNP1 of Saccharomyces cerevisiae, which are differently regulated
in early seed development
Mol. Gen. Genet. 260 (4), 388-394 (1998)
JOURNAL 99086251
MEDLINE 9870704
PUBMED 2 (bases 1 to 2209)
REFERENCE Takano,M.
AUTHORS Direct Submission
TITLE Submitted (15-DEC-1995) Makoto Takano, National Institute of
Agricultological Resources, Department of Molecular Genetics; 2-1-2
Kamondai, Tsukuba, Ibaraki 305-8602, Japan
(E-mail:mtakano@agr.affrc.go.jp, Tel:81-298-38-7446,
Fax:81-298-38-7408)
FEATURES
SOURCE Location/Qualifiers
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ORIGIN
Alignment Scores:
Pred. No.: 7.67e-171 Length: 2209
Score: 1977.00 Matches: 377
Percent Similarity: 84.28% Conservative: 52
Best Local Similarity: 74.07% Mismatches: 76
Query Match: 73.41% Indels: 4
DB: 8 Gaps: 2
US-09-857-522b-4 (1-509) x D82039 (1-2209)
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VERSION AX507962.1 GI:23389199
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Bukaraota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
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rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsids.
1
REFERENCE
AUTHORS Harper, J.F., Kreps, J., Wang, X. and Zhu, T.
TITLE Stress-regulated genes of plants, transgenic plants containing
same, and methods of use
JOURNAL Patent: WO 0216655-A 2657 28-FEB-2002;
The Scripps Research Institute (US) ; Syngenta Participations AG
(CH)
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Db 1363 TCCAGCATTAATAGGAACGAAGCAGCTGTTAAGTCGCCCAATGTTGTCAAGTTGAAATT 1422
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Db 1423 CAGTTGTATATAAACTCGGAGCAGACAGATCTACTGATTGTCAGAGATACAAAGTCTCT 1482
Qy 492 GlnLeuLeuPheLeuAspPheCysAlaAlaPheLeuThrLysLeuArgValLeu 509
Db 1483 CAGTTCTTGTCTGGATCTGTGTGCTCTTTCTTGCTCAGCTCCGAGTCTCTC 1536
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